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OM nucleic - nucleic search, using sw model

Run on:         July  5, 2003, 13:12:47 ; Search time 6749.08 Seconds
                                          (without alignments)
                                          11409.857 Million cell updates/sec

Title:          US-10-056-454A-14_COPY_145_2790
Perfect score:  2646
Sequence:       1 ATGGTGTATACACTCTCTGG..........AAGTAGTAGTAGAAGAAGAA 2646

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:      4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                1:  gb_ba:*
                2:  gb_htg:*
                3:  gb_in:*
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                23:  em_pat:*
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                30:  em_htg_hum:*
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                32:  em_htg_other:*
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                39:  em_htgo_hum:*
                40:  em_htgo_mus:*
                41:  em_htgo_other:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2646	100.0	2992	8	STU011890	AJ011890 Solanum t
2	2646	100.0	3033	6	A58164	A58164 Sequence 14
3	2581	97.5	3074	6	AR123355	AR123355 Sequence
4	2563.6	96.9	2982	8	STU011888	AJ011888 Solanum t
5	2558.2	96.7	3231	6	A58168	A58168 Sequence 18
6	2551	96.4	3003	6	A58162	A58162 Sequence 12
7	2538	95.9	2955	8	STU011885	AJ011885 Solanum t
8	2514	95.0	2975	6	A58163	A58163 Sequence 13
9	2486.8	94.0	2563	6	AX256072	AX256072 Sequence
10	2471.6	93.4	2529	6	A58167	A58167 Sequence 17
11	2470.6	93.4	2523	8	STU011889	AJ011889 Solanum t
12	2465.8	93.2	2578	6	A58169	A58169 Sequence 19
13	2455	92.8	2576	6	A58166	A58166 Sequence 16
14	2435.6	92.0	2493	8	STSBEII	AJ000004 Solanum t
15	1708.6	64.6	3123	8	AB071286	AB071286 Ipomoea b
16	1509	57.0	2517	8	AB042937	AB042937 Ipomoea b
17	1429.4	54.0	3090	6	A92164	A92164 Sequence 30
18	1414.6	53.5	3360	8	AB029548	AB029548 Phaseolus
19	1370.4	51.8	3549	8	PSSBEIGEN	X80009 P.sativum m
20	1369.8	51.8	1393	6	AR123356	AR123356 Sequence
21	1362	51.5	2913	6	A92162	A92162 Sequence 28
22	1317.4	49.8	2542	8	ATU22428	U22428 Arabidopsis
23	1290	48.8	2577	6	AX412751	AX412751 Sequence
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25	1285.2	48.6	2668	8	ATU18817	U18817 Arabidopsis
26	1270.8	48.0	1481	8	STU011891	AJ011891 Solanum t
27	1264.8	47.8	3015	6	E14723	E14723 Rice mRNA f
28	1264.8	47.8	3015	8	AB023498	AB023498 Oryza sat
29	1263.6	47.8	2364	6	E14724	E14724 Rice mRNA f
30	1260	47.6	2554	8	AF064560	AF064560 Hordeum v
31	1251.2	47.3	2918	8	RICBCE3	D16201 Rice mRNA f
32	1251.2	47.3	2919	6	E08183	E08183 Gene of sta
33	1245	47.1	2795	8	ZMU65948	U65948 Zea mays st
34	1243.6	47.0	2726	8	AF338432	AF338432 Triticum
35	1243.6	47.0	2970	8	AF286319	AF286319 Triticum
36	1242	46.9	2970	8	TASBA2	Y11282 T.aestivum
37	1240.4	46.9	2853	8	TAU66376	U66376 Triticum ae
38	1180.4	44.6	2725	6	AR106495	AR106495 Sequence
39	1180.4	44.6	2725	8	MZEGLUCTRN	L08065 Corn starch
40	1157.8	43.8	2780	8	AF064561	AF064561 Hordeum v
41	644.6	24.4	2732	8	AB029549	AB029549 Phaseolus
42	641.4	24.2	2843	8	MESBERNA	X77012 M.esculenta
43	637.8	24.1	2493	8	STY08786	Y08786 S.tuberosum
44	636.2	24.0	3114	8	STSBE	X69805 S.tuberosum
45	632.4	23.9	2745	8	AF286317	AF286317 Triticum

ALIGNMENTS

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RESULT 1
STU011890
LOCUS       STU011890            2992 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-6.
ACCESSION   AJ011890
VERSION     AJ011890.1  GI:4584512
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2992)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
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            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2992)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1..2992
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                     /cultivar="Desiree"
                     /db_xref="taxon:4113"
                     /note="sequence SBE A-6"
     gene            140..2788
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                     KILAEKSSYNSEFRPSTVAASGKVLVPGTQSDSSSSSTDQFEFTETSPENSPASTDVD
                     SSTMEHASQIKTENDDVEPSSDLTGSVEELDFASSLQLQEGGKLEESKTLNTSEETII
                     DESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
                     SRGYEKMGFTRSATGITYREWALGAQSAALIGDFNNWDANADIMTRNEFGVWEIFLPN
                     NVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIHYDPPEEERYI
                     FQHPRPKKPKSLRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYNALQIMAIQEH
                     SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                     MFDCTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDAFKFDGFRFDGV
                     TSMMYIHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
                     PTFCIPVQEGGVGFDYRLHMAIADKRIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEG
                     YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGDAEYLRYRGLQ
                     EFDRPMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHWTKSYSDYRIA
                     CLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYAPCKTAVVYAL
                     VDKEEEEEEEEEEVAAVEEVVVEEE"
     transit_peptide 140..283
                     /gene="SBE II"
     mat_peptide     284..2785
                     /gene="SBE II"
                     /product="starch branching enzyme II"
                     /EC_number="2.4.1.18"
BASE COUNT      893 a    542 c    701 g    856 t
ORIGIN

  Query Match            100.0%;  Score 2646;  DB 8;  Length 2992;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2646;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 199

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 259

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 319

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 379

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 439

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 499

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 559

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 619

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
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Db        620 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 679

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 739

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 799

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 859

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 919

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
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Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1039

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
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Db       1040 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1099

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1100 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1159

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1160 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1219

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
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Db       1220 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1279

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
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Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
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Db       1460 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1519

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Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
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Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
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Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
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Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
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Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
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Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
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Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
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Db       2060 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 2119

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
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Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
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Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
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Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
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Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
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Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
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Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
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Db       2720 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAA 2779

Qy       2641 GAAGAA 2646
              ||||||
Db       2780 GAAGAA 2785


RESULT 2
A58164
LOCUS       A58164                  3033 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 14 from Patent WO9634968.
ACCESSION   A58164
VERSION     A58164.1  GI:3713889
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3033)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 14 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
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ORIGIN

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Qy      301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
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Qy      901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
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Qy      961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
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Qy     1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
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Qy     1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
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Qy     1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
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Qy     1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Qy     1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
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Qy     1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
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Db     1885 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1944

Qy     1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
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Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
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Db       2485 GTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2544

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Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
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Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAA 2640
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Qy       2641 GAAGAA 2646
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RESULT 3
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VERSION     AR123355.1  GI:14108321
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SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 3074)
  AUTHORS   Ek,B., Khosnoodi,J., Larsson,C.-T., Larsson,H. and Rask,L.
  TITLE     Starch branching enzyme II of potato
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~~ktirf~~

see search 3

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Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
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Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
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Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
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Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
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Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
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Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
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Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
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Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
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Db       1089 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1148

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
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Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
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Db       1209 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1268

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
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Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
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Db       1329 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1388

Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Db       1389 CATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGGAACNCCCGACGACCTTAAGTCT 1448

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
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Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
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Db       1509 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1568

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1628

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1629 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTT 1688

Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1689 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1748

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
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Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
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Db       1809 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1868

Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
              |||||||||||||||||||||||||||| ||||||||| |||| ||||||||||||||||
Db       1869 GAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1928

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
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Db       1929 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1988

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
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Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
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Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
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Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
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Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
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Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
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Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
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Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
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Db       2409 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2468

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2469 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2528

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       2529 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTG 2588

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2589 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2648

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
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Db       2649 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2708

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
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Db       2709 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2768

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
              ||||||||||||||||| || || || || || || ||||| ||||| || |
Db       2769 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822


RESULT 4
STU011888
LOCUS       STU011888               2982 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-4.
ACCESSION   AJ011888
VERSION     AJ011888.1  GI:4584508
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2982)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2982)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1..2982
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                     /cultivar="Desiree"
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                     FQHPRPKKPKSVRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYNAVQIMAIQEH
                     SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
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                     TSMMCTHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
                     PTFCVPVQDGGVGFDYRLHMAIADKWIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEG
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                     EFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHWTKGYSDYRIG
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                     /EC_number="2.4.1.18"
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  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 2590;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

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Db        140 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 199

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
Db        200 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTCTGTATTCTTGAAAAAACAC 259

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
Db        260 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCT 319

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
Db        320 ACAATTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAATCCAGAGTGATAGCTCCTCATCC 379

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
Db        380 TCAACAGATCAATTTGAGTTCGCTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 439

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
Db        440 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 499

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
Db        500 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 559

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
Db        560 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 619

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
Db        620 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 679

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
Db        680 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 739

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
Db        740 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 799

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
Db        800 GGTTATGAAAGAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 859

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db        860 CCTGGTGCCCAGTCAGCTGCCCTCATTGGGGATTTCAACAATTGGGACGCAAATGCTGAC 919

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db        920 TTTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 979

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
Db        980 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1039

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
Db       1040 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1099

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
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Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
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Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
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Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
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Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
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Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
Db       1460 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1519

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
Db       1520 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAAC 1579

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
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Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
Db       1640 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTGTACTCACCACGGATTATCGGTG 1699

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
Db       1700 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1759

Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
Db       1760 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1819

Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
Db       1820 GAAGATGTTAGCGGAATGCCGACATTTTGTGTTCCCGTTCAAGATGGGGGTGTTGGCTTT 1879

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
Db       1880 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1939

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
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Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
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Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
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Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
Db       2120 ATAGATCGTGGGATAGCATTACACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2179

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
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Db       2180 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2239

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
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Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
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Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
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Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
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Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
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Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
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Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
Db       2660 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2719

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
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RESULT 5
A58168
LOCUS       A58168                  3231 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 18 from Patent WO9634968.
ACCESSION   A58168
VERSION     A58168.1  GI:3713893
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3231)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 18 07-NOV-1996;
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COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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BASE COUNT      960 a    577 c    739 g    947 t      8 others
ORIGIN

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  Matches 2584;  Conservative    2;  Mismatches   45;  Indels    0;  Gaps    0;
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Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
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Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
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Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
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Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
Db        528 GTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 587

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
Db        588 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAACTA 647

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
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Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
Db        708 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 767

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
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Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
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Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
Db        888 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 947

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db        948 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 1007

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db       1008 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1067

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
Db       1068 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTT 1127

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
Db       1128 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1187

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
Db       1188 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCA 1247

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
Db       1248 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1307

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
Db       1308 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGG 1367

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
Db       1368 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1427
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Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Db       1428 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1487

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1488 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1547

Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
              ||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||||
Db       1548 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1607

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
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Db       1608 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1667

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
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Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
              |:|||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1728 GRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1787

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
              |||||||||||||||||||||||||||||||||||||||||||||||:|||||| |  |||
Db       1788 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCCGCCGTG 1847

Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
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Db       1848 TATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1907

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Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
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Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
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Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
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Db       2148 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTA 2207

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
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Db       2208 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2267

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
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Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
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Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
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Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
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Db       2448 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2507

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
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Qy       2341 GTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
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Db       2628 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2687

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
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Db       2688 AGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2747

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
              ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db       2748 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2807

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTA 2631
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Db       2808 GAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2858
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RESULT 6
A58162
LOCUS       A58162                  3003 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 12 from Patent WO9634968.
ACCESSION   A58162
VERSION     A58162.1  GI:3713887
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3003)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 12 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1..3003
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      895 a    535 c    706 g    867 t
ORIGIN

  Query Match             96.4%;  Score 2551;  DB 6;  Length 3003;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 2589;  Conservative    0;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 202

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||
Db        203 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTCTGTATTCTTGAAAAAACAC 262

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        263 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCT 322

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        323 ACAATTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAATCCAGAGTGATAGCTCCTCATCC 382

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              |||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        383 TCAACAGATCAATTTGAGTTCGCTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 442
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Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
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Db        443 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 502

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
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Db        503 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 562

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
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Db        563 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 622

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
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Db        623 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 682

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
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Db        683 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 742

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
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Db        743 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 802

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 GGTTATGAAAGAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 862

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
              | ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        863 CCTGGTGCCCAGTCAGCTGCCCTCATTGGGGATTTCAACAATTGGGACGCAAATGCTGAC 922

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
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Db        923 TTTATGACTCGGAATGAATTTGGTGTCTGAGAGATTTTTCTGCCAAATAATGTGGATGGT 982

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1042

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
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Db       1043 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1102

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1162

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1163 AAGAAACCAAAGTCGGTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1222

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCAT-AAAAAAGCTTGG 1139
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Db       1223 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAAGCTTGG 1282

Qy       1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199
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Qy       1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1259
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Qy       1260 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1320 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT 1379
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Qy       1380 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1439
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Db       1523 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAA 1582

Qy       1440 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATT 1499
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Qy       1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559
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Qy       1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619
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Db       1703 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1762

Qy       1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
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Qy       1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
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Qy       1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
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Qy       1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
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Qy       2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
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Qy       2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
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Qy       2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
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Qy       2340 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCT 2399
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Qy       2460 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2519
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Db       2603 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2662

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              |||||||||||||||||||| || || || |||||| || | |||||||||| |
Db       2723 AGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2777


RESULT 7
STU011885
LOCUS       STU011885              2955 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-1.
ACCESSION   AJ011885
VERSION     AJ011885.1  GI:4584502
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2955)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2955)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
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  Matches 2568;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

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Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
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Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
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SOURCE      unidentified.
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REFERENCE   1  (bases 1 to 2975)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 13 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
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Qy      301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
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Db     1883 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1942

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Qy     2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
Db     2183 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2242

Qy     2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
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Qy     2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
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Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
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Db       2543 AAGCCTGGAAAATACAAGGTTGTCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2602

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
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Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
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Db       2663 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAACTA 2722

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGC 2618
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Db       2723 GAAGTAGCAGTAGTAGAAGAACCCATTGAAGAATGAAC 2760
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AX256072
LOCUS       AX256072              2563 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 1 from Patent WO0170942.
ACCESSION   AX256072
VERSION     AX256072.1  GI:16075112
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 2563)
  AUTHORS   Poulson,P. and s Rensen,I.S.
  TITLE     Enzyme
  JOURNAL   Patent: WO 0170942-A 1 27-SEP-2001;
            DANISCO A/S (DK)
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                     IDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAFSRGYEKMGFTRSATGITYREWA
                     PGAQSAALIGDFNNWDANADIMTRNEFGVWEIFLPNNVDGSPAIPHGSRVKIRMDTPS
                     GVKDSIPAWINYSLQLPDEIPYNGIYYDPPEEERYIFQHPRPKKPKSLRIYESHIGMS
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                     SRLFNYGNWEVLRYLLSNARWWLDEFKFDGFRFDGVTSMMCTHHGLSVGFTGNYEEYF
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                     ISRKDEGDRMIVFEKGNLVFVFNFHWTKSYSDYRIGCLKPGKYKVALDSDDPLFGGFG
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BASE COUNT      749 a    462 c    614 g    738 t
ORIGIN
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Qy         65 TCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTC 124
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Db          1 TCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTCTGTATTCTTGAAAAACACTCTC 60

Qy        125 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAG 184
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAG 120

Qy        185 TTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAA 244
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Qy        245 CAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAG 304
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Qy        305 ATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGT 364
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Qy        365 CAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAG 360

Qy        425 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATG 484
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        361 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTTTGAAGAGACAATTATTGATG 420

Qy        485 AATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATG 544
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Qy        545 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 604
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Qy        605 AGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTT 664
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        541 AGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTT 600

Qy        665 ATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTG 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 ATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG 660

Qy        725 GTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 720

Qy        785 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 780

Qy        845 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGG 904
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Db        781 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGG 840

Qy        905 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        965 GAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGA 1024
              | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGA 960

Qy       1025 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAA 1084
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        961 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAACCTAAAA 1020
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Qy       1085 TTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACA 1144
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Qy       1145 ATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATG 1204
Db       1081 ATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATG 1140

Qy       1205 TCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGA 1264
Db       1141 TCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACTCCCGACGACCTTAAGTCTTTGA 1200

Qy       1265 TTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCAT 1324
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Qy       1325 CAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACT 1384
Db       1261 CAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACT 1320

Qy       1385 CTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGG 1444
Db       1321 CTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGG 1380

Qy       1445 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATG 1504
Db       1381 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATG 1440

Qy       1505 GATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGAT 1564
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Qy       1565 TCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATC 1624
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Qy       1625 TGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAG 1684
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Qy       1685 ATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACT 1744
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Qy       1745 ATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGG 1804
Db       1681 ATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGG 1740

Qy       1805 ATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTG 1864
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Qy       1865 TTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGC 1924
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Qy       1925 TGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAG 1984
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Qy       1985 ATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAG 2044
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Qy       2045 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGG 2104
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Qy       2105 CTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAAT 2164
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Qy       2165 GCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAAT 2224
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Qy       2225 TTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2284
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Db       2221 TCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTT 2280

Qy       2345 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGC 2404
Db       2281 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGC 2340

Qy       2405 CTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAA 2464
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Qy       2465 TTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAA 2524
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Qy       2525 TTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAG 2584
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DEFINITION  Sequence 17 from Patent WO9634968.
ACCESSION   A58167
VERSION     A58167.1  GI:3713892
KEYWORDS    .
SOURCE      unidentified.
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            unclassified.
REFERENCE   1  (bases 1 to 2529)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 17 07-NOV-1996;
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COMMENT     Other publication AU 5509996 961121.
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Qy        147 AAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 206
Db         61 AAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 120

Qy        207 TGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 266
Db        121 TGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 180

Qy        267 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 326
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Db     181 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 240

Qy     327 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 386
Db     241 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 300

Qy     387 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 446
Db     301 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 360

Qy     447 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 506
Db     361 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 420

Qy     507 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 566
Db     421 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 480

Qy     567 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 626
Db     481 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 540

Qy     627 CAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 686
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Qy     687 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCAT 746
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Qy     747 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 806
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Qy     807 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 866
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Qy     867 AGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 926
Db     781 AGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 840

Qy     927 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGA 986
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Qy    1047 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1106
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Qy    1107 AGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTAT 1166
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Qy    1167 TCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1226
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Qy    1227 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1286
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Qy    1287 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1346
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Qy    1347 GAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1406
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Qy    1407 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1466
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Qy    1467 AAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1526
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Qy    1527 ATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1586
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Qy    1587 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1646
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Qy    1707 TTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1766
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Qy    1767 TGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1826
Db    1681 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1740

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Db    1741 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCATGA 1800

Qy    1887 TCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGA 1946
Db    1801 TCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTATGA 1860

Qy    1947 TTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 2006
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Qy    2007 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 2066
Db    1921 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 1980

Qy    2067 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2126
Db    1981 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGATGG 2040

Qy    2127 CTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2186
Db    2041 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2100

Qy    2187 AGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCT 2246
Db    2101 AGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2160

Qy    2247 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2306
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Qy    2307 AGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGAC 2366
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Qy    2367 AAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTT 2426
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Qy    2427 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2486
Db    2341 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2400
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Qy       2487 CACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAA 2546
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Db       2401 CACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAG 2460

Qy       2547 AACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 2606
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Db       2461 AACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCCGN 2520

Qy       2607 AGAAGTA 2613
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RESULT 11
STU011889
LOCUS       STU011889               2523 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-5.
ACCESSION   AJ011889
VERSION     AJ011889.1  GI:4584510
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2523)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2523)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1..2523
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                     /cultivar="Desiree"
                     /db_xref="taxon:4113"
                     /note="sequence SBE A-5"
     gene            2..2512
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                     EAIDKYEGGLEAFSRGYEKMGFTRSATGITYREWAPGAQSAALIGDFNNWDANADIMT
                     RNEFGVWEIFLPNNVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYN
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                     GYNALQIMAIQEHSYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIV
                     HSHASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWL
                     DEFKFDGFRFDGVTSMMYTHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLF
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                     LTNRRWSEKCVSYAESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHK
                     MIRLVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDDSVIPGNQFSYDKCRRRFD
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BASE COUNT      749 a    449 c    605 g    720 t
ORIGIN

  Query Match            93.4%;  Score 2470.6;  DB 8;  Length 2523;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 2485;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy        135 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 60

Qy        195 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 254
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         61 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 120

Qy        255 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 180

Qy        315 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 240

Qy        375 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 300

Qy        435 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 360

Qy        495 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 420

Qy        555 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 480

Qy        615 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAAT 674
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        481 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 540

Qy        675 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTC 734
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Db        541 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 600

Qy        735 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 660

Qy        795 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 854
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Db        661 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 720

Qy        855 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 780

Qy        915 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTA 974
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Qy        975 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1034
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Db        841 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 900

Qy       1035 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 960
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Qy       1095 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1020

Qy       1155 AATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTT 1214
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1021 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1080

Qy       1215 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1140

Qy       1275 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1200

Qy       1335 TTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1394
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1201 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1260

Qy       1395 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1454
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
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Qy       1455 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATT 1514
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Qy       1515 TGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAA 1574
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Db       1381 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1440

Qy       1575 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1634
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Qy       1635 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1694
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Qy       1755 TATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1814
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Qy       1815 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1874
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Db       1741 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1800

Qy       1935 GGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 1994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 1860

Qy       1995 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2054
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Db       1861 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1920

Qy       2055 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2114
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Qy       2115 CCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2174
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Db       1981 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2040

Qy       2175 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCC 2234
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Qy       2475 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2534
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Qy       2535 TGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2594
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Db       2401 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2460

Qy       2595 AGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAA 2643
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Db       2461 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGAAGAAGAA 2509
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RESULT 12
A58169

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LOCUS       A58169                  2578 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 19 from Patent WO9634968.
ACCESSION   A58169
VERSION     A58169.1  GI:3713894
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2578)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 19 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
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BASE COUNT      770 a     462 c     616 g     730 t
ORIGIN

  Query Match            93.2%;  Score 2465.8;  DB 6;  Length 2578;
  Best Local Similarity  98.9%;  Pred. No. 0;
  Matches 2482;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

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Qy        195 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 254
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        116 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 175

Qy        255 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 235
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Qy       315 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 374
Db       236 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 295

Qy       375 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 434
Db       296 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 355

Qy       435 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 494
Db       356 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 415

Qy       495 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 554
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Qy       555 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 614
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Qy       675 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTC 734
Db       596 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 655

Qy       735 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 794
Db       656 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 715

Qy       795 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 854
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Qy       855 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 914
Db       776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 835

Qy       915 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTA 974
Db       836 TGCTTGGATCAACTACTCTTCACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 895

Qy       975 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1034
Db       896 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 955

Qy      1035 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1094
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Qy      1095 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1154
Db      1016 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCA 1075

Qy      1155 AATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTT 1214
Db      1076 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1135

Qy      1215 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1274
Db      1136 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1195

Qy      1275 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1334
Db      1196 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1255

Qy      1335 TTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1394
Db      1256 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1315

Qy      1395 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1454
Db      1316 TGGTTATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAG 1375

Qy      1455 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATT 1514
Db      1376 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATT 1435

Qy      1515 TGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAA 1574
Db      1436 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1495

Qy      1575 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1634
Db      1496 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1555

Qy      1635 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1694
Db      1556 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1615

Qy      1695 AATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCA 1754
Db      1616 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1675

Qy      1755 TATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1814
Db      1676 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1735

Qy      1815 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1874
Db      1736 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1795

Qy      1875 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1934
Db      1796 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1855

Qy      1935 GGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 1994
Db      1856 GGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAT 1915

Qy      1995 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2054
Db      1916 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1975

Qy      2055 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2114
Db      1976 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2035

Qy      2115 CCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2174
Db      2036 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2095

Qy      2175 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCC 2234
Db      2096 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2155

Qy      2235 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2294
Db      2156 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2215

Qy      2295 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2354
Db      2216 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2275

Qy      2355 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATA 2414
Db      2276 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATA 2335

Qy      2415 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2474
Db      2336 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2395

Qy      2475 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2534
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Db       2396 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2455

Qy       2535 TGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2594
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2515

Qy       2595 AGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAA 2643
              |||||||||||||| || || || || ||||| |||||||| |||||||
Db       2516 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2564


RESULT 13
A58166
LOCUS       A58166                 2576 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 16 from Patent WO9634968.
ACCESSION   A58166
VERSION     A58166.1  GI:3713891
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2576)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 16 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1..2576
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BASE COUNT      770 a    462 c    615 g    729 t
ORIGIN

  Query Match             92.8%;  Score 2455;  DB 6;  Length 2576;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 2482;  Conservative    0;  Mismatches   25;  Indels    2;  Gaps    1;

Qy        135 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 115

Qy        195 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 254
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        116 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 175

Qy        255 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 235

Qy        315 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 295

Qy        375 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 355

Qy        435 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 415

Qy        495 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 475

Qy        555 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 535

Qy        615 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAAT 674
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Db        536 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 595

Qy        675 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGCTCTTGGTGCCCAGTC 734
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        596 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGCTCCTGGTGCCCAGTC 655

Qy        735 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 715

Qy        795 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 775

Qy        855 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 914
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Db        776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 835

Qy        915 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTA 974
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||| ||||
Db        836 TGCTTGGATCAACTACTC--TACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 893

Qy        975 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 953

Qy       1035 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1013

Qy       1095 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1073

Qy       1155 AATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTT 1214
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1074 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1133

Qy       1215 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1193

Qy       1275 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1334
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Db       1194 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1253

Qy       1335 TTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1394
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1254 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1313

Qy       1395 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1454
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1314 TGGTTATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAG 1373

Qy       1455 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATT 1514
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1374 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATT 1433

Qy       1515 TGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAA 1574
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Db       1434 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1493

Qy       1575 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1634
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Db       1494 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1553

Qy       1635 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1613

Qy       1695 AATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCA 1754
              |||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Db       1614 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1673
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Qy       1755 TATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1814
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Qy       1815 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1874
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Qy       1875 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1934
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Db       1794 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1853

Qy       1935 GGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 1994
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db       1854 GGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAT 1913

Qy       1995 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2054
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1973

Qy       2055 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2114
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Qy       2115 CCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2174
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Db       2034 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2093

Qy       2175 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCC 2234
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Qy       2235 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2294
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Db       2154 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2213

Qy       2295 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2354
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Db       2214 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2273

Qy       2355 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATA 2414
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Db       2274 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATA 2333

Qy       2415 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2334 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2393

Qy       2475 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2534
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Db       2394 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2453

Qy       2535 TGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2594
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2595 AGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAA 2643
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Db       2514 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2562
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RESULT 14
STSBEII
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LOCUS       STSBEII                 2493 bp    mRNA    linear   PLN 27-MAY-1998
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II.
ACCESSION   AJ000004
VERSION     AJ000004.1  GI:2764395
KEYWORDS    Sbe-II gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2493)
  AUTHORS   Larsson,C.T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell
            Research, Genetic Center, Swedish University of Agricultural
            Sciences, Box 7055, S-750 07 Uppsala, SWEDEN
REFERENCE   2  (bases 1 to 2493)
  AUTHORS   Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H.
  TITLE     Molecular cloning and characterization of starch-branching enzyme
            II from potato
  JOURNAL   Plant Mol. Biol. 37 (3), 505-511 (1998)
  MEDLINE   98278379
   PUBMED   9617817
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                     ITIGEDVSGMPTFCIPVQDGGVGFDYRLHMAIADKWIELLKKRDEDWRVGDIVHTLTN
                     RRWSEKCVSYAESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIR
                     LVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGD
                     AEYLRYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHW
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BASE COUNT      742 a    445 c    595 g    711 t
ORIGIN

  Query Match             92.0%;  Score 2435.6;  DB 8;  Length 2493;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 2456;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        145 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 204
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Db          1 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 60

Qy        205 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 120

Qy        265 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 324
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Db        121 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 180

Qy        325 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 384
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Db        181 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 240
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Qy    385 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 444
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Db    241 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 300

Qy    445 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 504
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 360

Qy    505 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 564
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Db    361 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 420

Qy    565 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 624
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Qy    865 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 924
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Qy    925 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCC 984
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Qy    985 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1044
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Qy   1045 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1104
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RESULT 15
AB071286
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DEFINITION  Ipomoea batatas SBE II mRNA for starch branching enzyme II,
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VERSION     AB071286.1  GI:15553090
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  AUTHORS   Kimura,T. and Saito,A.
  TITLE     Ipomoea batatas mRNA for starch branching enzyme II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3123)
  AUTHORS   Kimura,T. and Saito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2001) Takashi Kimura, National Agricultural
            Research Center for Kyushu Okinawa Region; 2421 Suya, Nishigoshi,
            Kumamoto 861-1192, Japan (E-mail:tkimura@affrc.go.jp,
            Tel:81-96-242-1150)
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ORIGIN

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                 Listing first 45 summaries

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                1:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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                22:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                23:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                24:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2646	100.0	3033	17	AAT42630	Class A starch bra
	2	2584.2	97.7	3074	18	AAT69587	Potato starch bran
	3	2558.2	96.7	3231	17	AAT42632	Class A starch bra
	4	2551	96.4	3003	17	AAT42634	Class A starch bra
	5	2512.4	95.0	2975	17	AAT42635	Class A starch bra
	6	2486.8	94.0	2563	23	ABK50301	Potato cDNA encodi
	7	2471.2	93.4	2531	17	AAT17267	Class A starch bra
	8	2468.4	93.3	2529	17	AAT42637	Class A starch bra
	9	2465.8	93.2	2578	17	AAT42631	Class A starch bra
	10	2451.8	92.7	2576	17	AAT42636	Class A starch bra
	11	1429.4	54.0	3090	19	AAV38720	Full length cassav
	12	1362	51.5	2913	19	AAV38719	Full length cassav
	13	1290	48.8	2715	21	AAC45939	Arabidopsis thalia
	14	1264.8	47.8	3015	19	AAV05639	Rice type IV starc
	15	1251.2	47.3	2919	15	AAQ73750	Rice starch branch
	16	1243.6	47.0	2726	22	AAH78337	Nucleotide sequenc
	17	1183.6	44.7	2640	19	AAV70961	DNA encoding maize
	18	1180.4	44.6	2665	18	AAT69729	Plasmid pBE240 ins
	19	1180.4	44.6	2725	19	AAV29757	Zea mays starch br
	20	1167.2	44.1	3039	24	ABK15494	Wheat starch branc
	21	1164	44.0	2968	22	AAH78342	Nucleotide sequenc
	22	1044.6	39.5	2307	21	AAZ99938	DNA encoding part
	23	1033	39.0	2087	18	AAT69737	Corn starch branch
c	24	1031.4	39.0	2165	18	AAT69736	Corn starch branch
	25	956.6	36.2	1919	19	AAV38722	cDNA encoding star
	26	728.8	27.5	1452	21	AAC36957	Arabidopsis thalia
	27	632.4	23.9	4563	22	AAF30910	Wheat starch branc
	28	631.4	23.9	3128	16	AAT00774	Potato starch bran
c	29	628.4	23.7	2487	18	AAT69747	Corn starch branch
	30	628.4	23.7	2565	18	AAT69752	Corn starch branch
	31	628.4	23.7	2763	19	AAV29758	Zea mays starch br
	32	628.4	23.7	2771	13	AAQ24257	Branching enzyme D
	33	628.4	23.7	2772	18	AAT69740	Plasmid pBE65 inse
	34	617.2	23.3	2909	13	AAQ27778	Potato amylose-amy
	35	610	23.1	2687	20	AAX34646	wSBE I-D4 cDNA seq
	36	603	22.8	2733	15	AAQ54674	Rice starch branch
	37	603	22.8	2733	15	AAQ62135	Rice starch branch
	38	589	22.3	2713	19	AAV70962	DNA encoding maize
	39	578.2	21.9	3075	24	AAS94880	Human DNA sequence
	40	576.6	21.8	2899	22	AAH02926	Human shear stress
	41	576.6	21.8	2955	24	ABN95650	Gene #2148 used to
	42	542	20.5	1809	18	AAT69753	Corn starch branch
	43	542	20.5	1865	18	AAT69748	Corn starch branch
	44	535.8	20.2	770	23	ABK50302	Potato starch bran
	45	501.6	19.0	728	23	ABK50303	Potato starch bran

ALIGNMENTS

```
RESULT 1
AAT42630
ID   AAT42630 standard; DNA; 3033 BP.
XX
AC   AAT42630;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (19con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             145..2793
FT                   /*tag=  a
FT   sig_peptide     145..288
FT                   /*tag=  b
FT   mat_peptide     289..2790
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;    96WO-GB01075.
XX
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
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PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAW06399.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 28-30; Page 42-46; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;

  Query Match             100.0%;  Score 2646;  DB 17;  Length 3033;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2646;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 204

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 264

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 324

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 384

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 444

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
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Db        445 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 504

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 564

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 624

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 684

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
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Db        685 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 744

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
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Db        745 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 804

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 864

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 924

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 984

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1044

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1104

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1164

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1224

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1284

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1285 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1344

Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTCT 1404

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
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Db       1405 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1464

Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
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Db       1465 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1524

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
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Db       1525 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1584

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
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Db       1585 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1644

Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
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Db       1645 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1704

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
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Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
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Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
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Db       1825 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1884

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1885 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1944

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1945 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2004

Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2005 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2064

Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
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Db       2065 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 2124

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2125 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2184

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
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Db       2185 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2244

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2245 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2304

Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
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Db       2305 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2364

Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
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Db       2365 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2424

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2425 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2484

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
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Db       2485 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2544

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
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Db       2545 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2604

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2605 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2664

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
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Db       2665 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2724

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAA 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2725 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAA 2784

Qy       2641 GAAGAA 2646
              ||||||
Db       2785 GAAGAA 2790
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RESULT 2
AAT69587
ID   AAT69587 standard; cDNA; 3074 BP.
XX
AC   AAT69587;
XX
DT   26-AUG-1997  (first entry)
XX
DE   Potato starch branching enzyme II gene (beII).
XX
KW   Starch branching enzyme II; beII gene; potato; transgenic plant;
KW   amylopectin; amylose; starch; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             189..2825
FT                   /*tag=  a
FT   sig_peptide     189..332
FT                   /*tag=  b
FT   mat_peptide     333..2822
FT                   /*tag=  c
XX
PN   WO9720040-A1.
XX
PD   05-JUN-1997.
XX
PF   28-NOV-1996;   96WO-SE01558.
XX
PR   19-APR-1996;   96SE-0001506.
PR   29-NOV-1995;   95SE-0004272.
XX
PA   (EKBB/) EK B.
PA   (KHOS/) KHOSNOODI J.
PA   (LARS/) LARSSON C.
PA   (LARS/) LARSSON H.
PA   (RASK/) RASK L.
PA   (AMYL-) AMYLOGENE HB.
XX
PI   Ek B,  Khosnoodi J,  Larsson C,  Larsson H,  Rask L;
XX
DR   WPI; 1997-310596/28.
DR   P-PSDB; AAW19113.
XX
PT   Isolated potato starch branching enzyme II - useful for altering
PT   degree of amylopectin branching and amylopectin/amylose ratio in
PT   potato starch
XX
PS   Claim 4; Page 12-15; 24pp; English.
XX
CC   A cDNA clone (AAT69587) codes for potato starch branching enzyme II
CC   (BEII) (AAW19113).  It was isolated from potato tuber cDNA by PCR
CC   amplification using primers (AAT69588-89) based on tryptic peptides
CC   of isolated BEII; the 5' and 3' ends of the sequence were detd. by
CC   RACE.  A vector comprising the whole or a functional active part of
CC   the isolated sequence (sense or antisense), plus regulatory
CC   sequences active in potato, can be used to produce transgenic
CC   potatoes.  The starch obtd. from such plants will show a changed
CC   pattern of amylopectin branching and an altered amylopectin/amylose
CC   ratio.
XX
SQ   Sequence 3074 BP; 902 A; 560 C; 710 G; 896 T; 6 other;

  Query Match             97.7%;  Score 2584.2;  DB 18;  Length 3074;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 2601;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 248

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        249 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTTGAAAAAGCAC 308

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        309 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCT 368

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 428

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 488
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Qy    301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
Db    489 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 548

Qy    361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
Db    549 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 608

Qy    421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
Db    609 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 668

Qy    481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
Db    669 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 728

Qy    541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
Db    729 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 788

Qy    601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
Db    789 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 848

Qy    661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
Db    849 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 908

Qy    721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db    909 CCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 968

Qy    781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db    969 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1028

Qy    841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
Db   1029 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1088

Qy    901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
Db   1089 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1148

Qy    961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
Db   1149 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1208

Qy   1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
Db   1209 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1268

Qy   1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
Db   1269 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1328

Qy   1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
Db   1329 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1388

Qy   1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
Db   1389 CATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGGAACNCCCGACGACCTTAAGTCT 1448

Qy   1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
Db   1449 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1508

Qy   1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
Db   1509 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1568

Qy   1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
Db   1569 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1628

Qy   1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
Db   1629 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTT 1688

Qy   1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
Db   1689 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1748

Qy   1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
Db   1749 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1808

Qy   1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
Db   1809 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1868

Qy   1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
Db   1869 GAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1928

Qy   1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
Db   1929 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1988

Qy   1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
Db   1989 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2048

Qy   1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
Db   2049 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2108

Qy   1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
Db   2109 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTCAACATCATTA 2168

Qy   1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
Db   2169 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2228

Qy   2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
Db   2229 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2288

Qy   2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
Db   2289 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2348

Qy   2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
Db   2349 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2408

Qy   2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
Db   2409 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2468

Qy   2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
Db   2469 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2528

Qy   2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
Db   2529 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTG 2588

Qy   2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
Db   2589 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2648

Qy   2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
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Db       2649 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2708

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
              |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||
Db       2709 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2768

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
              |||||||||||||||||| || || || || || || ||||| ||||| || |
Db       2769 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822


RESULT 3
AAT42632
ID   AAT42632 standard; DNA; 3231 BP.
XX
AC   AAT42632;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (psbe2con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        45..3200
FT                   /*tag=  a
FT                   /note= "claim 34"
FT   CDS             228..2855
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 31, 34; Page 53-55; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
CC   The same sequence is given in Figure 8, however, nucleotides
CC   1-44 omitted.
XX
SQ   Sequence 3231 BP; 960 A; 577 C; 739 G; 947 T; 8 other;

  Query Match             96.7%;  Score 2558.2;  DB 17;  Length 3231;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 2584;  Conservative    2;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 287

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 347

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              |||||||||||||||||||||||||||||||||||||| |||||||| |||||||||
Db        348 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCT 407

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              |||||||||||||||||||||||||||| |||||| ||||||||||||||||||||||||
Db        408 ACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCC 467

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        468 TCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACTGAT 527

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 GTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 587

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        588 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAACTA 647

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 707

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 767

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 827

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
              |||||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        828 TACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 887

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        888 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 947

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
              | |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        948 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 1007

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1008 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1067

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
              ||||||||||||||||||||||||||||||||||||| |||||||| |||||||||||||
Db       1068 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTT 1127

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1128 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1187

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
              |||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1188 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCA 1247

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1248 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1307

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1308 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGG 1367

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
              |||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1368 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1427
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Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
Db       1428 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1487

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
Db       1488 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1547

Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
Db       1548 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1607

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
Db       1608 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1667

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
Db       1668 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTT 1727

Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
Db       1728 GRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1787

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
Db       1788 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTG 1847

Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
Db       1848 TATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1907

Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
Db       1908 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1967

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
Db       1968 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 2027

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
Db       2028 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2087

Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
Db       2088 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2147

Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
Db       2148 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTA 2207

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
Db       2208 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2267

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
Db       2268 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2327

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
Db       2328 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2387

Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
Db       2388 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2447

Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
Db       2448 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2507

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
Db       2508 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2567

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
Db       2568 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTG 2627

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
Db       2628 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2687

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
Db       2688 AGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2747

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
Db       2748 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2807

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTA 2631
Db       2808 GAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2858
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RESULT 4
AAT42634
ID   AAT42634 standard; DNA; 3003 BP.
XX
AC   AAT42634;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (10con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 38-39; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;

  Query Match            96.4%;  Score 2551;  DB 17;  Length 3003;
  Best Local Similarity  98.3%;  Pred. No. 0;
  Matches 2589;  Conservative    0;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
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Db    143 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 202

Qy     61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
Db    203 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTCTGTATTCTTGAAAAAACAC 262

Qy    121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
Db    263 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCT 322

Qy    181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
Db    323 ACAATTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAATCCAGAGTGATAGCTCCTCATCC 382

Qy    241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
Db    383 TCAACAGATCAATTTGAGTTCGCTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 442

Qy    301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
Db    443 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 502

Qy    361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
Db    503 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 562

Qy    421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
Db    563 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 622

Qy    481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
Db    623 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 682

Qy    541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
Db    683 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 742

Qy    601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
Db    743 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 802

Qy    661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
Db    803 GGTTATGAAAGAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 862

Qy    721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db    863 CCTGGTGCCCAGTCAGCTGCCCTCATTGGGGATTTCAACAATTGGGACGCAAATGCTGAC 922

Qy    781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db    923 TTTATGACTCGGAATGAATTTGGTGTCTGAGAGATTTTTCTGCCAAATAATGTGGATGGT 982

Qy    841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
Db    983 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1042

Qy    901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
Db   1043 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1102

Qy    961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
Db   1103 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1162

Qy   1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
Db   1163 AAGAAACCAAAGTCGGTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1222

Qy   1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCAT-AAAAAAGCTTGG 1139
Db   1223 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAAGCTTGG 1282

Qy   1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199
Db   1283 GTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTA 1342

Qy   1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTC 1259
Db   1343 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTC 1402

Qy   1260 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1319
Db   1403 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1462

Qy   1320 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT 1379
Db   1463 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTT 1522

Qy   1380 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1439
Db   1523 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAA 1582

Qy   1440 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATT 1499
Db   1583 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATT 1642

Qy   1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559
Db   1643 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTGTACTCACCACGGATTATCGGT 1702

Qy   1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619
Db   1703 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1762

Qy   1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
Db   1763 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1822

Qy   1680 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTT 1739
Db   1823 TGAAGATGTTAGCGGAATGCCGACATTTTGTGTTCCCGTTCAAGATGGGGGTGTTGGCTT 1882

Qy   1740 TGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGA 1799
Db   1883 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1942

Qy   1800 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 1859
Db   1943 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2002

Qy   1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
Db   2003 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 2062

Qy   1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
Db   2063 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 2122

Qy   1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db   2123 AATAGATCGTGGGATAGCATTACACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2182

Qy   2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db   2183 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2242

Qy   2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db   2243 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCAGAAACCAATTCAGTTATGA 2302

Qy   2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db   2303 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2362
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Qy       2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2279
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2363 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2422

Qy       2280 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2423 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2482

Qy       2340 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCT 2399
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||||
Db       2483 AGTTTTTGTCTTTAATTTTCACTGGACAAAAGGCTATTCAGACTATCGCATAGGCTGCCT 2542

Qy       2400 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2543 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2602

Qy       2460 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2603 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2662

Qy       2520 TTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGA 2579
              |||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||
Db       2663 TTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGA 2722

Qy       2580 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
              |||||||||||||||||||| || || || || || || ||||| || || || |
Db       2723 AGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2777
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RESULT 5
AAT42635
ID   AAT42635 standard; DNA; 2975 BP.
XX
AC   AAT42635;
XX
DT   03-MAR-1997 (first entry)
XX
DE   Class A starch branching enzyme (11con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 40-41; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes. In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2975 BP; 871 A; 548 C; 693 G; 863 T; 0 other;

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  Query Match             95.0%;  Score 2512.4;  DB 17;  Length 2975;
  Best Local Similarity   98.0%;  Pred. No. 0;
  Matches 2565;  Conservative    0;  Mismatches   51;  Indels    2;  Gaps    2;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGTGTATATACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 204

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 264

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 324

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 384

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        385 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAAATCCCCAGCATCAACTGAT 444

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 504

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 564

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 624

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 684

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 744

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        745 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAG-CTTTTCTCGT 803

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 863

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 CCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 923

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 983

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1043

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1103

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1163

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
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Db       1164 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1223

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
Db       1224 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1283

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
Db       1284 TACAATGCGCTGCGAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1343

Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
Db       1344 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1403

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
Db       1404 TCGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATCGTTCACAGCCAT 1463

Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
Db       1464 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTT 1523

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
Db       1524 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATT-CCGCCTCTTTAACTATGGAAAC 1582

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
Db       1583 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTT 1642

Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
Db       1643 GATGGATTTAGATTCGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1702

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
Db       1703 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1762

Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
Db       1763 TATCTGATGCTGGTCAACGATCTTATTCATAGGCTTTTCCCAGATGCAATTACCATTGGT 1822

Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
Db       1823 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1882

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
Db       1883 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1942

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
Db       1943 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2002

Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
Db       2003 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2062

Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
Db       2063 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTA 2122

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
Db       2123 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2182

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
Db       2183 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2242

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
Db       2243 AGGGCTGAGCCACACCTTTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2302

Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
Db       2303 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCATGGGTTACAA 2362

Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
Db       2363 GAATTTGACTGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2422

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
Db       2423 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAGAGGAAACCTA 2482

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
Db       2483 GTTTTCGTCTTTAATTTTCACTGGACAAATAGCTATTCAGACTATCGCATAGGCTGCCTG 2542

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
Db       2543 AAGCCTGGAAAATACAAGGTTGTCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2602

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
Db       2603 AGAATTGATCATAATGCCGAATATTTCACCTCTGAAGGATCGTATGATGATCGTCCTTGT 2662

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
Db       2663 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAACTA 2722

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGC 2618
Db       2723 GAAGTAGCAGTAGTAGAAGAACCCATTGAAGAATGAAC 2760
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RESULT 6

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ABK50301
ID   ABK50301 standard; cDNA; 2563 BP.
XX
AC   ABK50301;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Potato cDNA encoding starch branching enzyme, SBE II.
XX
KW   Potato; starch branching enzyme; SBE II; glucan branching enzyme;
KW   GBE; ss; gene; plant; transgenic; antisense; food industry;
KW   paper industry; chemical industry.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..2552
FT                   /*tag=  a
FT                   /product= "SBE II"
FT                   /partial
FT                   /note= "No start codon shown"
XX
PN   GB2360521-A.
XX
PD   26-SEP-2001.
XX
PF   20-MAR-2000; 2000GB-0006733.
XX
PR   20-MAR-2000; 2000GB-0006733.
XX
PA   (DANI-) DANISCO AS.
XX
PI   Poulsen P,  Sorensen IS;
XX
DR   WPI; 2001-650142/75.
DR   P-PSDB; AAU80169.
XX
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PT   New transformed plants with reduced endogenous starch branching enzyme
PT   and heterologous glucan branching enzyme activities, useful for
PT   producing starch with improved properties, which is in the food, paper
PT   and chemical industries -
XX
PS   Example 1; Page 31-35; 61pp; English.
XX
CC   The invention relates to a transformed organism, preferably a transformed
CC   plant, having a reduced endogenous starch branching enzyme (SBE)
CC   activity, and having a heterologous glucan branching enzyme (GBE)
CC   activity. The reduced SBE activity is effected via expression of a
CC   nucleotide sequence that is antisense to at least part of a SBE exon.
CC   Also included are a method of producing starch with altered
CC   characteristics comprising (a) providing a plant having reduced
CC   endogenous SBE activity, and having heterologous GBE activity
CC   (b) propagating the plant of (a) and optionally (c) obtaining starch
CC   from the plant; starch obtainable from the transformed plant; and
CC   a nucleic acid construct system capable of directing the expression
CC   of all or part of one or more antisense SBE exons and optionally one or
CC   more heterologous GBE. The transformed plants are useful for producing
CC   starch with modified and improved properties, which is an important raw
CC   material and used in the food, paper and chemical industries. The
CC   present sequence encodes Potato SBE II, used to make transgenic plants of
CC   the invention.
XX
SQ   Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;

  Query Match             94.0%;  Score 2486.8;  DB 23;  Length 2563;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2512;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         65 TCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTC 124
              |||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||
Db          1 TCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTCTGTATTCTTGAAAAAACACTCTC 60

Qy        125 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAG 184
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAG 120

Qy        185 TTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAA 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAA 180

Qy        245 CAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAG 240

Qy        305 ATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGT 300

Qy        365 CAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAG 360

Qy        425 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATG 484
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        361 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTTTGAAGAGACAATTATTGATG 420

Qy        485 AATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATG 480

Qy        545 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 540

Qy        605 AGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTT 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTT 600

Qy        665 ATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTG 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 ATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG 660

Qy        725 GTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 720

Qy        785 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 780

Qy        845 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGG 904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGG 840

Qy        905 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 900

Qy        965 GAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGA 1024
              | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGA 960

Qy       1025 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAA 1084
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        961 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAACCTAAAA 1020

Qy       1085 TTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACA 1144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db       1021 TTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACG 1080

Qy       1145 ATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATG 1204
              ||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1081 ATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATG 1140

Qy       1205 TCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGA 1264
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1141 TCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACTCCCGACGACCTTAAGTCTTTGA 1200

Qy       1265 TTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCAT 1324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCAT 1260

Qy       1325 CAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACT 1384
              ||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||
Db       1261 CAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACT 1320

Qy       1385 CTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGG 1444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGG 1380

Qy       1445 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATG 1504
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1381 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATG 1440

Qy       1505 GATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGAT 1564
              ||||||||||||||||||||||||||||||||| || |||||||||||||||||||||||
Db       1441 GATTTAGATTTGATGGTGTGACATCAATGATGTGTACTCACCACGGATTATCGGTGGGAT 1500

Qy       1565 TCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATC 1624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATC 1560

Qy       1625 TGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAG 1684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAG 1620

Qy       1685 ATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACT 1744
              |||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||
Db       1621 ATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACT 1680

Qy       1745 ATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGG 1804
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1681 ATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGG 1740
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Qy     1805 ATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTG 1864
Db     1741 ATTGGAGAGTGAGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTG 1800

Qy     1865 TTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGC 1924
Db     1801 TTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGC 1860

Qy     1925 TGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAG 1984
Db     1861 TGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAG 1920

Qy     1985 ATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAG 2044
Db     1921 ATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAG 1980

Qy     2045 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGG 2104
Db     1981 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCCGAGTGGATTGATTTCCCTAGGG 2040

Qy     2105 CTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAAT 2164
Db     2041 CTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAAT 2100

Qy     2165 GCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAAT 2224
Db     2101 GCAGACGGAGATTTGACCTGGGAGATGCAGATTATTTAAGATACCGTGGGTTGCAAGAAT 2160

Qy     2225 TTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2284
Db     2161 TTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2220

Qy     2285 TCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTT 2344
Db     2221 TCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTT 2280

Qy     2345 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGC 2404
Db     2281 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGC 2340

Qy     2405 CTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAA 2464
Db     2341 CTGGAAAATACAAGGTTGCCTTGGACTCGGATGATCCACTTTTTGGTGGCTTTGGGAGAA 2400

Qy     2465 TTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAA 2524
Db     2401 TTGATCATAATGCCGAATACTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAA 2460

Qy     2525 TTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAG 2584
Db     2461 TTATGGTGTATGCACCTAGTAGGACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGCAG 2520

Qy     2585 AAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGC 2618
Db     2521 AAGAAGAAGTAGCAGTAGTAGAAGAAGAATGAAC 2554
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RESULT 7
AAT17267
ID   AAT17267 standard; DNA; 2531 BP.
XX
AC   AAT17267;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (direct sequencing).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAR93804.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Fig 9; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
CC   This sequence was obtained by direct sequencing of PCR fragments
CC   amplified from first strand cDNA.  Nucleotides which could not
CC   be unambiguously assigned are indicated using standard IUPAC
CC   notation.
XX
SQ   Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;

  Query Match             93.4%;  Score 2471.2;  DB 17;  Length 2531;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 2482;  Conservative   11;  Mismatches   34;  Indels    0;  Gaps    0;

Qy       87 GAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 146
Db        1 GGATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 60

Qy      147 AAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 206
Db       61 AAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 120

Qy      207 TGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 266
Db      121 TGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 180

Qy      267 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 326
Db      181 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 240

Qy      327 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 386
Db      241 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 300

Qy      387 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 446
Db      301 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 360

Qy      447 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 506
Db      361 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 420

Qy      507 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 566
Db      421 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 480

Qy      567 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 626
Db      481 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 540
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Qy     627 CAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 686
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     541 CAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 600

Qy     687 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCAT 746
           ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     601 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCAT 660

Qy     747 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 720

Qy     807 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 780

Qy     867 AGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 926
           ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 840

Qy     927 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGA 986
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     841 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 900

Qy     987 AGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 1046
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 960

Qy    1047 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1020

Qy    1107 AGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTAT 1166
           |||||||||||||||||||||||||||:||||||||||||||| ||||||||||||||||
Db    1021 AGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1080

Qy    1167 TCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1226
           |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    1081 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1140

Qy    1227 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1200

Qy    1287 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1260

Qy    1347 GAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1406
           ||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Db    1261 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1320

Qy    1407 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1380

Qy    1467 AAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1526
           ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    1381 AAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1440

Qy    1527 ATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1586
           |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1500

Qy    1587 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1560

Qy    1647 TCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1706
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1620

Qy    1707 TTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1766
           |||||||||||| ||||| |||||||||||||||||||||||||||||||||||||||||
Db    1621 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1680

Qy    1767 TGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1826
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1740

Qy    1827 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGA 1886
           ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db    1741 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCATGA 1800

Qy    1887 TCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGA 1946
           ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    1801 TCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTATGA 1860

Qy    1947 TTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 2006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 1920

Qy    2007 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGAAA 2066
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGAAA 1980

Qy    2067 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2126
           ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db    1981 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGATGG 2040

Qy    2127 CTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2186
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2100

Qy    2187 AGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCT 2246
           ||||||||||||||||||||||| ||||||||||||||||||||||| ||||||||||||
Db    2101 AGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2160

Qy    2247 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2220

Qy    2307 AGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGAC 2366
           |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db    2221 AGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGAC 2280

Qy    2367 AAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTT 2426
           ||| |||||||||||||||||||||| |||||||||||||||||||||||||||| |||
Db    2281 AAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGCTT 2340

Qy    2427 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2400

Qy    2487 CACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAA 2546
           ||||| |||||||| |||||||||||||||:||::|||||||||||||||||||| ||| 
Db    2401 CACCTCTGAAGGATCGTATGATGATCGTCCYCGYYCAATTATGGTGTATGCACCTAGTAG 2460

Qy    2547 AACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 2606
           |||||||||||||||||||||||||||||||  ||||| ||||||||||||||||   | 
Db    2461 AACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCCGN 2520

Qy    2607 AGAAGTA 2613
            |||| |
Db    2521 NGAAGAA 2527
```

RESULT 8
AAT42637
ID   AAT42637 standard; DNA; 2529 BP.
XX
AC   AAT42637;
XX
DT   03-MAR-1997 (first entry)
XX
DE   Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.

```
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 51-53; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;

  Query Match             93.3%;  Score 2468.4;  DB 17;  Length 2529;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 2481;  Conservative   10;  Mismatches   36;  Indels    0;  Gaps    0;

Qy         87 GAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 146
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 60

Qy        147 AAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 206
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         61 AAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 120

Qy        207 TGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 266
              |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 180

Qy        267 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 240

Qy        327 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 300

Qy        387 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 360

Qy        447 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 420

Qy        507 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 480

Qy        567 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 540

Qy        627 CAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 686
              ||||||||||||||||||  |||| |||||||||||||||||||||||||||||||||||
Db        541 CAAGTATGAGGGTGGTTTTCAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 600

Qy        687 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCAT 746
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        601 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCAT 660

Qy        747 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 720

Qy        807 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 780

Qy        867 AGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 926
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 840

Qy        927 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGA 986
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        841 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 900

Qy        987 AGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 1046
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 960

Qy       1047 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1020

Qy       1107 AGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTAT 1166
              |||||||||||||||||||||||||||:||||||||||||||| ||||||||||||||||
Db       1021 AGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1080

Qy       1167 TCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1226
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1081 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1140

Qy       1227 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1200

Qy       1287 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1260

Qy       1347 GAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1406
              ||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Db       1261 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1320

Qy       1407 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1380

Qy       1467 AAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1526
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1381 AAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1440

Qy       1527 ATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1586
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1500

Qy       1587 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1560

Qy       1647 TCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1706
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1620
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Qy        1707 TTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1766
               |||||||||||| ||||| |||||||||||||||||||||||||||||||||||||||||
Db        1621 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1680

Qy        1767 TGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1826
               ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1740

Qy        1827 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGA 1886
               ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        1741 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCATGA 1800

Qy        1887 TCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGA 1946
               ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        1801 TCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTATGA 1860

Qy        1947 TTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 2006
               ||||||||||||||||||||||:|||||:|||||||||||||||||||||||||||||||
Db        1861 TTTTATGGCTCTGGATAGACCGYCAACAYCATTAATAGATCGTGGGATAGCATTGCACAA 1920

Qy        2007 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGAAA 2066
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1921 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGAAA 1980

Qy        2067 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2126
               ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        1981 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGATGG 2040

Qy        2127 CTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2186
               ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2041 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2100

Qy        2187 AGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCT 2246
               ||||||||||||||||||||||| |||||||||||||||||||||| |||||||||||||
Db        2101 AGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2160

Qy        2247 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2161 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2220

Qy        2307 AGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGAC 2366
               |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        2221 AGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGAC 2280

Qy        2367 AAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTT 2426
               ||| |||||||||||||||||||||| ||||||||||||||||||||||||||||| |||
Db        2281 AAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGCTT 2340

Qy        2427 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2341 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2400

Qy        2487 CACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAA 2546
               ||||| |||||||| |||||||||||||||||||||||||||||||||||||| ||| 
Db        2401 CACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAG 2460

Qy        2547 AACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 2606
               |||||||||||||||||||||||||||||||  ||||| ||||||||||||||||   | 
Db        2461 AACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCCGN 2520

Qy        2607 AGAAGTA 2613
                |||| |
Db        2521 NGAAGAA 2527


RESULT 9
AAT42631
ID   AAT42631 standard; DNA; 2578 BP.
XX
AC   AAT42631;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (psbe2con.seq - clone pSJ90).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             24..2567
FT                   /*tag=  a
FT   sig_peptide     24..56
FT                   /*tag=  b
FT   mat_peptide     57..2564
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;    96WO-GB01075.
XX
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAW06400.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 32; Page 55-56; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;

  Query Match             93.2%;  Score 2465.8;  DB 17;  Length 2578;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 2482;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         135 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 194
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          56 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 115

Qy         195 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 254
               |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         116 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 175

Qy         255 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 314
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         176 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 235

Qy         315 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 374
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         236 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 295

Qy         375 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 434
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         296 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 355

Qy         435 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 494
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         356 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 415

Qy         495 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 554
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Db        416 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 475

Qy        555 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 535

Qy        615 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAAT 674
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        536 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 595

Qy        675 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTC 734
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        596 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 655

Qy        735 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 715

Qy        795 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 775

Qy        855 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 835

Qy        915 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTA 974
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||
Db        836 TGCTTGGATCAACTACTCTTCACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 895

Qy        975 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 955

Qy       1035 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1015

Qy       1095 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1016 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCA 1075

Qy       1155 AATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTT 1214
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1076 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1135

Qy       1215 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1195

Qy       1275 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1255

Qy       1335 TTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1394
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1256 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1315

Qy       1395 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1454
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1316 TGGTTATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAG 1375

Qy       1455 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATT 1514
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1376 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATT 1435

Qy       1515 TGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAA 1574
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1436 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1495

Qy       1575 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1555

Qy       1635 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1615

Qy       1695 AATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCA 1754
              |||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Db       1616 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1675

Qy       1755 TATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1814
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1676 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1735

Qy       1815 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1795

Qy       1875 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1855

Qy       1935 GGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 1994
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db       1856 GGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAT 1915

Qy       1995 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2054
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1975

Qy       2055 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2035

Qy       2115 CCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2174
              ||||||||||| ||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2095

Qy       2175 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCC 2234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       2096 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2155

Qy       2235 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2215

Qy       2295 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2275

Qy       2355 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATA 2414
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       2276 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATA 2335

Qy       2415 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2395

Qy       2475 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2455

Qy       2535 TGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2594
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2515

Qy       2595 AGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAA 2643
              |||||||||||||||  ||  ||  ||  ||  |||||  |||||||||  |||||||
Db       2516 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2564
```

RESULT 10
AAT42636

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ID   AAT42636 standard; DNA; 2576 BP.
XX
AC   AAT42636;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (86con.seq) cloned in QE32.
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 49-51; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;

  Query Match             92.7%;  Score 2451.8;  DB 17;  Length 2576;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 2480;  Conservative    0;  Mismatches   27;  Indels    2;  Gaps    1;

Qy        135 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 115

Qy        195 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        116 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 175

Qy        255 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 235

Qy        315 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 295

Qy        375 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 355

Qy        435 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 415

Qy        495 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 475

Qy        555 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 535

Qy        615 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAAT 674
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        536 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 595

Qy        675 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTC 734
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        596 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 655

Qy        735 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 715

Qy        795 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 775

Qy        855 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 835

Qy        915 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTA 974
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||| ||||
Db        836 TGCTTGGATCAACTACTC--TACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 893

Qy        975 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 953

Qy       1035 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1013

Qy       1095 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1073

Qy       1155 AATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTT 1214
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1074 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1133

Qy       1215 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1193

Qy       1275 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1253

Qy       1335 TTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1394
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1254 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1313

Qy       1395 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1454
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1314 TGGTTATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAG 1373

Qy       1455 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATT 1514
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||| | ||||
Db       1374 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATATTGATT 1433

Qy       1515 TGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAA 1574
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1434 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1493

Qy       1575 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1553

Qy       1635 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1694
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Db     1554 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1613

Qy     1695 AATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCA 1754
Db     1614 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1673

Qy     1755 TATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1814
Db     1674 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1733

Qy     1815 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1874
Db     1734 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1793

Qy     1875 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1934
Db     1794 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1853

Qy     1935 GGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 1994
Db     1854 GGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAT 1913

Qy     1995 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2054
Db     1914 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1973

Qy     2055 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2114
Db     1974 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2033

Qy     2115 CCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2174
Db     2034 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2093

Qy     2175 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCC 2234
Db     2094 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2153

Qy     2235 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2294
Db     2154 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2213

Qy     2295 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2354
Db     2214 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2273

Qy     2355 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATA 2414
Db     2274 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATA 2333

Qy     2415 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2474
Db     2334 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2393

Qy     2475 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2534
Db     2394 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2453

Qy     2535 TGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2594
Db     2454 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2513

Qy     2595 AGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAA 2643
Db     2514 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2562
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RESULT 11
AAV38720
ID   AAV38720 standard; DNA; 3090 BP.
XX
AC   AAV38720;
XX
DT   21-SEP-1998 (first entry)
XX
DE   Full length cassava tuber cDNA in pSJ146.
XX
KW   Starch branching enzyme; SBE; cassava; ss.
XX
OS   Manihot esculenta.
XX
FH   Key   Location/Qualifiers
FT   misc_feature   35..2760
FT   /*tag= a
FT   /note= "these nycleotides are SBE II sequence, the
FT   reminder are derived from the plamsid"
FT   CDS   131..2677
FT   /*tag= b
FT   /product= SBE II
XX
PN   WO9820145-A2.
XX
PD   14-MAY-1998.
XX
PF   04-NOV-1997;   97WO-GB03032.
XX
PR   05-NOV-1996;   96GB-0023095.
XX
PA   (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Jobling SA, Safford R;
XX
DR   WPI; 1998-286958/25.
DR   P-PSDB; AAW62600.
XX
PT   Starch branching gene from cassava - useful for producing altered
PT   plants giving modified starch
XX
PS   Claim 2; Fig 13; 67pp; English.
XX
CC   The present sequence encodes starch branching enzyme (SBE) II. It
CC   was isolated from cassava tubers. The products can be used for
CC   producing plants having altered starch quantities and qualities.
CC   They can also be used for producing altered plants such as cassava,
CC   banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
CC   and rice plants.
XX
SQ   Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;

Query Match 54.0%; Score 1429.4; DB 19; Length 3090;
Best Local Similarity 73.1%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 606; Indels 96; Gaps 2;

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Qy        7 TATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAATGGATTC 66
Db      140 TACACTGTATCAGGCATACGTTTTCCTTGTGCACCTTCACTCTACAAATCTCAGCTCACC 199

Qy       67 AGCAGTAATGGTGATCGGAGGAATGCTAATG---TTTCTGTATTCTTGAAAAAGCACTCT 123
Db      200 AGCTTCCATGGCGGTCGAAGGACCTCTTCTGGCCTTTCCTTCCTCTTGAAGAAGGAGCTG 259

Qy      124 CTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACA 183
Db      260 TTTCCTCGGAAGATCTTTGCTGGAAAGTCCTCTTATGAATCTGACTCCTCAAATTTAACT 319

Qy      184 GTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCA 243
Db      320 GTCTCTGCATCTGAGAAGGTCCTTGTTCCTGATGATCAGATTGATGGCTCTTCTTCTTCA 379

Qy      244 ACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTA 303
Db      380 ACATATCAATTAGAAACCACTGGCACAGTTTTGGAGGAATCCCAGGTTCTTGGTGATGCA 439

Qy      304 GATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCG 363
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Db    440 GAGAGTCTTGTGATGGAAGATGATAAGAATGTTGAGGAGGATGAAGTAAAAAAAGAGTCG 499

Qy    364 TCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAA 423

Db    500 ------------------------------------------------------------ 499

Qy    424 GAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGAT 483

Db    500 ---------------------------------GTTCCATTGCATGAGACAATTAGCATT 526

Qy    484 GAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTAT 543

Db    527 GGAAAAAGTGAATCTAAACCAAGGTCCATTCCTCCACCTGGCAGTGGGCAGAGAATATAT 586

Qy    544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603

Db    587 GACATAGATCCAAGCTTGGCAGGTTTCCGTCAGCATCTTGACTACCGATATTCACAGTAC 646

Qy    604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663

Db    647 AAAAGGCTGCGTGAGGAAATTGACAAGTATGAAGGTGGTTTGGATGCATTCTCTCGTGGA 706

Qy    664 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTT 723

Db    707 TTTGAAAAGTTTGGTTTCTTACGCAGTGAAACAGGAATAACTTATAGGGAATGGGCACCT 766

Qy    724 GGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATT 783

Db    767 GGAGCTACGTGGGCTGCACTTATTGGAGATTTCAACAATTGGAATCCTAATGCAGATGTC 826

Qy    784 ATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCT 843

Db    827 ATGACTCGGAATGAGTTTGGTGTCTGGGAGATTTTTTTGCCAAATAACGCAGATGGTTCA 886

Qy    844 CCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAG 903

Db    887 CCACCAATTCCTCATGGTTCTCGAGTAAAGATACGCATGGATACTCCATCTGGCATCAAA 946

Qy    904 GATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAAT 963

Db    947 GATTCAATTCCTGCTTGGATCAAGTTCTCAGTTCAGGCACCTGGTGAAATCCCATACAAT 1006

Qy    964 GGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAG 1023

Db   1007 GCCATATACTATGATCCACCAAAGGAGGAGAAGTATGTGTTCAAACATCCTCAGCCAAAG 1066

Qy   1024 AAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAA 1083

Db   1067 AGACCAAAATCACTTAGGATTTATGAATCTCATGTTGGGATGAGTAGTATGGAGCCAATA 1126

Qy   1084 ATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTAC 1143

Db   1127 ATTAACACATATGCCAACTTTAGAGATGATATGCTTCCTCGCATCAAAAAGCTTGGCTAC 1186

Qy   1144 AATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCAT 1203

Db   1187 AATGCTGTTCAGATCATGGCTATTCAAGAGCATTCCTATTATGCTAGTTTTGGGTACCAT 1246

Qy   1204 GTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTG 1263

Db   1247 GTCACAAACTTTTTTGCACCTAGCAGCCGATTTGGAACTCCTGATGATTTGAAGTCTTTA 1306

Qy   1264 ATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCA 1323

Db   1307 ATAGATAAAGCTCATGAGTTAGGGCTGCTTGTTCTCATGGATATTGTTCATAGCCATGCG 1366

Qy   1324 TCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCAC 1383

Db   1367 TCAAATAATACGTTGGATGGGCTGAACATGTTTGATGGTACGGATAGTCACTACTTCCAC 1426

Qy   1384 TCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGG 1443

Db   1427 TCCGGATCACGGGGTCATCATTGGTTGTGGGACTCTCGCCTTTTCAACTATGGAAGCTGG 1486

Qy   1444 GAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGAT 1503

Db   1487 GAGGTGCTAAGATTTCTTCTTTCAAATGCAAGATGGTGGTTGGAAGAGTACAGGTTTGAT 1546

Qy   1504 GGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGA 1563

Db   1547 GGTTTTAGATTTGATGGGGTGACTTCCATGATGTACACTCCCCATGGGTTGCAGGTAGCT 1606

Qy   1564 TTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTAT 1623

Db   1607 TTTACTGGCAACTACAATGAGTACTTTGGATATGCAACTGATGTAGATGCTGTGATTTAT 1666

Qy   1624 CTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAA 1683

Db   1667 TTGATGCTTGTGAATGATATGATTCACGGTCTTTTCCCTGAGGCTGTTACCATTGGTGAA 1726

Qy   1684 GATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGAC 1743

Db   1727 GATGTTAGCGGAAAGCCAACATTTTGCATTCCAGTGGAAGATGGTGGTGTTGGATTTGAT 1786

Qy   1744 TATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAG 1803

Db   1787 TACCGTCTCCACATGGCCATTGCCGATAAATGGATTGAGATTCTTAAGAAGAGAGATGAG 1846

Qy   1804 GATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGT 1863

Db   1847 GACTGGAAAATGGGTGACATTGTGCATACACTCACCAACAGAAGGTGGTTGGAAAAATGT 1906

Qy   1864 GTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGG 1923

Db   1907 GTTGCTTATGCTGAAAGTCATGACCAAGCTCTTGTTGGTGACAAAACTATTGCATTTTGG 1966

Qy   1924 CTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATA 1983

Db   1967 CTGATGGACAAGGACATGTACGACTTCATGGCTCGTGACAGACCATCTACTCCTCTTATA 2026

Qy   1984 GATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAA 2043

Db   2027 GATCGTGGAATAGCATTGCACAAAATGATCAGGCTTATTACCATGGGCTTAGGCGGAGAA 2086

Qy   2044 GGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGG 2103

Db   2087 GGATATTTGAATTTTATGGGAAATGAATTTGGACATCCTGAGTGGATTGATTTTCCAAGA 2146

Qy   2104 GCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAA 2163

Db   2147 GGGGATCGACATCTGCCCAATGGTAAAGTAATTCCAGGGAACAACCACAGTTATGATAAA 2206

Qy   2164 TGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAA 2223

Db   2207 TGCCGTCGTAGATTTGATCTAGGTGATGCAGACTATCTAAGATATCATGGAATGCAAGAG 2266

Qy   2224 TTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAG 2283

Db   2267 TTTGATCAGGCAATGCAACATCTTGAAGAAGCCTATGGTTTCATGACTTCTGAGCACCAG 2326

Qy   2284 TTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTT 2343

Db   2327 TATATATCACGGAAGGATGAAGGAGATCGGATCATTGTCTTTGAGAGGGGAAACCTTGTT 2386

Qy   2344 TTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAG 2403

Db   2387 TTTGTATTCAACTTTCATTGGACTAACAGCTATTCAGATTACCGAGTTGGCTGCTTCAAG 2446

Qy   2404 CCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGA 2463

Db   2447 TCAGGAAAGTACAAGATTGTTTTGGACTCGGATGATGGCTTGTTTGGAGGCTTCAACAGG 2506

Qy   2464 ATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCA 2523

Db   2507 CTTAGTCATGATGCCGAGCACTTCACCTTTGACGGGTGGTATGATAACCGGCCTCGGTCC 2566
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Qy       2524 ATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAA 2583
Db       2567 TTCATGGTATATGCACCATCTAGGACAGCAGTGGTCTATGCTTTAGTAGAAGATGAAGAG 2626

Qy       2584 GAAGAAGAAGAAGAAGAAGAAGAAGAAGTAG 2614
Db       2627 AATGAAGCAGAGAATGAAGTAGAAAGTGAAG 2657

RESULT 12
AAV38719
ID   AAV38719 standard; cDNA; 2913 BP.
XX
AC   AAV38719;
XX
DT   21-SEP-1998  (first entry)
XX
DE   Full length cassava tuber cDNA in pSJ107.
XX
KW   Starch branching enzyme; SBE; cassava; ss.
XX
OS   Manihot esculenta.
XX
FH   Key             Location/Qualifiers
FT   CDS             21..2531
FT                   /*tag=  a
FT                   /product= SBE II
XX
PN   WO9820145-A2.
XX
PD   14-MAY-1998.
XX
PF   04-NOV-1997;   97WO-GB03032.
XX
PR   05-NOV-1996;   96GB-0023095.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Jobling SA,  Safford R;
XX
DR   WPI; 1998-286958/25.
DR   P-PSDB; AAW62599.
XX
PT   Starch branching gene from cassava - useful for producing altered
PT   plants giving modified starch
XX
PS   Claim 2; Fig 4; 67pp; English.
XX
CC   The present sequence encodes starch branching enzyme (SBE) II. It
CC   was isolated from cassava tubers. The products can be used for
CC   producing plants having altered starch quantities and qualities.
CC   They can also be used for producing altered plants such as cassava,
CC   banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
CC   and rice plants.
XX
SQ   Sequence 2913 BP; 818 A; 549 C; 680 G; 866 T; 0 other;

  Query Match             51.5%;  Score 1362;  DB 19;  Length 2913;
  Best Local Similarity   75.9%;  Pred. No. 0;
  Matches 1683;  Conservative    0;  Mismatches  535;  Indels    0;  Gaps    0;

Qy        429 TGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATC 488
Db        347 TGTTGAAGATGAAGTAAATAAAGAATCTGTTCCAATGCGGGAGACAGTTAGCATCAGAAA 406

Qy        489 TGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAAT 548
Db        407 AATTGGATCTAAACCAAGGTCCATTCCTCCACCCGGCAGAGGGCAAAGAATATATGACAT 466

Qy        549 AGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAA 608
Db        467 AGATCCAAGCTTGACAGGCTTTCGTCAACACCTAGATTACCGGTATTCACAGTACAAAAG 526

Qy        609 ACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGA 668
Db        527 ACTCCGAGAAGAAATTGACAAGTATGAAGGTAGTCTGGATGCATTTTCTCGTGGCTATGA 586

Qy        669 AAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGC 728
Db        587 AAAGTTTGGTTTCTCACGCAGTGAAACAGGAATAACTTATAGAGAGTGGGCACCAGGAGC 646

Qy        729 CCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGAC 788
Db        647 TACGTGGGCTGCATTGATTGGAGATTTCAATAACTGGAATCCTAATGCAGATGTCATGAC 706

Qy        789 TCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGC 848
Db        707 TCAGAATGAGTGTGGTGTCTGGGAGATCTTTTTGCCGAATAATGCAGATGGTTCACCACC 766

Qy        849 AATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTC 908
Db        767 AATTCCCCATGGTTCTCGAGTAAAGATACGCATGGATACTCCATCTGGCAACAAAGATTC 826

Qy        909 CATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAAT 968
Db        827 TATTCCTGCTTGGATCAAGTTCTCAGTTCAAGCACCAGGTGAACTCCCATATAATGGCAT 886

Qy        969 ACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACC 1028
Db        887 ATACTATGATCCTCCCGAGGAGGAGAAGTATGTGTTCAAAAATCCTCAGCCAAAGAGACC 946

Qy       1029 AAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAA 1088
Db        947 AAAATCACTTCGGATTTATGAGTCGCACGTTGGAATGAGTAGTACGGAGCCAGTAATTAA 1006

Qy       1089 CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC 1148
Db       1007 CACATATGCCAACTTTAGAGATGATGTGCTTCCTCGCATCAAAAAGCTTGGCTACAATGC 1066

Qy       1149 GCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCAC 1208
Db       1067 TGTTCAGCTCATGGCTATTCAAGAGCATTCATATTATGCTAGTTTTGGGTATCACGTCAC 1126

Qy       1209 AAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGA 1268
Db       1127 AAACTTTTATGCAGCTAGCAGCCGATTTGGAACTCCTGATGATTTAAAGTCTCTAATAGA 1186

Qy       1269 TAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAA 1328
Db       1187 TAAAGCTCACGAGTTAGGTCTTCTTGTTCTCATGGATATTGTTCATAGCCATGCATCAAC 1246

Qy       1329 TAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGG 1388
Db       1247 TAATACGTTGGATGGGCTGAATATGTTTGATGGTACGGATGGTCACTACTTTCACTCTGG 1306

Qy       1389 AGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGT 1448
Db       1307 ACCACGGGGTCATCATTGGATGTGGGACTCTCGCCTTTTCAACTATGGAGCTGGGAGGT 1366

Qy       1449 ACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATT 1508
Db       1367 TCTAAGGTTTCTTCTTTCAAATGCAAGGTGGTGGTTGGATGAGTACAAGTTTGATGGGTT 1426

Qy       1509 TAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCAC 1568
Db       1427 CAGATTTGATGGGGTGACTTCAATGATGTACACCCATCATGGATTGCAGGTAGATTTTAC 1486

Qy       1569 TGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGAT 1628
Db       1487 CGGCAACTACAATGAATACTTTGGATATGCAACTGATGTAGATGCTGTGGTTTATTTGAT 1546

Qy       1629 GCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGT 1688
Db       1547 GCTGTTGAATGATATGATTCATGGTCTCTTCCCAGAGGCTGTCACCATTGGTGAAGATGT 1606

Qy       1689 TAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCG 1748
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Db     1607 TAGTGGAATGCCAACAGTTTGCATTCCGGTTGAAGATGGTGGTGTTGGCTTTGATTATCG 1666

Qy     1749 GCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTG 1808
Db     1667 TCTCCACATGGCTGTTGCTGATAAATGGGTTGAGATTATTCAGAAGAGAGATGAAGATTG 1726

Qy     1809 GAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTC 1868
Db     1727 GAAAATGGGTGACATTGTACATATGCTGACCAACAGGCGGTGGTTGGAAAAGTGTGTTTC 1786

Qy     1869 ATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGAT 1928
Db     1787 TTATGCTGAAAGTCATGACCAGGCCCTTGTTGGTGACAAAACTATTGCATTTTGGCTGAT 1846

Qy     1929 GGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCG 1988
Db     1847 GGACAAGGATATGTATGACTTCATGGCTCTTGACAGACCATCTACTCCTCTCATAGATCG 1906

Qy     1989 TGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTA 2048
Db     1907 TGGAGTAGCATTGCACAAAATGATCAGGCTTATTACCATGGGATTAGGCGGAGAAGGATA 1966

Qy     2049 CCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGA 2108
Db     1967 TTTGAATTTTATGGGAAATGAATTTGGACACCCCGAGTGGATTGATTTTCCAAGAGGTGA 2026

Qy     2109 ACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAG 2168
Db     2027 TCTACATCTTCCCAGTGGTAAATTTGTTCCTGGGAACAATTACAGTTATGATAAATGCCG 2086

Qy     2169 ACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGA 2228
Db     2087 GCGTAGGTTTGATCTAGGCAATTCAAAGCATCTGAGATATCATGGAATGCAAGAGTTTGA 2146

Qy     2229 CCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCAT 2288
Db     2147 TCAAGCAATTCAGCATCTTGAAGAAGCCTATGGTTTCATGACTTCTGAGCACCAATACAT 2206

Qy     2289 ATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGT 2348
Db     2207 ATCACGGAAGGATGAAAGGGATCGGATCATTGTCTTCGAGAGGGGAAACCTCGTTTTTGT 2266

Qy     2349 CTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGG 2408
Db     2267 ATTCAATTTTCATTGGACTAGCAGCTATTCGGATTACCGAGTTGGCTGCTTAAAGCCAGG 2326

Qy     2409 AAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGA 2468
Db     2327 AAAGTACAAGATAGTCTTGGATTCAGATGATCCTTTGTTTGGAGGCTTTGGCAGGCTTAG 2386

Qy     2469 TCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTAT 2528
Db     2387 TCATGATGCAGAGCACTTCAGCTTTGAAGGGTGGTACGATAACCGGCCTCGATCCTTCAT 2446

Qy     2529 GGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGA 2588
Db     2447 GGTGTACACACCATGTAGAACAGCAGTGGTCTATGCTTTAGTGGAGGATGAAGTGGAGAA 2506

Qy     2589 AGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2646
Db     2507 TGAATTGGAACCTGTCGCCGGTTAAGATATATCTTAACAACAGGTTCTGAAGCAGGAA 2564
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RESULT 13
AAC45939
ID   AAC45939 standard; DNA; 2715 BP.
XX
AC   AAC45939;
XX
DT   18-OCT-2000 (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
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PR   23-APR-1999;   99US-0130891.
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PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
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PR   06-MAY-1999;   99US-0132486.
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PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
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PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
PR   14-JUN-1999;   99US-0139119.
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PR   16-JUN-1999;   99US-0139453.
PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
PR   18-JUN-1999;   99US-0139457.
PR   18-JUN-1999;   99US-0139458.
PR   18-JUN-1999;   99US-0139459.
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PR   18-JUN-1999;   99US-0139462.
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PR   18-JUN-1999;   99US-0139750.
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PR   22-JUN-1999;   99US-0139899.

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PR   08-JUL-1999;   99US-0142803.
PR   09-JUL-1999;   99US-0142920.
PR   12-JUL-1999;   99US-0142977.
PR   13-JUL-1999;   99US-0143542.
PR   14-JUL-1999;   99US-0143624.
PR   15-JUL-1999;   99US-0144005.
PR   16-JUL-1999;   99US-0144085.
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PR   19-JUL-1999;   99US-0144325.
PR   19-JUL-1999;   99US-0144331.
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PR   23-JUL-1999;   99US-0145218.
PR   23-JUL-1999;   99US-0145224.
PR   26-JUL-1999;   99US-0145276.
PR   27-JUL-1999;   99US-0145913.
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PR   27-JUL-1999;   99US-0145919.
PR   28-JUL-1999;   99US-0145951.
PR   02-AUG-1999;   99US-0146386.
PR   02-AUG-1999;   99US-0146388.
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PR   03-AUG-1999;   99US-0147038.
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PR   04-AUG-1999;   99US-0147302.
PR   05-AUG-1999;   99US-0147192.
PR   05-AUG-1999;   99US-0147260.
PR   06-AUG-1999;   99US-0147303.
PR   06-AUG-1999;   99US-0147416.
PR   09-AUG-1999;   99US-0147493.
PR   09-AUG-1999;   99US-0147935.
PR   10-AUG-1999;   99US-0148171.
PR   11-AUG-1999;   99US-0148319.
PR   12-AUG-1999;   99US-0148341.
PR   13-AUG-1999;   99US-0148565.
PR   13-AUG-1999;   99US-0148684.
PR   16-AUG-1999;   99US-0149368.
PR   17-AUG-1999;   99US-0149175.
PR   18-AUG-1999;   99US-0149426.
PR   20-AUG-1999;   99US-0149722.
PR   20-AUG-1999;   99US-0149723.
PR   20-AUG-1999;   99US-0149929.
PR   23-AUG-1999;   99US-0149902.
PR   23-AUG-1999;   99US-0149930.
PR   25-AUG-1999;   99US-0150566.
PR   26-AUG-1999;   99US-0150884.
PR   27-AUG-1999;   99US-0151065.
PR   27-AUG-1999;   99US-0151066.
PR   27-AUG-1999;   99US-0151080.
PR   30-AUG-1999;   99US-0151303.
PR   31-AUG-1999;   99US-0151438.
PR   01-SEP-1999;   99US-0151930.
PR   07-SEP-1999;   99US-0152363.
PR   10-SEP-1999;   99US-0153070.
PR   13-SEP-1999;   99US-0153758.
PR   15-SEP-1999;   99US-0154018.
PR   16-SEP-1999;   99US-0154039.
PR   20-SEP-1999;   99US-0154779.
PR   22-SEP-1999;   99US-0155139.
PR   23-SEP-1999;   99US-0155486.
PR   24-SEP-1999;   99US-0155659.
PR   28-SEP-1999;   99US-0156458.
PR   29-SEP-1999;   99US-0156596.
PR   04-OCT-1999;   99US-0157117.
PR   05-OCT-1999;   99US-0157753.
PR   06-OCT-1999;   99US-0157865.
PR   07-OCT-1999;   99US-0158029.
PR   08-OCT-1999;   99US-0158232.
PR   12-OCT-1999;   99US-0158369.
PR   13-OCT-1999;   99US-0159293.
PR   13-OCT-1999;   99US-0159294.
PR   13-OCT-1999;   99US-0159295.
PR   14-OCT-1999;   99US-0159329.
PR   14-OCT-1999;   99US-0159330.
PR   14-OCT-1999;   99US-0159331.
PR   14-OCT-1999;   99US-0159637.
PR   14-OCT-1999;   99US-0159638.
PR   18-OCT-1999;   99US-0159584.
PR   21-OCT-1999;   99US-0160741.
PR   21-OCT-1999;   99US-0160767.
PR   21-OCT-1999;   99US-0160768.
PR   21-OCT-1999;   99US-0160770.
PR   21-OCT-1999;   99US-0160814.
PR   21-OCT-1999;   99US-0160815.
PR   22-OCT-1999;   99US-0160980.
PR   22-OCT-1999;   99US-0160981.
PR   22-OCT-1999;   99US-0160989.
PR   25-OCT-1999;   99US-0161404.
PR   25-OCT-1999;   99US-0161405.
PR   25-OCT-1999;   99US-0161406.
PR   26-OCT-1999;   99US-0161359.
PR   26-OCT-1999;   99US-0161360.
PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             48.8%;  Score 1290;  DB 21;  Length 2715;
  Best Local Similarity   76.1%;  Pred. No. 0;
  Matches 1590;  Conservative    0;  Mismatches  500;  Indels    0;  Gaps    0;

Qy        503 AGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGA 562
              |||||   || || || ||||||  |||  |||  || ||||| || || ||  | ||||
Db        443 AGAGGAAGATTCCACCTCCTGGAGATGGAAGAGAATATATGACATTGATCCTATGTTGA 502

Qy        563 CAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAA 622
                |   ||||| | || |||||||||  | |||  |||||||  |||||| | || | ||
Db        503 ACAGTCATCGTAATCATCTTGATTACCGATATGGGCAGTACAGAAAACTGCGTGAAGAAA 562

Qy        623 TTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCA 682
              |||||||| |||| ||||||||||| || ||||||||||||||||||| | | || ||||
Db        563 TTGACAAGAATGAAGGTGGTTTGGAGGCATTTTCTCGTGGTTATGAAATATTTGGCTTCA 622

Qy        683 CTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCC 742
              |||| || || || |||||||||||||| || ||||| |  || ||  || ||||  | |
Db        623 CTCGAAGCGCCACTGGTATCACTTACCGGGAATGGGCACCGGGAGCTAAGGCAGCATCAC 682

Qy        743 TCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTG 802
              | || |||||||| || || ||| | || ||  ||||  ||||| ||||||| || ||||
Db        683 TGATCGGAGATTTTAATAACTGGAATGCGAAATCTGATGTTATGGCTCGGAACGACTTTG 742

Qy        803 GTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGT 862
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Db        743 GTGTGTGGGAAATATTTCTGCCAAATAATGCTGATGGCTCACCAGCAATTCCCCATGGCT 802
Qy        863 CCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGA 922
Db        803 CCCGTGTGAAGATCCGCATGGATACCCCATCTGGTATTAAAGACTCCATTCCAGCTTGGA 862
Qy        923 TCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCAC 982
Db        863 TCAAGTATTCTGTCCAGCCACCTGGCGAGATCCCATATAATGGAGTATATTATGACCCTC 922
Qy        983 CCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAA 1042
Db        923 CTGAGGAGGATAAATATGCGTTCAAACATCCTCGTCCAAAGAAACCCACATCGCTGCGTA 982
Qy       1043 TATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATT 1102
Db        983 TATATGAATCACATGTTGGAATGAGTAGTACGGAACCAAAGATAAATACATATGCCAACT 1042
Qy       1103 TTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGG 1162
Db       1043 TTAGAGATGATGTACTTCCCCGTATAAAAAAGCTAGGCTATAATGCTGTGCAGATAATGG 1102
Qy       1163 CTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCAC 1222
Db       1103 CCATTCAAGAGCATGCCTACTATGCCAGCTTTGGGTATCATGTGACAAATTTTTTCGCAC 1162
Qy       1223 CAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGC 1282
Db       1163 CTAGCAGCCGCTTTGGAACACCTGATGACCTTAAATCTTTGATAGACAAAGCTCATGAGC 1222
Qy       1283 TAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATG 1342
Db       1223 TAGGTCTGGTTGTTCTGATGGATATTGTGCACAGCCATGCATCAAAAAACACACTGGATG 1282
Qy       1343 GACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATC 1402
Db       1283 GCCTGGACATGTTTGATGGTACTGATGGTCAATATTTCCACTCTGGATCGCGTGGTTATC 1342
Qy       1403 ATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTC 1462
Db       1343 ATTGGATGTGGGATTCTCGTCTTTTCAATTACGGAAGCTGGGAAGTGCTTAGGTATCTTC 1402
Qy       1463 TCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTG 1522
Db       1403 TTTCCAACGCGAGATGGTGGCTGGAAGAATACAAGTTTGATGGGTTCAGATTTGATGGTG 1462
Qy       1523 TGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGG 1582
Db       1463 TGACTTCCATGATGTACACTCATCATGGACTGCAGGTCGAATTTACTGGGAATTACAATG 1522
Qy       1583 AATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATC 1642
Db       1523 AGTACTTTGGATATTCTACTGATGTTGACGCTGTGGTCTATCTAATGCTGGTGAACGATT 1582
Qy       1643 TTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGA 1702
Db       1583 TGATTCATGGGCTATACCCTGAGGCTATTGTTGTCGGCGAAGATGTTAGCGGGATGCCAG 1642
Qy       1703 CATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAA 1762
Db       1643 CTTTTTGCGTTCCTGTCGAAGACGGTGGTGTGGGTTTTGACTACCGTCTACACATGGCAG 1702
Qy       1763 TTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATA 1822
Db       1703 TGGCAGATAAATGGATTGAGCTTCTTAAGAAGAGAGACGAGGACTGGCAGGTTGGTGATA 1762
Qy       1823 TTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTC 1882
Db       1763 TAACTTTCACGCTTACCAACAGGAGGTGGGGAGAAAAATGTGTCGTCTATGCAGAGAGTC 1822
Qy       1883 ATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGT 1942
Db       1823 ATGATCAAGCCCTTGTTGGAGACAAAACGATAGCTTTCTGGCTAATGGATAAGGACATGT 1882
Qy       1943 ATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGC 2002
Db       1883 ATGATTTCATGGCCGTTGATAGACAGGCCACTCCGCGTGTAGACCGTGGGATTGCTTTAC 1942
Qy       2003 ACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGG 2062
Db       1943 ACAAAATGATCCGTCTCATTACGATGGGATTGGGTGGAGAAGGATACCTCAATTTCATGG 2002
Qy       2063 GAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTG 2122
Db       2003 GAAACGAATTTGGACACCCAGAATGGATCGACTTCCCAAGGACCGACCAGCACCTTCCTG 2062
Qy       2123 ATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACC 2182
Db       2063 ATGGCAGAGTCATCGCTGGGAATAATGGTAGTTATGATAAATGCCGACGTAGGTTTGATC 2122
Qy       2183 TGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGT 2242
Db       2123 TGGGAGATGCAGAATATCTTAGATACCATGGACTACAAGAGTTTGATCGAGCAATGCAAA 2182
Qy       2243 ATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATG 2302
Db       2183 ATCTAGAGGAGACGTATGGTTTCATGACTTCAGAGCACCAGTACATATCCCGCAAGGATG 2242
Qy       2303 AAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACT 2362
Db       2243 AAGGAGACAGAGTCATTGTATTCGAGAGAGGTAACTTGCTCTTCGTCTTCAACTTCCACT 2302
Qy       2363 GGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTG 2422
Db       2303 GGACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAAGTACAAAATCG 2362
Qy       2423 CCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAAT 2482
Db       2363 TTTTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGACTCCGCGGAGT 2422
Qy       2483 ATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTT 2542
Db       2423 TTTTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGTGTATGCACCGT 2482
Qy       2543 GTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAA 2592
Db       2483 GCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGAA 2532
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RESULT 14
AAV05639
ID   AAV05639 standard; cDNA to mRNA; 3015 BP.
XX
AC   AAV05639;
XX
DT   01-MAY-1998  (first entry)
XX
DE   Rice type IV starch branching enzyme cDNA.
XX
KW   Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             129..2654
FT                   /*tag=  a
FT   sig_peptide     129..287
FT                   /*tag=  b
FT   mat_peptide     288..2651
FT                   /*tag=  c
FT                   /product= type_IV_starch_branching_enzyme
XX
PN   JP10004970-A.
XX
PD   13-JAN-1998.
```

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XX
PF   24-JUN-1996;    96JP-0162983.
XX
PR   24-JUN-1996;    96JP-0162983.
XX
PA   (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA   (MITK ) MITSUI TOATSU CHEN INC.
XX
DR   WPI; 1998-133625/13.
DR   P-PSDB; AAW41763.
XX
PT   Rice starch branching enzyme gene - synthesises amylopectin to yield
PT   high quality starch
XX
PS   Claim 4; Pages 5-8; 13pp; Japanese.
XX
CC   The present sequence encodes the rice type IV starch branching
CC   enzyme, which has the ability to synthesise amylopectin. The
CC   quality of starch is improved by the use of the protein.
XX
SQ   Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;

  Query Match            47.8%;  Score 1264.8;  DB 19;  Length 3015;
  Best Local Similarity  75.0%;  Pred. No. 0;
  Matches 1581;  Conservative    0;  Mismatches  527;  Indels    0;  Gaps    0;

Qy        480 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 539
Db        554 TGAACCAACTGTGGAGGATAAACCACGAGTTATCCCACCACCAGGAGATGGGCAGAAGAT 613

Qy        540 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 599
Db        614 ATACCAAATTGACCCAATGCTGGAAGGATTTCGGAACCATCTTGACTACCGATACAGTGA 673

Qy        600 GTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCG 659
Db        674 ATACAAGAGAATGCGTGCAGCTATTGACCAACATGAAGGTGGCTTGGATGCATTTTCTCG 733

Qy        660 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 719
Db        734 TGGTTACGAAAAGCTTGGATTCACCCGCAGCGCTGAAGGCATTACCTACCGAGAATGGGC 793

Qy        720 TCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 779
Db        794 ACCTGGAGCACAGTCTGCAGCATTAGTAGGTGACTTCAACAATTGGAACCCAAATGCAGA 853

Qy        780 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 839
Db        854 TACTATGACCAGAAATGAGTATGGTGTTTGGGAGATTTCCCTGCCTAACAATGCTGATGG 913

Qy        840 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGT 899
Db        914 ATCCCCTGCTATTCCTCATGGCTCACGTGTAAAGATTCGGATGGATACACCATCTGGCGT 973

Qy        900 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 959
Db        974 AAAGGATTCAATTCCTGCCTGGATTAAGTTTGCTGTGCAGGCTCCAGGTGAAATACCGTA 1033

Qy        960 TAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCC 1019
Db       1034 CAACGGTATATATTATGATCCACCTGAAGAAGAAAAATATGTATTCCAACATCCTCAACC 1093

Qy       1020 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1079
Db       1094 TAAACGACCAAATTCGCTGCGGATATATGAATCACATATTGGAATGAGTAGCCCGGAACC 1153

Qy       1080 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGG 1139
Db       1154 GAAGATAAACACATATGCTAATTTTAGGGATGAGGTGCTACCAAGAATTAAAAAGCTTGG 1213

Qy       1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199
Db       1214 GTACAATGCTGTACAGATAATGGCAATCCAGGAGCACTCTTATTACGCAAGCTTTGGGTA 1273

Qy       1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1259
Db       1274 TCATGTTACTAACTTCTTTGCGCCAAGTAGCCGTTTCGGAACCCCAGAAGACTTGAAATC 1333

Qy       1260 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1319
Db       1334 TCTGATTGATAAAGCTCACGAGCTTGGTTTGCTTGTACTTATGGATATTGTTCACAGTCA 1393

Qy       1320 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT 1379
Db       1394 TGCATCAAACAATACCCTGGATGGTTTGAATGGTTTTGATGGTACTGATACACATTACTT 1453

Qy       1380 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1439
Db       1454 CCATGGTGGACCACGGGGTCATCACTGGATGTGGGATTCTCGCCTGTTCAACTATGGGAG 1513

Qy       1440 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATT 1499
Db       1514 ITGGGAAGTTTTAAGATATTTACTGTCGAATGCAAGGTGGTGGCTTGAAGAATACAAGTT 1573

Qy       1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559
Db       1574 TGATGGGTTTCGATTTGATGGGGTGACCTCCATGATGTATACTCATCATGGTTTACAGGT 1633

Qy       1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619
Db       1634 GGCATTTACTGGCAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCAGTAGT 1693

Qy       1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
Db       1694 TTACTTGATGCTGGTGAACGATCTAATTCATGGGCTTTATCCTGAGGCTGTAGCCATTGG 1753

Qy       1680 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTT 1739
Db       1754 TGAAGATGTCAGCGGGATGCCCACATTTTGTATTCCTGTTCAAGATGGTGGTGTTGGTTT 1813

Qy       1740 TGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGA 1799
Db       1814 TGACTATCGTTTGCATATGGCTGTACCGGACAAATGGATCGAACTCCTCAAGCAAAGTGA 1873

Qy       1800 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 1859
Db       1874 CGAATATTGGAAAATGGGTGATATCGTGCACACCCTAACGAATAGAAGGTGGTCAGAGAA 1933

Qy       1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
Db       1934 GTGTGTTACTTATGCAGAAAGTCATGACCAAGCACTAGTTGGTGACAAGACTATTGCATT 1993

Qy       1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
Db       1994 CTGGTTGATGGATAAGGATATGTATGATTTTATGGCTCTAGACAGACCTTCAACACCTCG 2053

Qy       1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db       2054 CATTGATCGTGGGATAGCATTACATAAAATGATTAGGCTTGTCACCATGGGCTTAGGAGG 2113

Qy       2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db       2114 CGAAGGCTATCTTAATTTCATGGGAAATGAGTTTGGGCATCCTGAATGGATAGATTTCCC 2173

Qy       2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db       2174 AAGAGGCCCGCAAAGTCTTCCAAATGGCTCGGTCCTCCCAGGAAACAACTACAGTTTTGA 2233

Qy       2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db       2234 TAAATGCCGTCGTAGATTTGACCTTGGAGATGCAGATTATCTTAGATATCATGGTATGCA 2293

Qy       2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2279
Db       2294 AGAGTTTGATCAGGCCATGCAGCATCTTGAGGAAAAATATGGATTCATGACATCTGAGCA 2353
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Qy        2280 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2339
Db        2354 CCAGTATATATCGCGCAAACACGAGGAGGATAAGGTGATCATCTTCGAGAGAGGAGATTT 2413

Qy        2340 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCT 2399
Db        2414 GGTATTCGTGTTCAACTTCCACTGGAGTAATAGCTATTTTGACTATCGCGTCGGTTGTTT 2473

Qy        2400 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2459
Db        2474 AAAGCCTGGAAAGTACAAGATTGTGTTGGACTCAGACGATGGCCTCTTTGGTGGATTCAG 2533

Qy        2460 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2519
Db        2534 TCGGCTTGATCATGATGCTGAGTACTTCACTGCTGACTGGCCGCATGACAACAGACCATG 2593

Qy        2520 TTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGA 2579
Db        2594 TTCATTCTCGGTGTACACCCCAAGCAGAACCGCCGTCGTGTATGCACTTACAGAGGACTA 2653

Qy        2580 AGAAGAAG 2587
Db        2654 ATGATCAG 2661
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RESULT 15
AAQ73750
ID   AAQ73750 standard; cDNA to mRNA; 2919 BP.
XX
AC   AAQ73750;
XX
DT   05-JUL-1995  (first entry)
XX
DE   Rice starch branching enzyme.
XX
KW   Starch branching enzyme; rice; starch content; ds.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..127
FT                   /*tag=  a
FT   transit_peptide 128..322
FT                   /*tag=  b
FT   mat_peptide     323..2606
FT                   /*tag=  c
FT                   /product= branching_enzyme
FT   3'UTR           2603..2919
FT                   /*tag=  d
XX
PN   JP06261767-A.
XX
PD   20-SEP-1994.
XX
PF   22-OCT-1993;    93JP-0265171.
XX
PR   29-OCT-1992;    92JP-0291719.
XX
PA   (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX
DR   WPI; 1994-337418/42.
DR   P-PSDB; AAR60811.
XX
PT   New gene of branching enzyme of rice starch - useful for
PT   increasing starch yield of rice grains
XX
PS   Claim 1; Page 9-12; 13pp; Japanese.
XX
CC   The rice starch branching enzyme is encoded by the cDNA sequence
CC   AAQ73750. The starch content of rice grains can be increased by
CC   increasing the expression of branching enzyme in rice plants.
XX
SQ   Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 other;
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  Query Match             47.3%;  Score 1251.2;  DB 15;  Length 2919;
  Best Local Similarity   74.4%;  Pred. No. 1.1e-314;
  Matches 1577;  Conservative    0;  Mismatches  543;  Indels    0;  Gaps    0;

Qy         476 TTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGA 535
Db         504 TTGAAGAATTAGCTGCTGAGCAGAAACCACGAGTTGTCCCACCAACAGGAGATGGGCAAA 563

Qy         536 AGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATT 595
Db         564 AAATATTCCAGATGGACTCTATGCTTAATGGCTATAAGTACCATCTTGAATATCGATATA 623

Qy         596 CACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTT 655
Db         624 GCCTATATAGGAGACTGCGTTCAGACATTGATCAGTATGAAGGAGGACTGGAAACATTTT 683

Qy         656 CTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGT 715
Db         684 CTCGCGGTTATGAGAAGTTTGGATTTAATCACAGTGCTGAAGGTGTCACTTATCGAGAAT 743

Qy         716 GGGCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATG 775
Db         744 GGGCTCCCGGGGCACATTCTGCAGCATTAGTAGGTGACTTCAACAATTGGAATCCAAATG 803

Qy         776 CTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGG 835
Db         804 CAGACCGCATGAGCAAAAATGAGTTTGGTGTTTGGGAGATTTTTCTGCCTAACAATGCTG 863

Qy         836 ATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAG 895
Db         864 ATGGCTCATCTCCTATTCCACATGGCTCACGTGTAAAGGTGCGAATGGAAACTCCATCTG 923

Qy         896 GTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTC 955
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Job time : 565.364 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:31:27 ; Search time 115.381 Seconds
(without alignments)
7032.959 Million cell updates/sec

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Perfect score: 2646
Sequence: 1 ATGGTGTATACACTCTCTGG..........AAGTAGTAGTAGAAGAAGAA 2646

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2581	97.5	3074	4	US-09-087-277-1	Sequence 1, Appli
	2	2581	97.5	3074	4	US-09-658-499-1	Sequence 1, Appli
	3	1369.8	51.8	1393	4	US-09-087-277-3	Sequence 3, Appli
	4	1369.8	51.8	1393	4	US-09-658-499-3	Sequence 3, Appli
	5	1180.4	44.6	2665	4	US-09-257-894-1	Sequence 1, Appli
	6	1180.4	44.6	2725	3	US-08-941-445A-14	Sequence 14, Appl
	7	1033	39.0	2087	4	US-09-257-894-9	Sequence 9, Appli
c	8	1031.4	39.0	2165	4	US-09-257-894-8	Sequence 8, Appli
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	16	542	20.5	1865	4	US-09-257-894-20	Sequence 20, Appl
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ALIGNMENTS

RESULT 1
US-09-087-277-1
; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Unknown
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; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
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; NAME/KEY: mat_peptide
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; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
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; OTHER INFORMATION: or Phe.
; FEATURE:

✓ (2e date to late

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;   LOCATION: (1404)..(1406)
;   OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1428)..(1430)
;   OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
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;   LOCATION: (1896)..(1898)
;   OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
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;   LOCATION: (2154)..(2156)
;   OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

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Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
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Db       1989 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2048
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Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2049 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2108

Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
              ||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2109 TGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTCAACATCATTA 2168

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2169 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2228

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2229 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2288

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       2289 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2348

Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2349 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2408

Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       2409 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2468

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2469 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2528

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       2529 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTG 2588

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2589 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2648

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2649 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2708

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
              ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db       2709 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2768

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
              |||||||||||||||||| || || || || || ||||| ||||| || |
Db       2769 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822
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RESULT 2
US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/09/658,499
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER: 09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   NAME/KEY: CDS
;   LOCATION: (189)..(2825)
;   NAME/KEY: sig_peptide
;   LOCATION: (189)..(332)
;   NAME/KEY: mat_peptide
;   LOCATION: (333)..(2825)
;   NAME/KEY: misc_feature
;   LOCATION: (92)..(2156)
;   OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
;   OTHER INFORMATION: n wherein n = A, C, G or T.
;   NAME/KEY: misc_feature
;   LOCATION: (285)..(287)
;   OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1404)..(1406)
;   OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1428)..(1430)
;   OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;   NAME/KEY: misc_feature
;   LOCATION: (1896)..(1898)
;   OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (2154)..(2156)
;   OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

  Query Match             97.5%;  Score 2581;  DB 4;  Length 3074;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 2599;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;
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Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 248

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        249 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTTGAAAAAGCAC 308

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        309 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCT 368

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 428

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 488

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        489 GTAGATAGTTCAACAATGGAACACGCTAGGCAGATTAAAACTGAGAACGATGACGTTGAG 548

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 608
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Qy    421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
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Db    609 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 668

Qy    481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 728

Qy    541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 788

Qy    601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    789 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 848

Qy    661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 908

Qy    721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 CCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 968

Qy    781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1028

Qy    841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1088

Qy    901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
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Db   1089 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1148

Qy    961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1208

Qy   1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1268

Qy   1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1328

Qy   1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
          ||||||||| |||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1329 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1388

Qy   1201 CATGTCACAAATTTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Db   1389 CATGTCACAAATTTTTTTNGCACCAAGCAGCCGTTTGGAACNCCCGACGACCTTAAGTCT 1448

Qy   1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
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Db   1449 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1508

Qy   1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
          ||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||
Db   1509 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1568

Qy   1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1628

Qy   1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   1629 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTT 1688

Qy   1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
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Db   1689 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1748

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Qy   1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
          |||||||||||||||||||||||||||| ||||||||| ||||| |||||||||||||||
Db   1869 GAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1928

Qy   1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1929 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1988

Qy   1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2048

Qy   1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
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Db   2049 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2108

Qy   1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
          ||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2109 TGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTCAACATCATTA 2168

Qy   1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2228

Qy   2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2288

Qy   2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   2289 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2348

Qy   2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2408

Qy   2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2468

Qy   2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2528

Qy   2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   2529 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTG 2588

Qy   2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2648

Qy   2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2649 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2708

Qy   2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
          ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db   2709 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2768

Qy   2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
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Db     2769 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822

RESULT 3
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT: KHOSNOODI, Jamshid
;  APPLICANT: LARSSON, Clas-Tomas
;  APPLICANT: LARSSON, Hakan
;  APPLICANT: RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/09/087,277B
;  CURRENT FILING DATE: 1998-05-29
;  EARLIER APPLICATION NUMBER: PCT/SE96/01558
;  EARLIER FILING DATE: 1996-11-28
;  EARLIER APPLICATION NUMBER: SE 9504272-7
;  EARLIER FILING DATE: 1995-11-29
;  EARLIER APPLICATION NUMBER: SE 9601506-0
;  EARLIER FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-087-277-3

  Query Match             51.8%;  Score 1369.8;  DB 4;  Length 1393;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      819 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 878
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Db        1 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

Qy      879 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 938
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 120

Qy      939 GCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTA 998
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      121 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 180

Qy      999 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 1058
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 240

Qy     1059 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 1118
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 300

Qy     1119 TCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTC 1178
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      301 TCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 360

Qy     1179 TTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGG 1238
            |||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||| 
Db      361 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGA 420

Qy     1239 AACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 1298
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 480

Qy     1299 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 1358
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 540

Qy     1359 CTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 1418
            | |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 600

Qy     1419 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 1478
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 660

Qy     1479 GTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 1538
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 720

Qy     1539 TATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 1598
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 780

Qy     1599 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 1658
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 840

Qy     1659 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGT 1718
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      841 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGT 900

Qy     1719 CCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGAT 1778
             ||||| |||||||||||||||||||||||||||||||||||||||||||| ||||
Db      901 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 960

Qy     1779 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1838
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1020

Qy     1839 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1898
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1080

Qy     1899 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1958
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1140

Qy     1959 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2018
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 1200

Qy     2019 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2078
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 1260

Qy     2079 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCC 2138
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Db       1261 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 1320

Qy       2139 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 1380

Qy       2199 TTTAAGATACCGT 2211
              |||||||||||||
Db       1381 TTTAAGATACCGT 1393


RESULT 4
US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/09/658,499
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER: 09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-658-499-3

  Query Match             51.8%;  Score 1369.8;  DB 4;  Length 1393;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        819 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

Qy        879 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 120

Qy        939 GCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTA 998
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 180

Qy        999 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 240

Qy       1059 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 300

Qy       1119 TCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTC 1178
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        301 TCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 360

Qy       1179 TTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGG 1238
              |||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||| 
Db        361 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGA 420

Qy       1239 AACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 1298
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 480

Qy       1299 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 1358
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Db        481 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 540

Qy       1359 CTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 1418
              | |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 600

Qy       1419 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 1478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 660

Qy       1479 GTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 1538
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 720

Qy       1539 TATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 1598
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 780

Qy       1599 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 1658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 840

Qy       1659 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGT 1718
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        841 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGT 900

Qy       1719 CCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGAT 1778
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        901 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 960

Qy       1779 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1020

Qy       1839 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1080

Qy       1899 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1140

Qy       1959 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2018
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 1200

Qy       2019 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2078
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Db     1201 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 1260

Qy     2079 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCC 2138

Db     1261 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 1320

Qy     2139 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2198

Db     1321 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 1380

Qy     2199 TTTAAGATACCGT 2211

Db     1381 TTTAAGATACCGT 1393
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RESULT 5
US-09-257-894-1
; Sequence 1, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:    2665 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..2476
US-09-257-894-1

  Query Match            44.6%;  Score 1180.4;  DB 4;  Length 2665;
  Best Local Similarity  72.7%;  Pred. No. 0;
  Matches 1523;  Conservative    0;  Mismatches  571;  Indels    0;  Gaps    0;
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too late

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Qy      480 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 539

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Db      561 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 620

Qy      720 TCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 779

Db      621 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACTTCAACAACTGGGATCCAAATGCAGA 680

Qy      780 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 839

Db      681 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 740

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Qy      900 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 959

Db      801 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 860

Qy      960 TAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCC 1019

Db      861 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 920

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Qy     1080 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGG 1139

Db      981 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 1040

Qy     1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199

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Qy     1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTC 1259

Db     1101 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1160

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Qy     1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559

Db     1401 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 1460

Qy     1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619

Db     1461 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 1520
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Qy       1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
Db       1521 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 1580

Qy       1680 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTT 1739
Db       1581 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1640

Qy       1740 TGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGA 1799
Db       1641 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1700

Qy       1800 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 1859
Db       1701 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 1760

Qy       1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
Db       1761 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 1820

Qy       1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
Db       1821 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1880

Qy       1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db       1881 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1940

Qy       2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db       1941 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 2000

Qy       2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db       2001 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 2060

Qy       2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db       2061 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2120

Qy       2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2279
Db       2121 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATTCATGACATCTGATCA 2180

Qy       2280 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2339
Db       2181 CCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTGTGTTCGAAAAGGGAGATTT 2240

Qy       2340 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCT 2399
Db       2241 GGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTTGACTACCGTATTGGTTGTCG 2300

Qy       2400 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2459
Db       2301 AAAGCCTGGGGTGTATAAGGTGGTCTTGGACTCCGACGCTGGACTATTTGGTGGATTTAG 2360

Qy       2460 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2519
Db       2361 CAGGATCCATCACGCAGCCGAGCACTTCACCGCCGACTGTTCGCATGATAATAGGCCATA 2420

Qy       2520 TTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGA 2573
Db       2421 TTCATCCTCGGTTTATACACCAAGCAGAACATGTGTCGTCTATGCTCCAGTGGA 2474
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RESULT 6
US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/~~AGENT INFORMATION:~~
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..2487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..2490
US-08-941-445A-14

fav. late

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  Query Match             44.6%;  Score 1180.4;  DB 3;  Length 2725;
  Best Local Similarity   72.7%;  Pred. No. 0;
  Matches 1523;  Conservative    0;  Mismatches  571;  Indels    0;  Gaps    0;

Qy        480 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 539
Db        393 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 452

Qy        540 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 599
Db        453 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 512

Qy        600 GTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCG 659
Db        513 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 572

Qy        660 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 719
Db        573 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 632

Qy        720 TCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGACGCAAATGCTGA 779
Db        633 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACGTCAACAACTGGGATCCAAATGCAGA 692
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Qy    780 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 839
Db    693 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 752

Qy    840 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGT 899
Db    753 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 812

Qy    900 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 959
Db    813 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 872

Qy    960 TAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCC 1019
Db    873 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 932

Qy   1020 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1079
Db    933 TAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 992

Qy   1080 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGG 1139
Db    993 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 1052

Qy   1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199
Db   1053 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1112

Qy   1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1259
Db   1113 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1172

Qy   1260 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1319
Db   1173 TTTGATTGATAGAGCACATGAGCTTGGTTTGCTAGTTCTCATGGATGTGGTTCATAGTCA 1232

Qy   1320 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT 1379
Db   1233 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 1292

Qy   1380 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1439
Db   1293 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAA 1352

Qy   1440 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATT 1499
Db   1353 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 1412

Qy   1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559
Db   1413 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 1472

Qy   1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619
Db   1473 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 1532

Qy   1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
Db   1533 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 1592

Qy   1680 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTT 1739
Db   1593 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1652

Qy   1740 TGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGA 1799
Db   1653 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1712

Qy   1800 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 1859
Db   1713 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 1772

Qy   1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
Db   1773 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 1832

Qy   1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
Db   1833 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1892

Qy   1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db   1893 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1952

Qy   2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db   1953 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 2012

Qy   2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db   2013 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 2072

Qy   2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db   2073 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2132

Qy   2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2279
Db   2133 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATTCATGACATCTGATCA 2192

Qy   2280 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2339
Db   2193 CCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTGTGTTCGAAAAGGGAGATTT 2252

Qy   2340 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCT 2399
Db   2253 GGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTGACTACCGTATTGGTTGTCG 2312

Qy   2400 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2459
Db   2313 AAAGCCTGGGGTGTATAAGGTGGTCTTGGACTCCGACGCTGGACTATTTGGTGGATTTAG 2372

Qy   2460 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2519
Db   2373 CAGGATCCATCACGCAGCCGAGCACTTCACCGCCGACTGTTCGCATGATAATAGGCCATA 2432

Qy   2520 TTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGA 2573
Db   2433 TTCATTCTCGGTTTATACACCAAGCAGAACATGTGTCGTCTATGCTCCAGTGGA 2486
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RESULT 7
US-09-257-894-9
; Sequence 9, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2087 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-257-894-9

  Query Match             39.0%;  Score 1033;  DB 4;  Length 2087;
  Best Local Similarity   73.7%;  Pred. No. 1.3e-290;
  Matches 1315;  Conservative    0;  Mismatches  470;  Indels    0;  Gaps    0;

Qy        480 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 539
Db        303 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 362

Qy        540 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 599
Db        363 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 422

Qy        600 GTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCG 659
Db        423 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 482

Qy        660 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 719
Db        483 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 542

Qy        720 TCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 779
Db        543 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACTTCAACAACTGGGATCCAAATGCAGA 602

Qy        780 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 839
Db        603 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 662

Qy        840 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGT 899
Db        663 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 722

Qy        900 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 959
Db        723 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 782

Qy        960 TAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCC 1019
Db        783 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 842

Qy       1020 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1079
Db        843 TAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 902

Qy       1080 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGG 1139
Db        903 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 962

Qy       1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199
Db        963 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1022

Qy       1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1259
Db       1023 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1082

Qy       1260 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1319
Db       1083 TTTGATTGATAGAGCACATGAGCTTGGTTTGCTAGTTCTCATGGATGTGGTTCATAGTCA 1142

Qy       1320 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT 1379
Db       1143 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 1202

Qy       1380 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1439
Db       1203 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAA 1262

Qy       1440 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATT 1499
Db       1263 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 1322

Qy       1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559
Db       1323 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 1382

Qy       1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619
Db       1383 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 1442

Qy       1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
Db       1443 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 1502

Qy       1680 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTT 1739
Db       1503 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1562

Qy       1740 TGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGA 1799
Db       1563 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1622

Qy       1800 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 1859
Db       1623 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 1682

Qy       1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
Db       1683 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 1742

Qy       1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
Db       1743 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1802

Qy       1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db       1803 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1862

Qy       2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db       1863 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 1922

Qy       2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db       1923 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 1982

Qy       2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db       1983 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2042

Qy       2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTT 2264
Db       2043 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATT 2087
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RESULT 8
US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2165 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-257-894-8

  Query Match             39.0%;  Score 1031.4;  DB 4;  Length 2165;
  Best Local Similarity   73.6%;  Pred. No. 4e-290;
  Matches 1314;  Conservative    0;  Mismatches  471;  Indels    0;  Gaps    0;

Qy        480 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 539
Db       1785 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 1726

Qy        540 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 599
Db       1725 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 1666

Qy        600 GTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCG 659
Db       1665 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 1606

Qy        660 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 719
Db       1605 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 1546

Qy        720 TCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 779
Db       1545 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACGTCAACAACTGGGATCCAAATGCAGA 1486

Qy        780 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 839
Db       1485 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 1426

Qy        840 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGT 899
Db       1425 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 1366

Qy        900 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 959
Db       1365 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 1306

Qy        960 TAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCC 1019
Db       1305 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 1246

Qy       1020 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1079
Db       1245 TAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 1186

Qy       1080 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGG 1139
Db       1185 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 1126

Qy       1140 GTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTA 1199
Db       1125 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1066

Qy       1200 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1259
Db       1065 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1006

Qy       1260 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1319
Db       1005 TTTGATTGATAGAGCACATGAGCTTGGTTTGCTAGTTCTCATGGATGTGGTTCATAGTCA 946

Qy       1320 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT 1379
Db        945 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 886

Qy       1380 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1439
Db        885 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGAA 826

Qy       1440 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATT 1499
Db        825 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 766

Qy       1500 TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGT 1559
Db        765 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 706

Qy       1560 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGT 1619
Db        705 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 646

Qy       1620 GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1679
Db        645 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 586

Qy       1680 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTT 1739
Db        585 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 526

Qy       1740 TGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGA 1799
Db        525 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 466

Qy       1800 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 1859
Db        465 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 406
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Qy       1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 1919
Db        405 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 346

Qy       1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
Db        345 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 286

Qy       1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db        285 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 226

Qy       2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db        225 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 166

Qy       2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db        165 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 106

Qy       2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db        105 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 46

Qy       2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTT 2264
Db         45 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATT 1
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RESULT 9
US-08-716-449-1
; Sequence 1, Application US/08716449
; Patent No. 6103893
; GENERAL INFORMATION:
; APPLICANT: National Starch and Chemical Investment
; APPLICANT: Holding Corporation
; TITLE OF INVENTION: Method for Producing Altered Starch
; TITLE OF INVENTION: from Potato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott & Aylen
; STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
; CITY: Toronto
; STATE: Canada M5K 1H6
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IMB 1.44 MB High Density Diskette
; COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible)
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Word 7.0 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,449
; ~~FILING DATE: FILED CONCURRENTLY HEREWITH~~
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; ~~APPLICATION NUMBER:~~ PCT/GB95/00634
; FILING DATE: 22.03.95
; ATTORNEY/AGENT INFORMATION:
; NAME: Anita E.Nador
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1552
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 368-2400
; TELEFAX: (416) 363-7246
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA encoding starch branching enzyme
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE: clone 1.2.1 and E2
; ORGANISM: Solanum tuberosum
; STRAIN: cv desiree
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE: mature tuber
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY: lambda Zap tuber cDNA
; CLONE: 1.2.1 and E2
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE: open reading frame
; NAME/KEY: starch branching enzyme
; LOCATION: 44-2788
; IDENTIFICATION METHOD: lone ORF with homology to other starch
; IDENTIFICATION METHOD: branching enzymes
; OTHER INFORMATION: complements KV832 E. coli glycogen
; OTHER INFORMATION: branching enzyme mutant
US-08-716-449-1

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  Query Match             23.9%;  Score 631.4;  DB 3;  Length 3128;
  Best Local Similarity   60.1%;  Pred. No. 1.3e-173;
  Matches 1187;  Conservative    0;  Mismatches  731;  Indels   57;  Gaps    6;

Qy        548 TAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGA 607
Db        345 TGGATCCAACTTTGGAACCTTATCTAGATCACTTCAGACACAGAATGAAGAGATATGTGG 404

Qy        608 AACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATG 667
Db        405 ATCAGAAAATGCTCATTGAAAAATATGAGGGACCCCTTGAGGAATTTGCTCAAGGTTATT 464

Qy        668 AAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTG 727
Db        465 TAAAATTTGGATTCAACAGGGAAGATGGTTGCATAGTCTATCGTGAATGGGCTCCTGCTG 524

Qy        728 CCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGA 787
Db        525 CTCAGGAAGCAGAAGTTATTGGCGATTTCAATGGATGGAACGGTTCTAACCACATGATGG 584

Qy        788 CTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTG 847
Db        585 AGAAGGACCAGTTTGGTGTTTGGAGTATTAGAATTCC---TGATGTTGACAGTAAGCCAG 641

Qy        848 CAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAG---G 904
Db        642 TCATTCCACACAACTCCAGAGTTAAGTTTCGTTTCAAACATGGTAATGGAGTGTGGGTAG 701

Qy        905 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCC------TGATGAAATTCCAT 958
Db        702 ATCGTATCCCTGCTTGGATAAAGTATGCCACTGCAGACGCCACAAAGTTTGCAGCACCAT 761

Qy        959 ATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGC 1018
Db        762 ATGATGGTGTCTACTGGGACCCACCACCTTCAGAAAGGTACCACTTCAAATACCCTCGCC 821

Qy       1019 CAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGC 1078
Db        822 CTCCCAAACCCCGAGCCCCACGAATCTACGAAGCACATGTCGGCATGAGCAGCTCTGAGC 881

Qy       1079 CTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTG 1138
Db        882 CACGTGTAAATTCGTATCGTGAGTTTGCAGATGATGTTTTACCTCGGATTAAGGCAAATA 941

Qy       1139 GGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTT 1198
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Db    942 ACTATAATACTGTCCAGTTGATGGCCATAATGGAACATTCTTACTATGGATCATTTGGAT 1001

Qy   1199 ATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGT 1258
Db   1002 ATCATGTTACAAACTTTTTTGCTGTGAGCAATAGATATGGAAACCCGGAGGACCTAAAGT 1061

Qy   1259 CTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCC 1318
Db   1062 ATCTGATAGATAAAGCACATAGCTTGGGTTTACAGGTTCTGGTGGATGTAGTTCACAGTC 1121

Qy   1319 ATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGT---- 1374
Db   1122 ATGCAAGCAATAATGTCACTGATGGCCTCAATGGCTTTGATATTGGCCAAGGTTCTCAAG 1181

Qy   1375 -----TACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTA 1429
Db   1182 AATCCTACTTTCATGCTGGAGAGCGAGGGTACCATAAGTTGTGGGATAGCAGGCTGTTCA 1241

Qy   1430 ACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATG 1489
Db   1242 ACTATGCCAATTGGGAGGTTCTTCGTTTCCTTCTTTCCAACTTGAGGTGGTGGCTAGAAG 1301

Qy   1490 CGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACG 1549
Db   1302 AGTATAACTTTGACGGATTTCGATTTGATGGAATAACTTCTATGCTGTATGTTCATCATG 1361

Qy   1550 GATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGG 1609
Db   1362 GAATCAATATGGGATTTACAGGAAACTATAATGAGTATTTCAGCGAGGCTACAGATGTTG 1421

Qy   1610 ATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAA 1669
Db   1422 ATGCTGTGGTCTATTTAATGTTGGCCAATAATCTGATTCACAAGATTTTCCCAGACGCAA 1481

Qy   1670 TTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGG 1729
Db   1482 CTGTTATTGCCGAAGATGTTTCTGGTATGCCGGGCCTTAGCCGGCCTGTTTCTGAGGGAG 1541

Qy   1730 GTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCA 1789
Db   1542 GAATTGGTTTTGATTACCGCCTGGCAATGGCAATCCCAGATAAGTGGATAGATTATTTAA 1601

Qy   1790 AGAAACGG---GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAA 1846
Db   1602 AGAATAAGAATGATGAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGA 1661

Qy   1847 GATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATA 1906
Db   1662 GATATACAGAGAAGTGTATAGCATATGCGGAGAGCCATGATCAGTCTATTGTCGGTGACA 1721

Qy   1907 AAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGAC 1966
Db   1722 AGACCATTGCATTTCTCCTAATGGACAAAGAGATGTATTCTGGCATGTCTTGCTTGACAG 1781

Qy   1967 CGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTA 2026
Db   1782 ATGCTTCTCCTGTTGTTGATCGAGGAATTGCGCTTCACAAGATGATCCATTTTTTCACAA 1841

Qy   2027 TGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGT 2086
Db   1842 TGGCCTTGGGAGGAGAGGGGTACCTCAATTTCATGGGTAACGAGTTTGGCCATCCTGAGT 1901

Qy   2087 GGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACC 2146
Db   1902 GGATTGACTTCCCTAGAG-------------------------------AGGGCAATA 1928

Qy   2147 AATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGAT 2206
Db   1929 ATTGGAGTTATGACAAATGTAGACGCCAGTGGAACCTCGCAGATAGCGAACACTTGAGAT 1988

Qy   2207 ACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTA 2266
Db   1989 ACAAGTTTATGAATGCATTTGATAGAGCTATGAATTCGCTCGATGAAAAGTTCTCATTCC 2048

Qy   2267 TGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTG 2326
Db   2049 TCGCATCAGGAAAACAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTGTTTG 2108

Qy   2327 AAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATC 2386
Db   2109 AACGTGGTGACCTGGTATTTGTATTCAACTTCCACCCAAATAACACATACGAAGGGTATA 2168

Qy   2387 GCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTT 2446
Db   2169 AAGTTGGATGTGACTTGCCAGGGAAGTACAGAGTTGCACTGGGCAGTGATGCTTGGGAAT 2228

Qy   2447 TTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATG 2501
Db   2229 TTGGTGGCCATGGAAGAGCTGGTCATGATGTTGACCATTTCACATCACCAGAAGG 2283
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RESULT 10
US-09-257-894-19/c
; Sequence 19, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2487 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-257-894-19

  Query Match            23.7%;  Score 628.4;  DB 4;  Length 2487;
  Best Local Similarity  59.7%;  Pred. No. 8.7e-173;
  Matches 1177;  Conservative    0;  Mismatches  741;  Indels   54;  Gaps    5;

Qy    538 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 597
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Db       2124 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 2065

Qy        598 CAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCT 657
Db       2064 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 2005

Qy        658 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 717
Db       2004 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 1945

Qy        718 GCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 777
Db       1944 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 1885

Qy        778 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 837
Db       1884 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 1828

Qy        838 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
Db       1827 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 1768

Qy        898 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 953
Db       1767 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 1708

Qy        954 --TCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011
Db       1707 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 1648

Qy       1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071
Db       1647 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 1588

Qy       1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131
Db       1587 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 1528

Qy       1132 AAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGT 1191
Db       1527 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 1468

Qy       1192 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1251
Db       1467 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 1408

Qy       1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311
Db       1407 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1348

Qy       1312 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACTGC 1362
Db       1347 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1288

Qy       1363 ACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1422
Db       1287 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1228

Qy       1423 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1482
Db       1227 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1168

Qy       1483 TTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATT 1542
Db       1167 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1108

Qy       1543 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1602
Db       1107 CACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACA 1048

Qy       1603 GATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCA 1662
Db       1047 GCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCA 988

Qy       1663 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAA 1722
Db        987 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 928

Qy       1723 GAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAG 1782
Db        927 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 868

Qy       1783 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1839
Db        867 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 808

Qy       1840 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1899
Db        807 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 748

Qy       1900 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1959
Db        747 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 688

Qy       1960 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2019
Db        687 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 628

Qy       2020 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2079
Db        627 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 568

Qy       2080 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCC 2139
Db        567 CCAGAATGGATTGACTTTCCAAGAGAA--------------------------------- 541

Qy       2140 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2199
Db        540 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 481

Qy       2200 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATAT 2259
Db        480 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 421

Qy       2260 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2319
Db        420 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 361

Qy       2320 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2379
Db        360 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 301

Qy       2380 GACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2439
Db        300 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 241

Qy       2440 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCT 2491
Db        240 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 189
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RESULT 11
US-09-257-894-24
; Sequence 24, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
;   APPLICANT: Broglie, Karen E.
;   APPLICANT: Klein, Theodore M.
;   APPLICANT: Hubbard, Natalie L.
;   APPLICANT: Lightner, Jonathan E.
;   TITLE OF INVENTION: No. 6376749el Starches via Modification of
;   TITLE OF INVENTION: Expression of Starch Biosynthesis
;   TITLE OF INVENTION: Enzyme Genes
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: E. I. du Pont de Nemours and Company

```
;        STREET:  1007 Market Street
;        CITY:  Wilmington
;        STATE:  Delaware
;        COUNTRY:  USA
;        ZIP:  19898
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  Microsoft Windows 95
;        SOFTWARE:  Version 7.0A
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/09/257,894
;        FILING DATE:
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  09/091,052
;        FILING DATE:  JUNE 10, 1998
;     ATTORNEY/AGENT INFORMATION:
;        NAME:  Majarian, William R.
;        REGISTRATION NUMBER:  41,173
;        REFERENCE/DOCKET NUMBER:  BB-1066-A
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  302-992-4926
;        TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  24:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  2565 base pairs
;        TYPE:  nucleic acid
;        STRANDEDNESS:  single
;        TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-257-894-24

  Query Match             23.7%;  Score 628.4;  DB 4;  Length 2565;
  Best Local Similarity   59.7%;  Pred. No. 8.8e-173;
  Matches 1177;  Conservative    0;  Mismatches  741;  Indels   54;  Gaps    5;

Qy        538 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 597
Db        253 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 312

Qy        598 CAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCT 657
Db        313 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 372

Qy        658 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 717
Db        373 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 432

Qy        718 GCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 777
Db        433 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 492

Qy        778 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 837
Db        493 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 549

Qy        838 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
Db        550 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 609

Qy        898 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 953
Db        610 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 669

Qy        954 --TCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011
Db        670 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 729

Qy       1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071
Db        730 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 789

Qy       1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131
Db        790 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 849

Qy       1132 AAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGT 1191
Db        850 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 909

Qy       1192 TTTGGTTATCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1251
Db        910 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 969

Qy       1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311
Db        970 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1029

Qy       1312 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACTGC 1362
Db       1030 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1089

Qy       1363 ACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1422
Db       1090 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1149

Qy       1423 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1482
Db       1150 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1209

Qy       1483 TTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATT 1542
Db       1210 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1269

Qy       1543 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1602
Db       1270 CACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACA 1329

Qy       1603 GATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCA 1662
Db       1330 GCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCA 1389

Qy       1663 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAA 1722
Db       1390 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 1449

Qy       1723 GAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAG 1782
Db       1450 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 1509

Qy       1783 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1839
Db       1510 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 1569

Qy       1840 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1899
Db       1570 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1629

Qy       1900 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1959
Db       1630 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1689

Qy       1960 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2019
Db       1690 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 1749

Qy       2020 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2079
Db       1750 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 1809

Qy       2080 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCC 2139
Db       1810 CCAGAATGGATTGACTTTCCAAGAGAA------------------------------ 1836

Qy       2140 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2199
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Db     1837 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 1896

Qy     2200 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATAT 2259

Db     1897 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 1956

Qy     2260 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2319

Db     1957 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 2016

Qy     2320 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2379

Db     2017 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 2076

Qy     2380 GACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2439

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Qy     2440 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCT 2491

Db     2137 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 2188

RESULT 12
US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060
;  GENERAL INFORMATION:
;    APPLICANT:  Keeling, Peter
;    APPLICANT:  Guan, Hanping
;    TITLE OF INVENTION:  Starch Encapsulation
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Greenlee, Winner and Sullivan, P.C.
;      STREET:  5370 Manhattan Circle
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/941,445A
;      FILING DATE:  30-SEP-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,855
;      FILING DATE:  30-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winner, Ellen P
;      REGISTRATION NUMBER:  28,547
;      REFERENCE/DOCKET NUMBER:  89-97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  mRNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Zea mays
;    FEATURE:
;      NAME/KEY:  transit_peptide
;      LOCATION:  2..190
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  191..2467
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..2470
US-08-941-445A-16

  Query Match             23.7%;  Score 628.4;  DB 3;  Length 2763;
  Best Local Similarity   59.7%;  Pred. No. 9.2e-173;
  Matches 1177;  Conservative    0;  Mismatches  741;  Indels   54;  Gaps    5;

Qy      538 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 597

Db      251 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 310

Qy      598 CAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCT 657

Db      311 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 370

Qy      658 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 717

Db      371 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 430

Qy      718 GCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 777

Db      431 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 490

Qy      778 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 837

Db      491 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 547

Qy      838 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897

Db      548 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 607

Qy      898 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 953

Db      608 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 667

Qy      954 --TCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011

Db      668 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 727

Qy     1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071

Db      728 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 787

Qy     1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131

Db      788 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 847

Qy     1132 AAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGT 1191

Db      848 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 907

Qy     1192 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1251

Db      908 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 967

Qy     1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311

Db      968 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1027

Qy     1312 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACTGC 1362

Db     1028 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1087

Qy     1363 ACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1422

Db     1088 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1147

Qy     1423 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1482
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Db   1148 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1207

Qy   1483 TTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATT 1542
Db   1208 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1267

Qy   1543 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1602
Db   1268 CACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACA 1327

Qy   1603 GATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCA 1662
Db   1328 GCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCA 1387

Qy   1663 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAA 1722
Db   1388 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 1447

Qy   1723 GAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAG 1782
Db   1448 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 1507

Qy   1783 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1839
Db   1508 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 1567

Qy   1840 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1899
Db   1568 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1627

Qy   1900 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1959
Db   1628 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1687

Qy   1960 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2019
Db   1688 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 1747

Qy   2020 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2079
Db   1748 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 1807

Qy   2080 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCC 2139
Db   1808 CCAGAATGGATTGACTTTCCAAGAGAA--------------------------------- 1834

Qy   2140 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2199
Db   1835 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 1894

Qy   2200 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATAT 2259
Db   1895 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 1954

Qy   2260 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2319
Db   1955 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 2014

Qy   2320 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2379
Db   2015 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 2074

Qy   2380 GACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2439
Db   2075 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 2134

Qy   2440 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCT 2491
Db   2135 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 2186
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RESULT 13
US-09-257-894-12

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; Sequence 12, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2772 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  49..2580
US-09-257-894-12

  Query Match             23.7%;  Score 628.4;  DB 4;  Length 2772;
  Best Local Similarity   59.7%;  Pred. No. 9.2e-173;
  Matches 1177;  Conservative    0;  Mismatches  741;  Indels   54;  Gaps    5;

Qy    538 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 597
Db    364 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 423

Qy    598 CAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCT 657
Db    424 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 483

Qy    658 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 717
Db    484 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 543

Qy    718 GCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 777
Db    544 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 603

Qy    778 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 837
Db    604 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 660
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Qy     838 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
Db     661 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 720

Qy     898 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 953
Db     721 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 780

Qy     954 --TCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011
Db     781 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 840

Qy    1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071
Db     841 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 900

Qy    1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131
Db     901 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 960

Qy    1132 AAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGT 1191
Db     961 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 1020

Qy    1192 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGAC 1251
Db    1021 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 1080

Qy    1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311
Db    1081 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1140

Qy    1312 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACTGC 1362
Db    1141 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1200

Qy    1363 ACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1422
Db    1201 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1260

Qy    1423 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1482
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Qy    1483 TTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATT 1542
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Qy    1543 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1602
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Qy    1603 GATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCA 1662
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Qy    1663 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAA 1722
Db    1501 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 1560

Qy    1723 GAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAG 1782
Db    1561 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 1620

Qy    1783 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1839
Db    1621 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 1680

Qy    1840 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1899
Db    1681 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1740

Qy    1900 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1959
Db    1741 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1800

Qy    1960 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2019
Db    1801 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 1860

Qy    2020 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2079
Db    1861 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 1920

Qy    2080 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCC 2139
Db    1921 CCAGAATGGATTGACTTTCCAAGAGAA-------------------------------- 1947

Qy    2140 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2199
Db    1948 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 2007

Qy    2200 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATAT 2259
Db    2008 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 2067

Qy    2260 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2319
Db    2068 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 2127

Qy    2320 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2379
Db    2128 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 2187

Qy    2380 GACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2439
Db    2188 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 2247

Qy    2440 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCT 2491
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RESULT 14
US-08-104-158-1
; Sequence 1, Application US/08104158
; Patent No. 6215042
; GENERAL INFORMATION:
; APPLICANT: Willmitzer, Lothar
; APPLICANT: Sonnewald, Uwe
; APPLICANT: Kossmann, Jens
; APPLICANT: Mueller-Roeber, Bernd
; APPLICANT: Visser, Richard Gerardus Francisus
; APPLICANT: Jacobsen, Evert
; TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
; TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
; TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
; TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,158
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

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;       APPLICATION NUMBER:  EP PCT/EP92/00302
;       FILING DATE:  11-FEB-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  DE P 41 04 782.6
;       FILING DATE:  13-FEB-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meilman, Edward A.
;       REGISTRATION NUMBER:  24,735
;       REFERENCE/DOCKET NUMBER:  FA-1996 PCT (951-91)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-382-0700
;       TELEFAX:  212-382-0888
;       TELEX:  236925
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2909 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Solanum tuberosum cv. Desiree
;       STRAIN:  Desiree
;       DEVELOPMENTAL STAGE:  growing tuber
;       TISSUE TYPE:  tuber
;       CELL TYPE:  total tuber
;     IMMEDIATE SOURCE:
;       LIBRARY:  cDNA of total tuber mRNA in pUC 19 (Hinc II)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  2..1699
;       OTHER INFORMATION:  /note= "for Branching enzyme I
;       OTHER INFORMATION:  (partial) truncated protein; 97,11 % identity to
;       OTHER INFORMATION:  active potato branching enzyme"
US-08-104-158-1

  Query Match             23.3%;  Score 617.2;  DB 4;  Length 2909;
  Best Local Similarity   60.0%;  Pred. No. 1.7e-169;
  Matches 1185;  Conservative    0;  Mismatches  733;  Indels   58;  Gaps    7;

Qy        548 TAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGA 607
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Qy        608 AACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATG 667
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Qy        668 AAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTG 727
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Qy        728 CCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGA 787
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Qy        848 CAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAG---G 904
Db        462 TCATTCCACACAACTCCAGAGTTAAGTTTCGTTTCAAACATGGTAATGGAGTGTGGGTAG 521

Qy        905 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCC------TGATGAAATTCCAT 958
Db        522 ATCGTATCCCTGCTTGGATAAAGTATGCCACTGCAGACGCCACAAAGTTTGCAGCACCAT 581

Qy        959 ATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGC 1018
Db        582 ATGATGGTGTCTACTGGGACCCACCACCTTCAGAAAGGTACCACTTCAAATACCCTCGCC 641

Qy       1019 CAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGC 1078
Db        642 CTCCCAAACCCCGAGCCCCACGAATCTACGAAGCACATGTCGGCATGAGCAGCTCTGAGC 701

Qy       1079 CTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTG 1138
Db        702 CACGTGTAAATTCGTATCGTGAGTTTGCAGATGATGTTTTACCTCGGATTAAGGCAAATA 761

Qy       1139 GGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTT 1198
Db        762 ACTATAATACTGTCCAGTTGATGGCCATAATGGAACATTCTTACTATGGATCATTTGGAT 821

Qy       1199 ATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGT 1258
Db        822 ATCATGTTACAAACTTTTTTGCTGTGAGCAATAGATATGGAAACCCGGAGGACCTAAAGT 881

Qy       1259 CTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCC 1318
Db        882 ATCTGATAGATAAAGCACATAGCTTGGGTTTACAGGTTCTGGTGGATGTAGTTCACAGTC 941

Qy       1319 ATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGT---- 1374
Db        942 ATGCAAGCAATAATGTCACTGATGGCCTCAATGGCTTTGATATTGGCCAAGGTTCTCAAG 1001

Qy       1375 -----TACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTA 1429
Db       1002 AATCCTACTTTCATGCTGGAGAGCGAGGGTACCATAAGTTGTGGGATAGCAGGCTGTTCA 1061

Qy       1430 ACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATG 1489
Db       1062 ACTATGCCAATTGGGAGGTTCTTCGTTTCCTTCTTTCCAACTTGAGGTGGTGGCTAGAAG 1121

Qy       1490 CGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACG 1549
Db       1122 AGTATAACTTTGACGGATTTCGATTTGATGGAATAACTTCTATGCTGTATGTTCATCATG 1181

Qy       1550 GATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGG 1609
Db       1182 GAATCAATATGGGATTTACAGGAAACTATAATGAGTATTTCAGCGAGGCTACAGATGTTG 1241

Qy       1610 ATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGCTTTTCCCAGATGCAA 1669
Db       1242 ATGCTGTGGTCTATTTAATGTTGGCCAATAATCTGATTCACAAGATTTTCCCAGACGCAA 1301

Qy       1670 TTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGG 1729
Db       1302 CTGTTATTGCCGAAGATGTTTCTGGTATGCCGGGCCTTAGCCGGCCTGTTTCTGAGGGAG 1361

Qy       1730 GTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCA 1789
Db       1362 GAATTGGTTTTGATTACCGCCTGGCAATGGCAATCCCAGATAAGTGGATAGATTATTTAA 1421

Qy       1790 AGAAACGG---GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAA 1846
Db       1422 AGAATAAGAATGATGAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGA 1481

Qy       1847 GATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATA 1906
Db       1482 GATATACAGAGAAGTGTATAGCATATGCGGAGAGCCATGATCAGTCTATTGTCGGTGACA 1541

Qy       1907 AAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGAC 1966
Db       1542 AGACCATTGCATTTCTCCTAATGAACAAAGAGATGTATTCTGGCATGTCTTGCTTGACAG 1601

Qy       1967 CGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGAT-TAGGCTTGTAACT 2025
Db       1602 ATGCTTCTCCTGTTGTTGATGCAGGAATTGCGCTTGACAAGATGATCCATTTTTTCACA 1661

Qy       2026 ATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAG 2085
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Qy       2086 TGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAAC 2145
Db       1722 TGGATTGACTTCCCTAGTGAG-------------------------------GGCAAT 1748

Qy       2146 CAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGA 2205
Db       1749 AATTGGAGTTATGACAAATGTAGACGCCAGTGGAACCTCGCAGATAGCGAACACTTGAGA 1808

Qy       2206 TACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTT 2265
Db       1809 TACAAGTTTATGAATGCATTTGATAGAGCTATGAATTCGCTCGATGAAAAGTTCTCATTC 1868

Qy       2266 ATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTT 2325
Db       1869 CTCGCATCAGGAAAACAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTGTTT 1928

Qy       2326 GAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTAT 2385
Db       1929 GAACGTGGTGACCTGGTATTTGTATTCAACTTCCACCCAAATAACACATACGAAGGGTAT 1988

Qy       2386 CGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTT 2445
Db       1989 AAAGTTGGATGTGACTTGCCAGGGAAGTACAGAGTTGCACTGGACAGTGATGCTTGGGAA 2048

Qy       2446 TTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATG 2501
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RESULT 15
US-09-257-894-25
; Sequence 25, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1809 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-257-894-25

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Matches  954;  Conservative    0;  Mismatches  585;  Indels   21;  Gaps    4;

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Qy        598 CAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCT 657
Db        313 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 372

Qy        658 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 717
Db        373 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 432

Qy        718 GCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 777
Db        433 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 492

Qy        778 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 837
Db        493 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 549

Qy        838 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
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Qy        898 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 953
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Qy        954 --TCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011
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Qy       1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071
Db        730 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 789

Qy       1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131
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Qy       1132 AAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGT 1191
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Db        910 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 969

Qy       1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311
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Qy       1312 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACTGC 1362
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Qy       1483 TTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATT 1542
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Qy   1603 GATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCA 1662
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Qy   1663 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAA 1722
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Qy   1840 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1899
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GenCore version 5.1.6

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10130.730 Million cell updates/sec

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Perfect score: 2646
Sequence: 1 ATGGTGTATACACTCTCTGG..........AAGTAGTAGTAGAAGAAGAA 2646

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2581	97.5	3074	9	US-10-254-534-1	Sequence 1, Appli
	2	1369.8	51.8	1393	9	US-10-254-534-3	Sequence 3, Appli
	3	1317.4	49.8	2418	9	US-09-938-842A-872	Sequence 872, App
	4	1290	48.8	2577	9	US-09-938-842A-337	Sequence 337, App
	5	1167.2	44.1	3039	10	US-09-792-127-3	Sequence 3, Appli
	6	1166.6	44.1	2559	10	US-09-792-127-1	Sequence 1, Appli
	7	578.2	21.9	2994	9	US-10-084-817-92	Sequence 92, Appl
	8	576.6	21.8	2955	9	US-09-918-624B-30	Sequence 30, Appl
	9	576.6	21.8	2955	10	US-09-880-107-2148	Sequence 2148, Ap
c	10	257.8	9.7	602	10	US-09-770-149-955	Sequence 955, App
	11	136	5.1	604	10	US-09-925-300-453	Sequence 453, App
	12	114.6	4.3	441	10	US-09-770-444-893	Sequence 893, App
c	13	104.8	4.0	601	9	US-10-025-380-304	Sequence 304, App
c	14	104.8	4.0	601	10	US-09-922-217-304	Sequence 304, App
c	15	104.8	4.0	601	10	US-09-833-263-304	Sequence 304, App
	16	88.8	3.4	204	10	US-09-878-574-12567	Sequence 12567, A
	17	88.6	3.3	1877	10	US-09-974-300-653	Sequence 653, App
	18	86.2	3.3	1830121	9	US-10-329-960-1	Sequence 1, Appli
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	26	66.8	2.5	90650	9	US-10-175-523-80	Sequence 80, Appl
c	27	66.6	2.5	16299	9	US-10-175-523-64	Sequence 64, Appl
	28	65.8	2.5	288	9	US-09-728-444-165	Sequence 165, App
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c	30	65.8	2.5	496	10	US-09-864-761-2534	Sequence 2534, Ap
	31	65.8	2.5	6944	9	US-10-172-086-111	Sequence 111, App
	32	65.8	2.5	225883	9	US-10-175-523-57	Sequence 57, Appl
c	33	65.8	2.5	1691139	9	US-10-067-514-1	Sequence 1, Appli
	34	65.4	2.5	419	10	US-09-864-761-6432	Sequence 6432, Ap
c	35	65	2.5	659158	9	US-09-771-208-20	Sequence 20, Appl
c	36	64.2	2.4	157	10	US-09-864-761-21717	Sequence 21717, A
	37	64.2	2.4	301	10	US-09-864-761-17047	Sequence 17047, A
c	38	64.2	2.4	462	10	US-09-864-761-3829	Sequence 3829, Ap
	39	64.2	2.4	471	10	US-09-864-761-2776	Sequence 2776, Ap
	40	64	2.4	576	10	US-09-815-343-924	Sequence 924, App
c	41	63.6	2.4	232	10	US-09-864-761-19928	Sequence 19928, A
c	42	63.6	2.4	312	10	US-09-864-761-22972	Sequence 22972, A
c	43	63.4	2.4	483	10	US-09-864-761-1384	Sequence 1384, Ap
	44	63.2	2.4	261	10	US-09-864-761-19524	Sequence 19524, A
c	45	63.2	2.4	261	10	US-09-864-761-25517	Sequence 25517, A

ALIGNMENTS

RESULT 1
US-10-254-534-1
; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beII gene
; OTHER INFORMATION: (branching enzyme II) from *Solanum tuberosum*
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:

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;   NAME/KEY: misc_feature
;   LOCATION: (92)..(2156)
;   OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
;   OTHER INFORMATION: n wherein n = A, C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (285)..(287)
;   OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1404)..(1406)
;   OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1428)..(1430)
;   OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1896)..(1898)
;   OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2154)..(2156)
;   OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-10-254-534-1

  Query Match             97.5%;  Score 2581;  DB 9;  Length 3074;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 2599;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAAT 248

Qy         61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCAC 120
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        249 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTTGAAAAAGCAC 308

Qy        121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        309 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCT 368

Qy        181 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCC 428

Qy        241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGAT 488

Qy        301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        489 GTAGATAGTTCAACAATGGAACACGCTAGGCAGATTAAAACTGAGAACGATGACGTTGAG 548

Qy        361 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTA 608

Qy        421 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATT 668

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 728

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 788

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        789 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 848

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 908

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 CCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 968

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1028

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 1088

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1148

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1208

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1268

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1328

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
              ||||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1329 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1388

Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAGTCT 1260
              ||||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
Db       1389 CATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTGGAACNCCCGACGACCTTAAGTCT 1448

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1508

Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
              ||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||||
Db       1509 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1568

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1628

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1629 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTT 1688

Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1689 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1748

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1749 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1808

Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1868

Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
              |||||||||||||||||||||||||||| ||||||||| ||||| |||||||||||||||
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Db       1869 GAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1928

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1929 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1988

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1989 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2048

Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2049 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2108

Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
              ||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2109 TGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTCAACATCATTA 2168

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2169 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2228

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2229 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2288

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       2289 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2348

Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2349 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2408

Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       2409 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2468

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2469 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2528

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       2529 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTG 2588

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2589 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2648

Qy       2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2649 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2708

Qy       2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
              ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db       2709 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2768

Qy       2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTA 2634
              |||||||||||||||||  || ||  || ||  || ||  |||||  |||||  || |
Db       2769 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822
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RESULT 2
US-10-254-534-3
; Sequence 3, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-10-254-534-3

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  Query Match             51.8%;  Score 1369.8;  DB 9;  Length 1393;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        819 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

Qy        879 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 120

Qy        939 GCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTA 998
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        121 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 180

Qy        999 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 240

Qy       1059 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 300

Qy       1119 TCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTC 1178
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        301 TCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 360
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Qy  1179 TTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGG 1238
Db   361 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGA 420

Qy  1239 AACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 1298
Db   421 AACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 480

Qy  1299 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 1358
Db   481 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 540

Qy  1359 CTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 1418
Db   541 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 600

Qy  1419 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 1478
Db   601 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 660

Qy  1479 GTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 1538
Db   661 GTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 720

Qy  1539 TATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 1598
Db   721 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 780

Qy  1599 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 1658
Db   781 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 840

Qy  1659 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGT 1718
Db   841 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGT 900

Qy  1719 CCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGAT 1778
Db   901 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 960

Qy  1779 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1838
Db   961 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1020

Qy  1839 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1898
Db  1021 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1080

Qy  1899 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1958
Db  1081 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1140

Qy  1959 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2018
Db  1141 GGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 1200

Qy  2019 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2078
Db  1201 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 1260

Qy  2079 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCC 2138
Db  1261 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 1320

Qy  2139 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2198
Db  1321 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 1380

Qy  2199 TTTAAGATACCGT 2211
Db  1381 TTTAAGATACCGT 1393
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RESULT 3
US-09-938-842A-872
; Sequence 872, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 872
;   LENGTH: 2418
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

  Query Match             49.8%;  Score 1317.4;  DB 9;  Length 2418;
  Best Local Similarity   75.3%;  Pred. No. 0;
  Matches 1655;  Conservative    0;  Mismatches  541;  Indels    3;  Gaps    1;

Qy   384 TGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGA 443
Db   216 TGATGATGATCCCAGAGGTTTTTCACAGATATTTGATCTAGAAAGTCAAACAATGGAATA 275

Qy   444 GTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATA---GGATCAG 500
Db   276 TACTGAGGCAGTAAGAACAGAAGACCAAACAATGAACGTTGTCAAGGAGAGAGGGGTGAA 335

Qy   501 AGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTT 560
Db   336 ACCAAGAATAGTTCCCCCACCGGGTGATGGCAAGAAAATTTATGAGATAGACCCCATGTT 395

Qy   561 GACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGC 620
Db   396 ACGAACTTACAACAATCATCTTGATTACCGTTATGGACAGTATAAAAGATTGCGTGAGGA 455

Qy   621 AATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTT 680
Db   456 AATAGACAAGTATGAGGGTGGTCTTGAGGCATTCTCTCGTGGCTATGAAAAGTTAGGATT 515

Qy   681 CACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGC 740
Db   516 TTCGCGCAGTGATGCCGGTATAACTTATAGAGAGTGGGCGCCTGGAGCTAAGGCTGCATC 575

Qy   741 CCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATT 800
Db   576 ACTTATCGGAGATTTCAACAACTGGAATTCTAATGCAGATATCATGACTCGGAATGAATT 635

Qy   801 TGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGG 860
Db   636 TGGTGTTTGGGAGATCTTTTTGCCCAACAACACTGATGGTTCGCCTGCAATTCCTCATGG 695

Qy   861 GTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTG 920
Db   696 CTCACGTGTAAAGATTCGTATGGATACTCCATCTGGCATTAAAGACTCAATTCCTGCTTG 755

Qy   921 GATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCC 980
Db   756 GATCAAGTTCTCGGTGCAAGCTCCAGGTGAAATCCCATTCAATGGCATATACTATGATCC 815

Qy   981 ACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAG 1040
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Db      816 TCCAGAAGAGGAGAAGTATGTATTCAAACATCCTCAACCAAAGAGACCTAAGTCGCTAAG 875

Qy     1041 AATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAA 1100
Db      876 GATTTATGAAGCACATGTTGGCATGAGTAGCACGGAACCAATGGTCAATACGTATGCTAA 935

Qy     1101 TTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTAT 1160
Db      936 CTTTAGAGATGATGTTCTTCCCCGCATCAAAAAGCTTGGATATAATGCTGTTCAAATTAT 995

Qy     1161 GGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGC 1220
Db      996 GGCCATACAAGAACATTCATATTATGCCAGCTTTGGGTACCATGTCACAAACTTTTTTGC 1055

Qy     1221 ACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGA 1280
Db     1056 CCCAAGCAGTCGCTGTGGGACCCCAGAGGAACTAAAATCACTGATAGATAGAGCTCACGA 1115

Qy     1281 GCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGA 1340
Db     1116 GTTAGGCCTGGTAGTTCTGATGGATATCGTTCATAGCCATGCTTCAAAAAACACATTGGA 1175

Qy     1341 TGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTA 1400
Db     1176 TGGACTGAACATGTTTGATGGAACTGATGCTCACTATTTTCACTCTGGACCTCGGGGATA 1235

Qy     1401 TCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCT 1460
Db     1236 CCATTGGATGTGGGATTCACGACTTTTCAATTATGGGAGCTGGGAAGTATTACGATATCT 1295

Qy     1461 TCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGG 1520
Db     1296 CCTTTCAAATGCACGGTGGTGGCTAGAAGAATACAAGTTTGATGGATTTAGATTTGATGG 1355

Qy     1521 TGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGA 1580
Db     1356 TGTAACCTCAATGATGTATACTCATCATGGACTCTCGGTTGGATTTACTGGGAACTACAC 1415

Qy     1581 GGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGA 1640
Db     1416 CGAATACTTTGGATTGGAAACTGATGTGGATGCTGTGAATTATCTCATGCTGGTTAATGA 1475

Qy     1641 TCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCC 1700
Db     1476 TATGATTCATGGGCTCTACCCTGAAGCGATTACCGTTGGTGAAGATGTTAGTGGTATGCC 1535

Qy     1701 GACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGC 1760
Db     1536 AACATTCTGTATTCCTGTCCAAGATGGTGGCGTTGGATTTGACTACCGTTTACACATGGC 1595

Qy     1761 AATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGA 1820
Db     1596 CATAGCTGATAAGTGGATAGAAATGCTCAAGAAGAGAGATGAAGACTGGCAAATGGGCGA 1655

Qy     1821 TATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAG 1880
Db     1656 CATCATTTACACACTTACCAACAGAAGGTGGTCAGAGAAGTGTATCTCTTATGCTGAAAG 1715

Qy     1881 TCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATAT 1940
Db     1716 TCACGATCAAGCTCTTGTTGGTGATAAAACAATTGCCTTCTGGTTAATGGACAAGGATAT 1775

Qy     1941 GTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATT 2000
Db     1776 GTATGATTTCATGGCAGTAGACAGACCATCAACTCCTCTTATCGATAGAGGAATAGCTTT 1835

Qy     2001 GCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCAT 2060
Db     1836 GCACAAAATGATTAGGCTTATAACTATGGGATTAGGCGGTGAAGGTTACTTAAATTTTAT 1895

Qy     2061 GGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTC 2120
Db     1896 GGGAAACGAATTCGGACATCCAGAATGGATTGATTTTCCCAGAGGCGAGCAGCGTCTTTC 1955

Qy     2121 TGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGA 2180
Db     1956 TGATGGTAGCGTGATTCCTGGCAACAATTTCAGTTATGACAAATGCCGCCGCAGATTTGA 2015

Qy     2181 CCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCA 2240
Db     2016 TCTTGGGGATGCAGATTATCTCAGATACCGCGGACTACAAGAATTTGATCAGGCAATGCA 2075

Qy     2241 GTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGA 2300
Db     2076 ACATCTTGAAGAGAATTACGGTTTTATGACTTCGGAGCACCAATTCATATCACGAAAAGA 2135

Qy     2301 TGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCA 2360
Db     2136 CGAAGCAGATAGAGTAATCGTATTCGAAAGAGGTGATCTCGTCTTTGTCTTTAACTTTCA 2195

Qy     2361 CTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGT 2420
Db     2196 CTGGACCAGCAGCTACTTTGATTACCGCATTGGTTGCTCCAAGCCTGGAAAATATAAGAT 2255

Qy     2421 TGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGA 2480
Db     2256 CGTATTGGACTCGGACGATCCTCTCTTTGGTGGATTCAATAGGCTCGATCGCAAGGCAGA 2315

Qy     2481 ATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACC 2540
Db     2316 GTACTTCACTTATGATGGCTTATACGACGAACGACCCTGCTCCTTCATGGTCTATGCACC 2375

Qy     2541 TTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGA 2579
Db     2376 GTGTAGAACCGCCGTGGTTTATGCTTTAGCAAACCACGA 2414
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RESULT 4
US-09-938-842A-337
; Sequence 337, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
;   LENGTH: 2577
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

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  Query Match             48.8%;  Score 1290;  DB 9;  Length 2577;
  Best Local Similarity   76.1%;  Pred. No. 0;
  Matches 1590;  Conservative    0;  Mismatches  500;  Indels    0;  Gaps    0;

Qy      503 AGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGA 562
Db      443 AGAGGAAGATTCCACCTCCTGGAGATGGGAAGAGAATATATGACATTGATCCTATGTTGA 502

Qy      563 CAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAA 622
Db      503 ACAGTCATCGTAATCATCTTGATTACCGATATGGGCAGTACAGAAAACTGCGTGAAGAAA 562
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Qy    623 TTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCA 682
Db    563 TTGACAAGAATGAAGGTGGTTTGGAGGCATTTTCTCGTGGTTATGAAATATTTGGCTTCA 622

Qy    683 CTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCC 742
Db    623 CTCGAAGCGCCACTGGTATCACTTACCGGGAATGGGCACCGGGAGCTAAGGCAGCATCAC 682

Qy    743 TCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTG 802
Db    683 TGATCGGAGATTTTAATAACTGGAATGCGAAATCTGATGTTATGGCTCGGAACGACTTTG 742

Qy    803 GTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGT 862
Db    743 GTGTGTGGGAAATATTTCTGCCAAATAATGCTGATGGCTCACCAGCAATTCCCCATGGCT 802

Qy    863 CCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGA 922
Db    803 CCCGTGTGAAGATCCGCATGGATACCCCATCTGGTATTAAAGACTCCATTCCAGCTTGGA 862

Qy    923 TCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCAC 982
Db    863 TCAAGTATTCTGTCCAGCCACCTGGCGAGATCCCATATAATGGAGTATATTATGACCCTC 922

Qy    983 CCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAA 1042
Db    923 CTGAGGAGGATAAATATGCGTTCAAACATCCTCGTCCAAAGAAACCCACATCGCTGCGTA 982

Qy   1043 TATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATT 1102
Db    983 TATATGAATCACATGTTGGAATGAGTAGTACGGAACCAAAGATAAATACATATGCCAACT 1042

Qy   1103 TTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGG 1162
Db   1043 TTAGAGATGATGTACTTCCCCGTATAAAAAAGCTAGGCTATAATGCTGTGCAGATAATGG 1102

Qy   1163 CTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCAC 1222
Db   1103 CCATTCAAGAGCATGCCTACTATGCCAGCTTTGGGTATCATGTGACAAATTTTTTCGCAC 1162

Qy   1223 CAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGC 1282
Db   1163 CTAGCAGCCGCTTTGGAACACCTGATGACCTTAAATCTTTGATAGACAAAGCTCATGAGC 1222

Qy   1283 TAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATG 1342
Db   1223 TAGGTCTGGTTGTTCTGATGGATATTGTGCACAGCCATGCATCAAAAAACACACTGGATG 1282

Qy   1343 GACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATC 1402
Db   1283 GCCTGGACATGTTTGATGGTACTGATGGTCAATATTTCCACTCTGGATCGCGTGGTTATC 1342

Qy   1403 ATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTC 1462
Db   1343 ATTGGATGTGGGATTCTCGTCTTTTCAATTACGGAAGCTGGGAAGTGCTTAGGTATCTTC 1402

Qy   1463 TCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTG 1522
Db   1403 TTTCCAACGCGAGATGGTGGCTGGAAGAATACAAGTTTGATGGGTTCAGATTTGATGGTG 1462

Qy   1523 TGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGG 1582
Db   1463 TGACTTCCATGATGTACACTCATCATGGACTGCAGGTCGAATTTACTGGGAATTACAATG 1522

Qy   1583 AATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATC 1642
Db   1523 AGTACTTTGGATATTCTACTGATGTTGACGCTGTGGTCTATCTAATGCTGGTGAACGATT 1582

Qy   1643 TTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGA 1702
Db   1583 TGATTCATGGGCTATACCCTGAGGCTATTGTTGTCGGCGAAGATGTTAGCGGGATGCCAG 1642

Qy   1703 CATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAA 1762
Db   1643 CTTTTTGCGTTCCTGTCGAAGACGGTGGTGTGGGTTTTGACTACCGTCTACACATGGCAG 1702

Qy   1763 TTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATA 1822
Db   1703 TGGCAGATAAATGGATTGAGCTTCTTAAGAAGAGAGACGAGGACTGGCAGGTTGGTGATA 1762

Qy   1823 TTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTC 1882
Db   1763 TAACTTTCACGCTTACCAACAGGAGGTGGGGAGAAAAATGTGTCGTCTATGCAGAGAGTC 1822

Qy   1883 ATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGT 1942
Db   1823 ATGATCAAGCCCTTGTTGGAGACAAAACGATAGCTTTCTGGCTAATGGATAAGGACATGT 1882

Qy   1943 ATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGC 2002
Db   1883 ATGATTTCATGGCCGTTGATAGACAGGCCACTCCGCGTGTAGACCGTGGGATTGCTTTAC 1942

Qy   2003 ACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGG 2062
Db   1943 ACAAAATGATCCGTCTCATTACGATGGGATTGGGTGGAGAAGGATACCTCAATTTCATGG 2002

Qy   2063 GAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTG 2122
Db   2003 GAAACGAATTTGGACACCCAGAATGGATCGACTTCCCAAGGACCGACCAGCACCTTCCTG 2062

Qy   2123 ATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACC 2182
Db   2063 ATGGCAGAGTCATCGCTGGGAATAATGGTAGTTATGATAAATGCCGACGTAGGTTTGATC 2122

Qy   2183 TGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGT 2242
Db   2123 TGGGAGATGCAGAATATCTTAGATACCATGGACTACAAGAGTTTGATCGAGCAATGCAAA 2182

Qy   2243 ATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATG 2302
Db   2183 ATCTAGAGGAGACGTATGGTTTCATGACTTCAGAGCACCAGTACATATCCCGCAAGGATG 2242

Qy   2303 AAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACT 2362
Db   2243 AAGGAGACAGAGTCATTGTATTCGAGAGAGGTAACTTGCTCTTCGTCTTCAACTTCCACT 2302

Qy   2363 GGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTG 2422
Db   2303 GGACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAAGTACAAAATCG 2362

Qy   2423 CCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAAT 2482
Db   2363 TTTTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGACTCCGCGGAGT 2422

Qy   2483 ATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTT 2542
Db   2423 TTTTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGTGTATGCACCGT 2482

Qy   2543 GTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAA 2592
Db   2483 GCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGAA 2532
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RESULT 5
US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIb
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23

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;  PRIOR APPLICATION NUMBER:  60/186098
;  PRIOR FILING DATE:  2000-03-01
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  Microsoft Office 97
; SEQ ID NO 3
;   LENGTH: 3039
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-792-127-3

  Query Match             44.1%;  Score 1167.2;  DB 10;  Length 3039;
  Best Local Similarity   72.0%;  Pred. No. 7.6e-312;
  Matches 1523;  Conservative    0;  Mismatches  593;  Indels    0;  Gaps    0;

Qy        481 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 540
Db        474 GAATCATCTACGAGGGAGAAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATA 533

Qy        541 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 600
Db        534 TACGAGATTGACCCAACGCTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA 593

Qy        601 TACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGT 660
Db        594 TACAGGAGAATACGTTCAGACATTGATGAACACGAAGGAGGCATGGATGTATTTTCCCGC 653

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
Db        654 GGTTACGAGAAGTTTGGATTTATGCGCAGCGCTGAAGGTATCACTTACCGAGAATGGGCT 713

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGACGCAAATGCTGAC 780
Db        714 CCTGGAGCAGATTCTGCAGCATTAGTTGGCGACTTCAACAATTGGGATCCAAATGCAGAC 773

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db        774 CATATGAGCAAAAATGACCTTGGTGTTTGGGAGATTTTTCTGCCAAACAATGCAGATGGT 833

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
Db        834 TCGCCACCAATTCCTCACGGCTCACGGGTGAAGGTGAGAATGGATACTCCATCTGGGATA 893

Qy        901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
Db        894 AAGGATTCAATTCCTGCTTGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATAC 953

Qy        961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
Db        954 AATGGAATATATTATGATCCTCCCGAAGAGGAGAAGTATGTATTCAAGCATCCTCAACCT 1013

Qy       1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
Db       1014 AAACGACCAAAATCATTGCGGATATATGAAACACATGTTGGCATGAGTAGCCCGGAACCA 1073

Qy       1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
Db       1074 AAGATCAACACATATGCAAACTTCAGGGATGAGGTGCTTCCAAGAATTAAAAGACTTGGA 1133

Qy       1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
Db       1134 TACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATACTATGGAAGCTTTGGGTAC 1193

Qy       1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
Db       1194 CATGTTACCAATTTCTTTGCACCAAGTAGCCGTTTTGGGTCCCCAGAAGATTTAAAATCT 1253

Qy       1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
Db       1254 TTGATTGATAGAGCTCACGAGCTTGGCTTGGTTGTCCTCATGGATGTTGTTCACAGTCAC 1313

Qy       1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
Db       1314 GCGTCAAATAATACCTTGGACGGGTTGAATGGTTTTGATGGCACGGATACACATTACTTC 1373

Qy       1381 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1440
Db       1374 CATGGCGGTTCACGGGGCCATCACTGGATGTGGGATTCCCGTGTGTTTAACTATGGGAAT 1433

Qy       1441 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTT 1500
Db       1434 AAGGAAGTTATAAGGTTTCTACTTTCCAATGCAAGATGGTGGCTAGAGGAGTATAAGTTT 1493

Qy       1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTG 1560
Db       1494 GATGGTTTCCGATTCGATGGCGCGACCTCCATGATGTATACCCATCATGGATTACAAGTA 1553

Qy       1561 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG 1620
Db       1554 ACCTTTACAGGAAGCTACCATGAATATTTTGGCTTTGCCACTGATGTAGATGCGGTCGTT 1613

Qy       1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1680
Db       1614 TACTTGATGCTGATGAATGATCTAATTCATGGGTTTTATCCTGAAGCCGTAACTATCGGT 1673

Qy       1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTT 1740
Db       1674 GAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGGTTGGTTTT 1733

Qy       1741 GACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACGGGAT 1800
Db       1734 GACTATCGCTTACATATGGCTGTTGCCGACAAATGGATTGAACTTCTCAAAGGAAACGAT 1793

Qy       1801 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 1860
Db       1794 GAAGCTTGGGAGATGGGTAATATTGTGCACACACTAACAAACAGAAGGTGGCTGGAAAAG 1853

Qy       1861 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 1920
Db       1854 TGTGTTACTTATGCTGAAAGTCACGATCAAGCACTTGTTGGAGACAAGACTATTGCATTC 1913

Qy       1921 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
Db       1914 TGGTTGATGGACAAGGATATGTATGATTTCATGGCGCTGAACGGACCTTCGACGCCTAAT 1973

Qy       1981 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2040
Db       1974 ATTGATCGTGGAATAGCACTGCATAAAATGATTAGACTTATCACAATGGGTCTAGGAGGA 2033

Qy       2041 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2100
Db       2034 GAGGGTTATCTTAACTTTATGGGAAATGAGTTCGGGCATCCTGAATGGATAGACTTTCCA 2093

Qy       2101 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGAT 2160
Db       2094 AGAGGCCCACAAGTACTTCCAAGTGGTAAGTTCATCCCAGGAAACAACAACAGTTACGAC 2153

Qy       2161 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2220
Db       2154 AAATGCCGTCGAAGATTTGACCTGGGTGATGCAGAATTTCTTAGGTATCATGGTATGCAG 2213

Qy       2221 GAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2280
Db       2214 CAGTTTGATCAGGCAATGCAGCATCTTGAGGAAAAATATGGTTTTATGACATCAGACCAC 2273

Qy       2281 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2340
Db       2274 CAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTGTTTGAAAAAGGGGACTTG 2333

Qy       2341 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTG 2400
Db       2334 GTATTTGTGTTCAACTTCCACTGGAGTAGTAGCTATTTCGACTACCGGGTCGGCTGTTTA 2393

Qy       2401 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2460
Db       2394 AAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGACTCTTTGGTGGATTTGGT 2453
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Qy      2461 AGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2520
Db      2454 AGGATCCATCACACTGCAGAGCACGTCACTTCTGACTGCCAACATGACAACAGGCCCCAT 2513

Qy      2521 TCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2580
Db      2514 TCATTCTCAGTGTACACTCCTAGCAGAACCTGTGTTGTCTATGCTCCAATGAACTAACAG 2573

Qy      2581 GAAGAAGAAGAAGAAG 2596
Db      2574 CAAAGTGCAGCATACG 2589
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RESULT 6
US-09-792-127-1
; Sequence 1, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIb
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-1

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  Query Match             44.1%;  Score 1166.6;  DB 10;  Length 2559;
  Best Local Similarity   72.5%;  Pred. No. 9.9e-312;
  Matches 1511;  Conservative    0;  Mismatches  574;  Indels    0;  Gaps    0;

Qy       512 TCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATC 571
Db        25 TGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACGCTCCGAGACTTTA 84

Qy       572 GTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGT 631
Db        85 AGTACCATCTTGAGTATCGATATAGCCTATACAGGAGAATACGTTCAGACATTGATGAAC 144

Qy       632 ATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTG 691
Db       145 ACGAAGGAGGCATGGATGTATTTTCCCGCGGTTACGAGAAGTTTGGATTTATGCGCAGCG 204

Qy       692 CTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAG 751
Db       205 CTGAAGGTATCACTTACCGAGAATGGGCTCCTGGAGCAGATTCTGCAGCATTAGTTGGCG 264

Qy       752 ATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGG 811
Db       265 ACTTCAACAATTGGGATCCAAATGCAGACCATATGAGCAAAAATGACCTTGGTGTTTGGG 324

Qy       812 AGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGA 871
Db       325 AGATTTTTCTGCCAAACAATGCAGATGGTTCGCCACCAATTCCTCACGGCTCACGGGTGA 384

Qy       872 AGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACT 931
Db       385 AGGTGAGAATGGATACTCCATCTGGGATAAAGGATTCAATTCCTGCTTGGATCAAGTACT 444

Qy       932 CTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGG 991
Db       445 CCGTGCAGACTCCAGGAGATATACCATACAATGGAATATATTATGATCCTCCCGAAGAGG 504

Qy       992 AGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAAT 1051
Db       505 AGAAGTATGTATTCAAGCATCCTCAACCTAAACGACCAAAATCATTGCGGATATATGAAA 564

Qy      1052 CTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATG 1111
Db       565 CACATGTTGGCATGAGTAGCCCGGAACCAAAGATCAACACATATGCAAACTTCAGGGATG 624

Qy      1112 AAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAG 1171
Db       625 AGGTGCTTCCAAGAATTAAAAGACTTGGATACAATGCAGTGCAAATAATGGCAATCCAAG 684

Qy      1172 AGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTGCACCAAGCAGCC 1231
Db       685 AGCACTCATACTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTTGCACCAAGTAGCC 744

Qy      1232 GTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTG 1291
Db       745 GTTTTGGGTCCCCAGAAGATTTAAAATCTTTGATTGATAGAGCTCACGAGCTTGGCTTGG 804

Qy      1292 TTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACA 1351
Db       805 TTGTCCTCATGGATGTTGTTCACAGTCACGCGTCAAATAATACCTTGGACGGGTTGAATG 864

Qy      1352 TGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGT 1411
Db       865 GTTTTGATGGCACGGATACACATTACTTCCATGGCGGTTCACGGGGCCATCACTGGATGT 924

Qy      1412 GGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATG 1471
Db       925 GGGATTCCCGTGTGTTTAACTATGGGAATAAGGAAGTTATAAGGTTTCTACTTTCCAATG 984

Qy      1472 CGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAA 1531
Db       985 CAAGATGGTGGCTAGAGGAGTATAAGTTTGATGGTTTCCGATTCGATGGCGCGACCTCCA 1044

Qy      1532 TGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTG 1591
Db      1045 TGATGTATACCCATCATGGATTACAAGTAACCTTTACAGGAAGCTACCATGAATATTTTG 1104

Qy      1592 GACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATG 1651
Db      1105 GCTTTGCCACTGATGTAGATGCGGTCGTTTACTTGATGCTGATGAATGATCTAATTCATG 1164

Qy      1652 GGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTA 1711
Db      1165 GGTTTTATCCTGAAGCCGTAACTATCGGTGAAGATGTTAGTGGAATGCCTACATTTGCCC 1224

Qy      1712 TTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATA 1771
Db      1225 TTCCTGTTCAAGTTGGTGGGGTTGGTTTTGACTATCGCTTACATATGGCTGTTGCCGACA 1284

Qy      1772 AACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATA 1831
Db      1285 AATGGATTGAACTTCTCAAAGGAAACGATGAAGCTTGGGAGATGGGTAATATTGTGCACA 1344

Qy      1832 CACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAG 1891
Db      1345 CACTAACAAACAGAAGGTGGCTGGAAAAGTGTGTTACTTATGCTGAAAGTCACGATCAAG 1404

Qy      1892 CTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTA 1951
Db      1405 CACTTGTTGGAGACAAGACTATTGCATTCTGGTTGATGGACAAGGATATGTATGATTTCA 1464

Qy      1952 TGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGA 2011
Db      1465 TGGCGCTGAACGGACCTTCGACGCCTAATATTGATCGTGGAATAGCACTGCATAAAATGA 1524

Qy      2012 TTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAAT 2071
Db      1525 TTAGACTTATCACAATGGGTCTAGGAGGAGAGGGTTATCTTAACTTTATGGGAAATGAGT 1584

Qy      2072 TCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAG 2131
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Db   1585 TCGGGCATCCTGAATGGATAGACTTTCCAAGAGGCCCACAAGTACTTCCAAGTGGTAAGT 1644

Qy   2132 TAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATG 2191
Db   1645 TCATCCCAGGAAACAACAACAGTTACGACAAATGCCGTCGAAGATTTGACCTGGGTGATG 1704

Qy   2192 CAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAG 2251
Db   1705 CAGAATTTCTTAGGTATCATGGTATGCAGCAGTTTGATCAGGCAATGCAGCATCTTGAGG 1764

Qy   2252 ATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATA 2311
Db   1765 AAAAATATGGTTTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATA 1824

Qy   2312 GGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAA 2371
Db   1825 AGGTGATCGTGTTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAGTA 1884

Qy   2372 GCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACT 2431
Db   1885 GCTATTTCGACTACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACT 1944

Qy   2432 CAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCT 2491
Db   1945 CGGACGCTGGACTCTTTGGTGGATTTGGTAGGATCCATCACACTGCAGAGCACGTCACTT 2004

Qy   2492 TTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAG 2551
Db   2005 CTGACTGCCAACATGACAACAGGCCCCATTCATTCTCAGTGTACACTCCTAGCAGAACCT 2064

Qy   2552 CAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAG 2596
Db   2065 GTGTTGTCTATGCTCCAATGAACTAACAGCAAAGTGCAGCATACG 2109
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RESULT 7
US-10-084-817-92
; Sequence 92, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 92
;   LENGTH: 2994
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CB1
US-10-084-817-92

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  Query Match             21.9%;  Score 578.2;  DB 9;  Length 2994;
  Best Local Similarity   57.5%;  Pred. No. 6.2e-149;
  Matches 1164;  Conservative    0;  Mismatches  813;  Indels   48;  Gaps    5;

Qy    544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603
Db    215 GAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 274

Qy    604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663
Db    275 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 334

Qy    664 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 720
Db    335 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAATGGGCC 394

Qy    721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db    395 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 454

Qy    781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db    455 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 514

Qy    841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898
Db    515 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 574

Qy    899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957
Db    575 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 634

Qy    958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017
Db    635 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGA 688

Qy   1018 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1077
Db    689 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 748

Qy   1078 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTT 1137
Db    749 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTT 808

Qy   1138 GGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGT 1197
Db    809 GGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGT 868

Qy   1198 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCCGACGACCTTAAG 1257
Db    869 TACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAA 928

Qy   1258 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1317
Db    929 GAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGC 988

Qy   1318 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTAC 1377
Db    989 CATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTAT 1048

Qy   1378 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1437
Db   1049 TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC 1108

Qy   1438 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAA 1497
Db   1109 AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC 1168

Qy   1498 TTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCG 1557
Db   1169 TTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGT 1228

Qy   1558 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTT 1617
Db   1229 CAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTG 1288

Qy   1618 GTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1677
Db   1289 ACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATA 1348

Qy   1678 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGC 1737
Db   1349 GCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGT 1408

Qy   1738 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCA---AGAAA 1794
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Db     1409 TTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1468

Qy     1795 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 1854
Db     1469 AAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTT 1528

Qy     1855 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 1914
Db     1529 GAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTG 1588

Qy     1915 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACA 1974
Db     1589 GCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACT 1648

Qy     1975 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2034
Db     1649 CCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTT 1708

Qy     2035 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2094
Db     1709 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGGCATCCTGAATGGTTAGAC 1768

Qy     2095 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGT 2154
Db     1769 TTCCCAAGAAAA--------------------------------GGAAATAATGAGAGT 1795

Qy     2155 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2214
Db     1796 TACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1855

Qy     2215 TTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2274
Db     1856 CTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCT 1915

Qy     2275 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2334
Db     1916 CCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTGAAAGAGCA 1975

Qy     2335 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCC 2394
Db     1976 GGTCTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGA 2035

Qy     2395 TGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2454
Db     2036 ACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGG 2095

Qy     2455 TTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGT 2514
Db     2096 CATCAGAGACTGGACCACAGCACTGACTTTTTTCTGAGGCTTTTGAACATAATGGCGT 2155

Qy     2515 CCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTC 2559
Db     2156 CCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATC 2200
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RESULT 8
US-09-918-624B-30
; Sequence 30, Application US/09918624B
; Publication No. US20030113720A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
; FILE REFERENCE: PA-0033 US
; CURRENT APPLICATION NUMBER: US/09/918,624B
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/222,470
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
US-09-918-624B-30

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  Query Match             21.8%;  Score 576.6;  DB 9;  Length 2955;
  Best Local Similarity   57.4%;  Pred. No. 1.7e-148;
  Matches 1163;  Conservative    0;  Mismatches  814;  Indels   48;  Gaps    5;

Qy      544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603
Db      187 GAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 246

Qy      604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663
Db      247 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 306

Qy      664 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 720
Db      307 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTCCAAAGAATGGGCC 366

Qy      721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db      367 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 426

Qy      781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db      427 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 486

Qy      841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898
Db      487 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 546

Qy      899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957
Db      547 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 606

Qy      958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017
Db      607 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGA 660

Qy     1018 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1077
Db      661 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720

Qy     1078 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTT 1137
Db      721 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTT 780

Qy     1138 GGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGT 1197
Db      781 GGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGT 840

Qy     1198 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1257
Db      841 TACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAA 900

Qy     1258 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1317
Db      901 GAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGC 960

Qy     1318 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTAC 1377
Db      961 CATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTAT 1020

Qy     1378 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGATTCCCGCCTCTTTAACTATGGA 1437
Db     1021 TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC 1080

Qy     1438 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAA 1497
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Db     1081 AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC 1140

Qy     1498 TTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCG 1557
Db     1141 TTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGT 1200

Qy     1558 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTT 1617
Db     1201 CAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTG 1260

Qy     1618 GTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1677
Db     1261 ACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATA 1320

Qy     1678 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGC 1737
Db     1321 GCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGT 1380

Qy     1738 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCA---AGAAA 1794
Db     1381 TTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1440

Qy     1795 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 1854
Db     1441 AAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTT 1500

Qy     1855 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 1914
Db     1501 GAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTG 1560

Qy     1915 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACA 1974
Db     1561 GCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACT 1620

Qy     1975 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2034
Db     1621 CCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTT 1680

Qy     2035 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2094
Db     1681 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGGCATCCTGAATGGTTAGAC 1740

Qy     2095 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGT 2154
Db     1741 TTCCCAAGAAAA---------------------------------GGAAATAATGAGAGT 1767

Qy     2155 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2214
Db     1768 TACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1827

Qy     2215 TTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2274
Db     1828 CTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCT 1887

Qy     2275 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2334
Db     1888 CCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCA 1947

Qy     2335 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCC 2394
Db     1948 GGTCTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGA 2007

Qy     2395 TGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2454
Db     2008 ACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGG 2067

Qy     2455 TTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGT 2514
Db     2068 CATCAGAGACTGGACCACAGCACTGACTTTTTTTCTGAGGCTTTGAACATAATGGGCGT 2127

Qy     2515 CCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTC 2559
Db     2128 CCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATC 2172
```

RESULT 9
US-09-880-107-2148
; Sequence 2148, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2148
;   LENGTH: 2955
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

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  Query Match            21.8%;  Score 576.6;  DB 10;  Length 2955;
  Best Local Similarity  57.4%;  Pred. No. 1.7e-148;
  Matches 1163;  Conservative    0;  Mismatches  814;  Indels   48;  Gaps    5;

Qy      544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603
Db      187 GAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 246

Qy      604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663
Db      247 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 306

Qy      664 TATGAAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 720
Db      307 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTCCAAAGAATGGGCC 366

Qy      721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db      367 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 426

Qy      781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db      427 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 486

Qy      841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898
Db      487 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 546

Qy      899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957
Db      547 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 606

Qy      958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017
Db      607 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGA 660

Qy     1018 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1077
Db      661 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720

Qy     1078 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTT 1137
Db      721 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTT 780
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Qy   1138 GGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGT 1197
Db    781 GGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGT 840

Qy   1198 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1257
Db    841 TACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAA 900

Qy   1258 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1317
Db    901 GAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGC 960

Qy   1318 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTAC 1377
Db    961 CATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTAT 1020

Qy   1378 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1437
Db   1021 TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC 1080

Qy   1438 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAA 1497
Db   1081 AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC 1140

Qy   1498 TTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCG 1557
Db   1141 TTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGT 1200

Qy   1558 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTT 1617
Db   1201 CAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTG 1260

Qy   1618 GTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1677
Db   1261 ACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATA 1320

Qy   1678 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGC 1737
Db   1321 GCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGT 1380

Qy   1738 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCA---AGAAA 1794
Db   1381 TTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1440

Qy   1795 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 1854
Db   1441 AAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTT 1500

Qy   1855 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 1914
Db   1501 GAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTG 1560

Qy   1915 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACA 1974
Db   1561 GCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACT 1620

Qy   1975 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2034
Db   1621 CCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTT 1680

Qy   2035 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2094
Db   1681 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGGCATCCTGAATGGTTAGAC 1740

Qy   2095 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGT 2154
Db   1741 TTCCCAAGAAAA--------------------------------GGAAATAATGAGAGT 1767

Qy   2155 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2214
Db   1768 TACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1827

Qy   2215 TTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2274
Db   1828 CTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTCAGCT 1887

Qy   2275 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2334
Db   1888 CCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCA 1947

Qy   2335 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCC 2394
Db   1948 GGTCTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGA 2007

Qy   2395 TGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2454
Db   2008 ACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGG 2067

Qy   2455 TTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGT 2514
Db   2068 CATCAGAGACTGGACCACAGCACTGACTTTTTTTCTGAGGCTTTTGAACATAATGGGCGT 2127

Qy   2515 CCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTC 2559
Db   2128 CCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATC 2172
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RESULT 10
US-09-770-149-955/c
; Sequence 955, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-955

Query Match 9.7%; Score 257.8; DB 10; Length 602;
Best Local Similarity 75.1%; Pred. No. 9.3e-61;
Matches 322; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

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Qy   2151 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2210
Db    602 CAGTTATGACAAATGCCGCCGCAGATTTGATCTTGGGGATGCAGATTATCTCAGATACCG 543

Qy   2211 TGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2270
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Db       542 CGGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGAC 483

Qy      2271 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2330
             ||| || ||||| ||||||||||||| || |||| ||||||  | || ||||| ||||
Db       482 TTCGGAGCACCAATTCATATCACGAAAAGACGAAGCAGATAGAGTAATCGTATTCGAAAG 423

Qy      2331 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2390
             |||  | || || ||||||||||| |||||||||| |  ||||| |  || || |||||
Db       422 AGGTGATCTCGTCTTTGTCTTTAACTTTCACTGGACCAGCAGCTACTTTGATTACCGCAT 363

Qy      2391 AGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2450
               |  |||    |||||||||||||| ||| | |  |||||||| || ||||| || |||||
Db       362 TGGTTGCTCCAAGCCTGGAAAATATAAGATCGTATTGGACTCGGACGATCCTCTCTTTGG 303

Qy      2451 TGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGA 2510
             ||| |||     || | ||||  || || || || || ||||| | ||| || |  || || ||
Db       302 TGGATTCAATAGGCTCGATCGCAAGGCAGAGTACTTCACTTATGATGGCTTATACGACGA 243

Qy      2511 TCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGT 2570
               || ||   | ||  | ||||| |||||||| |||| ||| || ||||| |||||  |||
Db       242 ACGACCCTGCTCCTTCATGGTCTATGCACCGTGTAGAACCGCCGTGGTTTATGCTTTAGC 183

Qy      2571 AGACAAAGA 2579
              | || | ||
Db       182 AAACCACGA 174
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RESULT 11
US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
;   LENGTH: 604
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (12)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (517)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (540)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (567)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (593)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-453

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  Query Match             5.1%;  Score 136;  DB 10;  Length 604;
  Best Local Similarity   58.8%;  Pred. No. 4.6e-27;
  Matches  254;  Conservative    1;  Mismatches  171;  Indels    6;  Gaps    1;

Qy       903 GGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAA 962
              | ||   ||| |  | |||   || ||       | |        |||| |  |     ||| |
Db        47 GTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAATTATGA 106

Qy       963 TGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAA 1022
             | | ||||| |  |||||        |||  |     |||    ||  | ||  |  | |||||
Db       107 TTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGACCAAA 160

Qy      1023 GAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAA 1082
             ||| |||  |      || ||||| ||||||||||| | |||||      |    | ||    ||
Db       161 GAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAAGGAAA 220

Qy      1083 AATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTA 1142
             | |       || ||       |||||| |      | || || ||   |  || |||   ||||| ||
Db       221 AGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTTGGATA 280

Qy      1143 CAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCA 1202
             |||     | ||  | ||||| ||     |||||| |||| || || || |||||||| ||
Db       281 CAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTTACCA 340

Qy      1203 TGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTT 1262
               |||||| || |||||| |    |||||||| |||||| || || || ||   |      |
Db       341 AATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAAGAACT 400

Qy      1263 GATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGC 1322
             | | || | ||||||     | || ||    | || ||| | ||    | || ||     :|||||
Db       401 GGTAGACACAGCTCATTYCATGGGTATCATAGTCCTCTTAGATGTGGTACAAGCSCATGC 460

Qy      1323 ATCAAATAATAC 1334
              ||||| ||| |
Db       461 TTCAAAAAATTC 472
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RESULT 12
US-09-770-444-893
; Sequence 893, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 893
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-770-444-893

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  Query Match             4.3%;  Score 114.6;  DB 10;  Length 441;
  Best Local Similarity   67.2%;  Pred. No. 3.1e-21;
  Matches  162;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;
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Qy       2352 TAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAA 2411

Db          1 TAACTTCCACTGGACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAA 60

Qy       2412 ATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCA 2471

Db         61 GTACAAAATCGTTTTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGA 120

Qy       2472 TAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGT 2531

Db        121 CTCCGCGGAGTTTTTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGT 180

Qy       2532 GTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGA 2591

Db        181 GTATGCACCGTGCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGA 240

Qy       2592 A 2592

Db        241 A 241
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RESULT 13
US-10-025-380-304/c
; Sequence 304, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-304

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  Query Match             4.0%;  Score 104.8;  DB 9;  Length 601;
  Best Local Similarity   52.2%;  Pred. No. 1.9e-18;
  Matches  310;  Conservative    0;  Mismatches  272;  Indels   12;  Gaps    3;

Qy        544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603

Db        590 GAGATCGACCGGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 531

Qy        604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663

Db        530 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 471

Qy        664 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 720

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Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780

Db        410 CCGGGAGCAGAAGGAGTTTTTCTTACTGGAGATTTAATGGTTGGAATCCATTTTCGTAC 351

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Db        350 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 291

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898

Db        290 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 231

Qy        899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957

Db        230 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 171

Qy        958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017

Db        170 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCGGA 117

Qy       1018 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1077

Db        116 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 57

Qy       1078 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131

Db         56 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAA 3
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RESULT 14
US-09-922-217-304/c
; Sequence 304, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-304

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  Query Match             4.0%;  Score 104.8;  DB 10;  Length 601;
  Best Local Similarity   52.2%;  Pred. No. 1.9e-18;
  Matches  310;  Conservative    0;  Mismatches  272;  Indels   12;  Gaps    3;

Qy        544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603

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Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db        410 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 351

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db        350 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 291

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898
Db        290 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 231

Qy        899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957
Db        230 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 171

Qy        958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017
Db        170 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCGGA 117

Qy       1018 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1077
Db        116 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 57

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RESULT 15
US-09-833-263-304/c
; Sequence 304, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Aijun
;  APPLICANT:  Clapper, Jonathan D.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Meagher, Madeleine J.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.471C12
;  CURRENT APPLICATION NUMBER: US/09/833,263
;  CURRENT FILING DATE:  2001-04-10
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 304
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-833-263-304

  Query Match             4.0%;  Score 104.8;  DB 10;  Length 601;
  Best Local Similarity   52.2%;  Pred. No. 1.9e-18;
  Matches  310;  Conservative    0;  Mismatches  272;  Indels   12;  Gaps    3;

Qy        544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603
Db        590 GAGATCGACCGGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 531

Qy        604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663
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Qy        664 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 720
Db        470 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAATGGGCC 411

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db        410 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 351

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
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Db        290 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 231

Qy        899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957
Db        230 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 171

Qy        958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table:   IDENTITY_NUC
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Searched:        16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 7:  em_estro:*
                 8:  em_htc:*
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                 12:  gb_est3:*
                 13:  gb_est4:*
                 14:  gb_est5:*
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                 17:  gb_gss:*
                 18:  em_gss_hum:*
                 19:  em_gss_inv:*
                 20:  em_gss_pln:*
                 21:  em_gss_vrt:*
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                 25:  em_gss_other:*
                 26:  em_gss_pro:*
                 27:  em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1122.6	42.4	2732	11	AY109532	AY109532 Zea mays
3	615.8	23.3	3012	11	AY105679	AY105679 Zea mays
4	564.4	21.3	2738	11	AK009815	AK009815 Mus muscu
5	482.2	18.2	728	14	BU008463	BU008463 QGH7K17.y
6	473	17.9	713	14	BQ986883	BQ986883 QGF10L08.
7	436.2	16.5	689	13	BI308555	BI308555 EST529965
8	436	16.5	801	10	BE195628	BE195628 HVSMEh008
9	424.2	16.0	678	10	AV939010	AV939010 AV939010
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35	342	12.9	592	14	BQ608128	BQ608128 BRY_4030
36	340	12.8	516	14	BQ253050	BQ253050 sao05e05.
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38	336.8	12.7	761	13	BM411030	BM411030 EST585357
39	332.8	12.6	568	14	BQ240653	BQ240653 TaE05014F
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44	307.6	11.6	751	13	BI920158	BI920158 EST540093
45	306.4	11.6	898	14	BQ716536	BQ716536 AGENCOURT

ALIGNMENTS

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DEFINITION  Zea mays CL1245_1 mRNA sequence.
ACCESSION   AY109521
VERSION     AY109521.1  GI:21213273
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 2766)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 2766)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
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                     /db_xref="MaizeDB:630161"
                     /db_xref="taxon:4577"
                     /clone="CL1245_1"
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            /clone_lib="Maize Mapping Project/DuPont Cornsensus
            Library"
            /note="this sequence is part of a project of EST
            assemblies resulting from the application of public
            contigs to seed DuPont contigs; this resource was
            assembled by DuPont as part of a collaboration for the
            overgo addressing of BACs in conjunction with the Maize
            Mapping Project"
BASE COUNT     715 a    546 c    689 g    718 t     98 others
ORIGIN

  Query Match          44.5%;  Score 1177.6;  DB 11;  Length 2766;
  Best Local Similarity  70.8%;  Pred. No. 1.2e-257;
  Matches 1486;  Conservative    0;  Mismatches  612;  Indels    0;  Gaps    0;

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Qy        626 ACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTC 685
Db        483 ATCAACATGAAGGTGGTTTGGATGCATTTTCACGCGGTTACGAAAAGCTTGGATTTACTC 542

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Qy        746 TTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTG 805
Db        603 TAGGTGACTTCAACAACTGGAACCCAAATGCTGATGCTATGGCCAGAAATGAGTACGGCG 662

Qy        806 TCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCA 865
Db        663 TTTGGGAGATTTTCCTGCCTAACAATGCTGATGGTTCCCCTGCTATTCCTCATGGCTCAC 722

Qy        866 GAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCA 925
Db        723 GTGTAAAGATACGGATGGACACACCATCTGGTGTTAAGGATTCCATTCCTGCCTGGATCA 782

Qy        926 ACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCG 985
Db        783 AGTTTTCTGTGCAGGCTCCAGGTGAAATACCATACAACGGTATATATTATGACCCACCTG 842

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Qy       1586 ACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTA 1645
Db       1443 ATTTTGGATTTGCCACTGATGTTGATGCAGTAGTTTACCTAATGCTGGTAAACGATCTTA 1502

Qy       1646 TTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACAT 1705
Db       1503 TTCGTGGGCTTTATCCAGAAGCTGTATCCATTGGCGAAGATGTCAGCGGAATGCCNNNNN 1562

Qy       1706 TTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTG 1765
Db       1563 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1622

Qy       1766 CTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTG 1825
Db       1623 NNNNNNNNNNNNNNNNNNNNNTGAAGCAAAGTGACGAATATTGGGAAATGGGTGACATCG 1682

Qy       1826 TTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATG 1885
Db       1683 TGCACACCTTAACAAATAGAAGGTGGCTTGAAAAGTGTGTCACTTATTGTGAAAGTCATG 1742

Qy       1886 ATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATG 1945
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Qy       2306 GAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGA 2365
Db       2163 AGGATAAGGTGATCATCTTTGAGAGAGGAGATTTGGTCTTCGTGTTCAACTTCCACTGGA 2222

Qy       2366 CAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCT 2425
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Qy       2426 TGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATT 2485
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RESULT 2
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LOCUS       AY109532                2732 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays CL1742_1 mRNA sequence.
ACCESSION   AY109532
VERSION     AY109532.1  GI:21213287
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 2732)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 2732)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
     source          1..2732
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                     /clone="CL1742_1"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      659 a    506 c    679 g    710 t    178 others
ORIGIN

  Query Match             42.4%;  Score 1122.6;  DB 11;  Length 2732;
  Best Local Similarity   69.3%;  Pred. No. 4.1e-245;
  Matches 1452;  Conservative    0;  Mismatches  642;  Indels    0;  Gaps    0;

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Qy        540 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 599
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Qy       1920 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATT 1979
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Qy       1980 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2039
Db       1903 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1962

Qy       2040 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2099
Db       1963 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 2022

Qy       2100 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGA 2159
Db       2023 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 2082

Qy       2160 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2219
Db       2083 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2142

Qy       2220 AGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2279
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Qy       2280 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2339
Db       2203 CCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTGTGTTCGAAAAGGGAGATTT 2262

Qy       2340 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCT 2399
Db       2263 GGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTTGACTACCGTATTGGTTGTCG 2322

Qy       2400 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2459
Db       2323 AAAGCCTGGGGTGTATAAGGTGGTCTTGGACTCCGACGCTGGACTATTTGGTGGATTTAG 2382

Qy       2460 GAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2519
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Qy       2520 TTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTATGCACTAGTAGA 2573
Db       2443 TTCGTTCTCGGTTTATACACCAAGCAGAACATGTGTCGTCTATGCTCCAGTGGA 2496
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DEFINITION  Zea mays PCO072723 mRNA sequence.
ACCESSION   AY105679
VERSION     AY105679.1  GI:21208757
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 3012)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 3012)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
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                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      837 a    628 c    790 g    756 t      1 others
ORIGIN

  Query Match             23.3%;  Score 615.8;  DB 11;  Length 3012;
  Best Local Similarity   59.6%;  Pred. No. 1.2e-129;
  Matches 1176;  Conservative    0;  Mismatches  742;  Indels   55;  Gaps    6;

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Qy        598 CAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCT 657
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Qy        658 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 717
Db        527 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 586

Qy        718 GCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 777
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Qy        778 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 837
Db        647 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 703

Qy        838 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
Db        704 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 763

Qy        898 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 953
Db        764 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 823

Qy        954 --TCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011
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Qy       1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071
Db        884 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 943

Qy       1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131
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Qy       1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311
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Qy  1542 TCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAAC 1601
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Qy  1662 AGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCA 1721
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Qy  1839 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1898
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Qy  1899 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1958
Db  1784 TGGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGA 1843

Qy  1959 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2018
Db  1844 CTTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTT 1903

Qy  2019 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2078
Db  1904 CATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCA 1963

Qy  2079 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCC 2138
Db  1964 CCCAGAATGGATTGACTTTCCAAGAGAA-------------------------------- 1991

Qy  2139 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2198
Db  1992 -GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCA 2050

Qy  2199 TTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATA 2258
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Qy  2259 TGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGAT 2318
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Qy  2319 TGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTCACTGGACAAAAAGCTATTC 2378
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Qy  2379 AGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGA 2438
Db  2231 GGGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGC 2290

Qy  2439 TCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCT 2491
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RESULT 4
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LOCUS       AK009815                2738 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
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            ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME) (BRANCHER ENZYME),
            full insert sequence.
ACCESSION   AK009815
VERSION     AK009815.1  GI:12844841
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
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            clone:2310045H19.
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
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PUBMED      11217851
REFERENCE   5  (bases 1 to 2738)
AUTHORS     Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
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            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0 and subtraction to
            Rot = 25.0. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
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                     /db_xref="FANTOM_DB:2310045H19"
                     /db_xref="MGD:MGI:1907315"
                     /db_xref="taxon:10090"
                     /clone="2310045H19"
                     /sex="male"
                     /tissue_type="tongue"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             21. .2129
                     /note="data source:SPTR, source key:Q04446, evidence:ISS
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                     (GLYCOGEN BRANCHING ENZYME) (BRANCHER ENZYME)
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                     EFSGWNPFSHPYKKLEYGKWELYIPPKQNKSPLIPHGSKLKVVITSKSGEILYRISPW
                     AKYVVRENNNVNYDWIHWAPEDPYKFKHSRPKKPRSLRIYESHVGISSHEGKIASYKH
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                     LRFLLSNIRWWLEEYCFDGFRFDGVTSMLYHHHGMGQGFSGDYNEYFGLQVDEDALIY
                     LMLANHLAHTLYPDSITIAEDVSGMPALCSPTSQGGGGFDYRLAMAIPDKWIQLLKEF
                     KDEDWNMGNIVYTLTNRRYLEKCVAYAESHDQALVGDKTLAFWLMDAEMYTNMSVLAP
                     FTPVIDRGIQLHKMIRLITHGLGGEGYLNFMGNEFGHPEWLDFPRKGNNESYHYARRQ
                     FNLTDDDLLRYKFLNNFDRDMNRLEERCGWLSAPQAYVSEKHEANKTITFERAGLLFI
                     FNFHPSKSYTDYRVGTATPGKFKIVLDSDAAEYGGHQRLDHNTNYFAEAFEHNGRPYS
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                     /note="putative"
BASE COUNT      780 a    562 c    624 g    772 t
ORIGIN

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  Best Local Similarity   57.3%;  Pred. No. 6.3e-118;
  Matches 1146;  Conservative    0;  Mismatches  806;  Indels   48;  Gaps    5;

Qy        544 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603
Db        117 GAGATTGACCCGTACCTGAAGCCCTTCGCCGCGGACTTCCAGCGCAGGTATAAGAAGTTT 176

Qy        604 AAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGT 663
Db        177 AGCCAGGTTTTGCATGACATTGGAGAGAATGAAGGTGGGATCGATAAGTTCTCCAGAGGC 236

Qy        664 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 720
Db        237 TATGAGTCATTTGGCATCCACAGATGTTCTGATGGTGGCATCTACTGCAAAGAATGGGCC 296

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db        297 CCAGGAGCAGAAGGAGTTTTTCTTACTGGAGAATTCAGTGGTTGGAATCCATTTTCTCAC 356

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db        357 CCATATAAAAAGCTGGAATACGGAAAATGGGAGCTGTATATCCCACCCAAGCAGAACAAA 416

Qy        841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898
Db        417 TCCCCCCTGATACCTCATGGGTCCAAGCTGAAGGTAGTTATTACTAGTAAGAGTGGCGAG 476

Qy        899 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 957
Db        477 ATACTGTATCGCATTTCCCCATGGGCAAAGTATGTGGTTCGTGAGAACAACAACGTGAAC 536

Qy        958 TATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGG 1017
Db        537 TATGATTGGATACACTGGGCTCC------AGAAGACCCCTATAAATTCAAGCATTCCAGA 590

Qy       1018 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1077
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Qy       1078 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTT 1137
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Qy       1138 GGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGT 1197
Db        711 GGGTATAACTGCATTCAGTTGATGGCGATCATGGAACATGCTTACTATGCCAGTTTTGGG 770

Qy       1198 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1257
Db        771 TACCAAATCACGAGCTTTTTTGCAGCTTCAAGTCGTTATGGAACTCCTGAAGAGCTGAAA 830

Qy       1258 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1317
Db        831 GAACTTGTTGACACAGCACATTCGATGGGCATTGTAGTCCTCCTAGATGTGGTTCATAGC 890

Qy       1318 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTAC 1377
Db        891 CATGCTTCAAAAAATTCAGAAGATGGGTTAAACATGTTTGATGGGACCGATTCCTGTTAT 950

Qy       1378 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1437
Db        951 TTTCACTCTGGACCCCGAGGGACCCATGATCTTTGGGACAGTAGATTATTTATCTATTCC 1010

Qy       1438 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAAA 1497
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Db     1011 AGCTGGGAAGTTTTAAGATTCCTTCTGTCGAACATAAGATGGTGGTTGGAGGAGTACTGC 1070

Qy     1498 TTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCG 1557
Db     1071 TTTGATGGCTTCCGTTTTGATGGTGTCACCTCTATGCTCTATCATCACCACGGAATGGGT 1130

Qy     1558 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTT 1617
Db     1131 CAAGGTTTTTCGGGTGACTATAATGAATATTTTGGACTACAAGTAGATGAAGATGCTTTG 1190

Qy     1618 GTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1677
Db     1191 ATTTATCTCATGTTGGCAAATCATTTGGCTCACACGTTGTACCCAGACTCGATAACAATA 1250

Qy     1678 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGC 1737
Db     1251 GCAGAGGATGTATCAGGGATGCCGGCTCTCTGTTCTCCAACTTCCCAGGGAGGCGGTGGT 1310

Qy     1738 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAA--- 1794
Db     1311 TTTGACTACAGATTAGCAATGGCTATTCCAGATAAATGGATCCAATTACTTAAGGAATTT 1370

Qy     1795 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 1854
Db     1371 AAAGATGAAGACTGGAATATGGGCAATATAGTGTATACTCTCACCAATCGACGCTACCTT 1430

Qy     1855 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 1914
Db     1431 GAAAAATGTGTGGCTTATGCAGAGAGTCATGATCAGGCATTGGTTGGTGACAAGACACTG 1490

Qy     1915 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACA 1974
Db     1491 GCGTTTTGGTTGATGGACGCTGAGATGTACACGAACATGAGCGTTCTGGCCCCTTTCACT 1550

Qy     1975 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2034
Db     1551 CCAGTAATTGATCGAGGAATACAGCTTCATAAGATGATTCGTCTCATCACTCACGGGCTC 1610

Qy     2035 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2094
Db     1611 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAGTTTGGGCATCCTGAATGGTTGGAC 1670

Qy     2095 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCGGAAACCAATTCAGT 2154
Db     1671 TTCCCAAGGAAA-------------------------------GGAAATAATGAGAGT 1697

Qy     2155 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2214
Db     1698 TACCATTATGCCAGAAGGCAGTTTAATTTAACCGACGATGACCTTCTTCGCTATAAGTTC 1757

Qy     2215 TTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2274
Db     1758 CTAAATAACTTTGACAGAGATATGAATAGACTGGAAGAAAGATGTGGTTGGCTTTCAGCT 1817

Qy     2275 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2334
Db     1818 CCACAGGCCTACGTGAGTGAAAAACATGAAGCCAATAAGACAATCACCTTTGAGAGAGCA 1877

Qy     2335 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGCC 2394
Db     1878 GGACTTCTCTTTATTTTCAACTTCCACCCAAGCAAGAGCTATACGGACTACCGAGTCGGG 1937

Qy     2395 TGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2454
Db     1938 ACAGCAACACCAGGGAAGTTCAAAATTGTACTAGATTCTGACGCAGCGGAGTATGGAGGT 1997

Qy     2455 TTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGT 2514
Db     1998 CATCAGAGACTGGACCACAACACCAACTACTTTGCTGAGGCTTTTGAACATAATGGGCGC 2057

Qy     2515 CCTCGTTCAATTATGGTGTA 2534
Db     2058 CCCTATTCTCTTCTGGTGTA 2077
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RESULT 5
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LOCUS       BU008463                728 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGH7K17.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGH7K17, mRNA sequence.
ACCESSION   BU008463
VERSION     BU008463.1  GI:22442858
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGH7  row: K  column: 17.
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                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=leaves dark grow
                     TAG_SEQ=GCTAGTCGGG"
BASE COUNT      227 a    133 c    149 g    218 t      1 others
ORIGIN

  Query Match             18.2%;  Score 482.2;  DB 14;  Length 728;
  Best Local Similarity   78.8%;  Pred. No. 2.8e-99;
  Matches  574;  Conservative    0;  Mismatches  154;  Indels    0;  Gaps    0;

Qy        661 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 720
Db          1 GGTTATGAAAAATTAGGTTTCACTCGAAGCAAAACAGGTATCACTTATAGAGAATGGGCA 60

Qy        721 CTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 780
Db         61 CCTGGGGCAAAGTCTGCTTCACTTACTGGAGATTTCAACAACTGGAATCCAAATGCTGAT 120

Qy        781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 840
Db        121 GTTATGACCCGGAATGAATTTGGTGTGTGGGAGATCTTTTTGCCAAACAATGTTGATGAT 180
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Qy         841 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTT 900
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Qy         901 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 960
Db         241 AAAGACTCGATTCCTGCTTGGATCAAGTTTTCAGTACAAGCACCTGGTGAGATTCCTTAT 300

Qy         961 AATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCA 1020
Db         301 AATGGAATATACTATGATCCCCCACAAGAGGAAAAATACGTGTTTCAACATCCAAGACCA 360

Qy        1021 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1080
Db         361 AAGAAGCCGAAATCTCTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCA 420

Qy        1081 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGG 1140
Db         421 ATGATCAACACGTATGCTAACTTTAGAGACGATGTTCTCCCTCGCATAAAAAAACTCGGT 480

Qy        1141 TACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTAT 1200
Db         481 TACAATGCAGTTCAAATCATGGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTAC 540

Qy        1201 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1260
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Qy        1261 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1320
Db         601 ATGATTGATAAAGCACATGAATTAGGTCTTGTTGTTCTCATGGATATTGTGCATAGTCAT 660

Qy        1321 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTT 1380
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Qy        1381 CACTCTGG 1388
Db         721 CATTCTGG 728
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RESULT 6
BQ986883

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LOCUS       BQ986883                713 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  QGF10L08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGF10L08, mRNA sequence.
ACCESSION   BQ986883
VERSION     BQ986883.1  GI:22404408
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGF10  row: L  column: 08.
FEATURES             Location/Qualifiers
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                     /clone="QGF10L08"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=flowers post-fertilized
                     TAG_SEQ=TGCCATCGGG"
BASE COUNT      221 a    132 c    146 g    214 t
ORIGIN

  Query Match            17.9%;  Score 473;  DB 14;  Length 713;
  Best Local Similarity  79.0%;  Pred. No. 3.5e-97;
  Matches  563;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy         676 GGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCA 735
Db           1 GGTTTCACTCGAAGCAAAACAGGTATCACTTATAGAGAATGGGCACCTGGGGCAAAGTCT 60

Qy         736 GCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAAT 795
Db          61 GCTTCACTTATTGGAGATTTCAACAACTGGAATCCAAATGCTGATGTTATGACCCGGAAT 120

Qy         796 GAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCT 855
Db         121 GAATTTGGTGTGTGGGAGATCTTTTTGCCAAACAATGTTGATGATTCTTCACCTATTCCT 180

Qy         856 CATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCT 915
Db         181 CATGGTTCTCGAGTAAAGATTCGTATGGATACGCCATCTGGCATTAAAGACTCGATTCCT 240

Qy         916 GCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTAT 975
Db         241 GCTTGGATCAAGTTTTCAGTACAAGCACCTGGTGAGATTCCTTATAATGGAATATACTAT 300

Qy         976 GATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCG 1035
Db         301 GATCCCCCACAAGAGGAAAAATACGTGTTTCAACATCCAAGACCAAAGAAGCCGAAATCT 360

Qy        1036 CTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATAC 1095
Db         361 CTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCAATGATCAACACGTAT 420

Qy        1096 GTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAA 1155
Db         421 GCTAACTTTAGAGACGATGTTCTCCCTCGCATAAAAAAACTCGGTTACAATGCAGTTCAA 480

Qy        1156 ATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTT 1215
Db         481 ATCATGGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTACCATGTGACAAATTTT 540

Qy        1216 TTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCT 1275
Db         541 TTTGCACCAAGTAGTCGATGTGGAACTCCAGATGATCTTAAATCAATGATTGATAAAGCA 600

Qy        1276 CATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACT 1335
Db         601 CATGAATTAGGTCTTGTTGTTCTCATGGATATTGTGCATAGTCATTCATCAAACAACACA 660

Qy        1336 TTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGG 1388
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Db       661 TTAGATGGATTAAATATGTTTGATGGAACTGATAGTCAATACTTTCATTCTGG 713

RESULT 7
BI308555
LOCUS       BI308555                 689 bp    mRNA    linear   EST 20-JUL-2001
DEFINITION  EST529965 GPOD Medicago truncatula cDNA clone pGPOD-7017 5' end,
            mRNA sequence.
ACCESSION   BI308555
VERSION     BI308555.1  GI:14982882
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
            ,J. and Fraser,C.M.
  TITLE     ESTs from developing reproductive tissues of Medicago truncatula
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Michael A. Grusak
            USDA/ARS Children's Nutrition Research Center
            Baylor College of Medicine
            1100 Bates Street, Houston, TX 77030-2600, USA
            Tel: 713-798-7044
            Fax: 713-798-7078
            Email: mgrusak@bcm.tmc.edu
            B395410e
             TIGR sequence name: MTOAQ93TK
             More information is available at: www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
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                     /dev_stage="Immature pods, ranging in age from 15 to 30
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                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Immature pods, ranging in age from 15 to 30 days
                     after pollination,  were collected from greenhouse-grown
                     plants.  At harvest, seeds were removed from pods and
                     isolated pod walls were collected and  immediately frozen
                     in liquid nitrogen.  Pod walls were pooled for  mRNA
                     extraction. cDNA was prepared from polyA+ enriched RNA.
                     The cDNA was directionally  ligated into the Unizap XR
                     vector from Stratagene and packaged using  Gigapack III
                     Gold packaging extracts.  Plasmids containing cDNA inserts
                     were excised from the recombinant lambda-Zap phage using
                     Ex-assist helper phage and propogated in XLOLR cells."
BASE COUNT     198 a    112 c    165 g    214 t
ORIGIN

  Query Match            16.5%;  Score 436.2;  DB 13;  Length 689;
  Best Local Similarity  77.1%;  Pred. No. 8.5e-89;
  Matches  531;  Conservative    0;  Mismatches  158;  Indels    0;  Gaps    0;

Qy      1895 TAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGG 1954
             | || ||||| || ||  |||||| ||| |||||||||||||||||||| || ||||
Db         1 TGGTTGGTGACAAGACACTAGCATTTTGGTTGATGGACAAGGATATGTATGACTTCATGG 60

Qy      1955 CTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTA 2014
             || | || ||||| || ||  |  |||| |||||||| || ||||| ||||| |||||||
Db        61 CTTTAGACAGACCATCTACTCCTCTAATCGATCGTGGTATTGCATTACACAAAATGATTA 120

Qy      2015 GGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCG 2074
             ||||| | ||||||||  | || || ||||||||  ||||||| ||||| |||||||||
Db       121 GGCTTATTACTATGGGCCTTGGTGGTGAAGGGTATTTAAATTTTATGGGGAATGAATTCG 180

Qy      2075 GCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAA 2134
             |||| |||||||||||| ||||| || |||| ||| ||||| ||  || ||||| |||||
Db       181 GCCATCCTGAGTGGATCGATTTTCCAAGGGGTGATCAACATCTTCCTAATGGCACAGTAG 240

Qy      2135 TCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAG 2194
             | || || ||  |    ||||||||||||||||| || |||||||||| |||| |||||||
Db       241 TTCCTGGGAATAACAACAGTTATGATAAATGCAGGCGTAGATTTGACTTGGGTGATGCAG 300

Qy      2195 AATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATA 2254
             ||||| ||||||| | |||  |||||||||||| || ||||||| | || ||||| |
Db       301 AATATCTAAGATATCATGGAATGCAAGAATTTGATCGAGCTATGCAGCACCTAGAAGAAA 360

Qy      2255 AATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGA 2314
              ||||| || |||| ||| || ||||| |  || ||| | ||  ||||||| || ||
Db       361 GATATGGTTTCATGATTTCTGAGCACCAATATATTTCAAGGAAAAATGAAGGTGACAGAG 420

Qy      2315 TGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCT 2374
             | ||  |||||||  |   ||||| || ||||| || ||||||||||||| || | ||
Db       421 TTATAATCTTTGAAAGGGACAACCTGGTCTTTGTATTCAATTTTCACTGGACCAACAGTT 480

Qy      2375 ATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAG 2434
             ||||||| ||       | | |||  | ||||| |||||  ||| || ||||||| ||||
Db       481 ATTCAGATTACAAAGTTGGCTGTTTAAAGCCAGGGAAATATAAGATTGTCTTGGATTCAG 540

Qy      2435 ATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTG 2494
             ||||  |  | |||||||||||    ||  |  |||||| ||| || || ||||| |  |
Db       541 ATGAGTCCTTGTTTGGTGGCTTCAATAGGCTCAATCATACTGCTGAGTACTTCACTTCGG 600

Qy      2495 AAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAG 2554
             |||||||||||||||| || ||||||||   |  | || ||||||||||||| |||||||
Db       601 AAGGATGGTATGATGACCGGCCTCGTTCCTTCCTCGTTTATGCACCTTGTAGAACAGCAG 660

Qy      2555 TGGTCTATGCACTAGTAGACAAAGAAGAA 2583
             |||| ||||| || |||||   ||  |||
Db       661 TGGTATATGCTCTTGTAGATGGAGTTGAA 689


RESULT 8
BE195628
LOCUS       BE195628                 801 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0089P20f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0089P20f,
            mRNA sequence.
ACCESSION   BE195628
VERSION     BE195628.2  GI:13188305
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 26, 2000 this sequence version replaced gi:8707823.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 408
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 611.
FEATURES             Location/Qualifiers
     source          1..801
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                    /cultivar="Morex"
                    /db_xref="taxon:4513"
                    /clone="HVSMEh0089P20f"
                    /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                    HVcDNA0009 (5 to 45 DAP)"
                    /tissue_type="5-45 DAP Spike"
                    /lab_host="SOLR"
                    /note="Vector: lambdaZAP; Site_1: EcoRl; Site_2: Xhol;
                    Plants were grown in the greenhouse at the University of
                    California, Riverside (Fenton, SJ Close, TJ Close). Whole
                    spikes with awns trimmed were collected at 5, 10, 15, 20,
                    30 and 45 DAP (Fenton). Total RNA was prepared from each
                    pool, equal quantities of all six RNA pools were combined,
                    poly(A) RNA was purified from the mixture, one primary
                    unamplified cDNA library was made, and 1 million pfu were
                    in vivo excised to give pBluescript SK(-) cDNA phagemids
                    (Choi)in the TJ Close lab at the University of California,
                    Riverside. Phagemids were plated and picked at the Clemson
                    University Genomics Institute (CUGI) (Begum, Palmer,
                    Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                    sequencing and sequence analysis were performed at CUGI
                    (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                    The sequence has been trimmed to remove vector sequence
                    and contains a minimum of 100 bases of phred value 20 or
                    above. For more details on library preparation and
                    sequence analysis see
                    http://www.genome.clemson.edu/projects/barley. To order
                    this clone see http://www.genome.clemson.edu/orders Also
                    see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                    Genetically and physically anchored EST resources for
                    barley genomics. Barley Genetics Newsletter 31:29-30.
                    (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      220 a    146 c    198 g    236 t      1 others
ORIGIN

  Query Match             16.5%;  Score 436;  DB 10;  Length 801;
  Best Local Similarity   76.1%;  Pred. No. 9.6e-89;
  Matches  549;  Conservative    0;  Mismatches  171;  Indels    1;  Gaps    1;

Qy       1645 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1704
              |||||||| ||||  || |||||  |  |||||||||||||||| ||||||||||| |||
Db          2 ATTCATGGACTTTATCCGGATGCTGTATCCATTGGTGAAGATGTCAGCGGAATGCCTACA 61

Qy       1705 TTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1764
              ||||| || || |||| ||| || |||||||| |||||||||||| |||||||||||    |
Db         62 TTTTGCATCCCTGTCCCAGATGGTGGTGTTGGTTTTGACTATCGCCTGCATATGGCTGTA 121

Qy       1765 GCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1824
              || |||||| |||||||   | |||||| || | || ||       ||||| | |||| ||||||
Db        122 GCAGATAAATGGATTGAACTCCTCAAGCAAAGTGACGAATCTTGGAAAATGGGCGATATT 181

Qy       1825 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1884
              || || || || ||||||||||| |||      || ||||||||  | || || |||||||||
Db        182 GTGCACACCCTAACAAATAGAAGGTGGCTTGAGAAGTGTGTCACTTATGCAGAAAGTCAT 241

Qy       1885 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1944
              |||||||| ||||| ||||| || ||||| ||||||||| ||||||| ||||||||||||
Db        242 GATCAAGCACTAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTAT 301

Qy       1945 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2004
              ||||| |||||||||||||||||| |||||    |       || |||||||| |||||||| ||
Db        302 GATTTCATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACAT 361

Qy       2005 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2064
              || ||||| |||||||| || ||||| ||||| || |||||  || || |||||||||||||
Db        362 AAAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTAATTTCATGGGA 421

Qy       2065 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2124
              ||||| || || || ||||| ||||| ||||| |||||  || |    ||     ||    |
Db        422 AATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGGGGTCCGCANACTCTTCCAACC 481

Qy       2125 GGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2184
              |||  |||  |||| || ||  |        |||||||||||||| | || | |||||| ||
Db        482 GGCAAAGTTCTCCCTGGCAATAACAATAGTTATGATAAATGCCGCCGTAAATTTGATCTT 541

Qy       2185 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTAT 2244
              |||||||||||  |  | |||||  |||||   ||||||| || || |  |  | ||||   ||
Db        542 GGAGATGCAGATTTTCTTAGATATCGTGGAATGCAAGAGTTCGATCAGGCAATGCCCCAT 601

Qy       2245 CTTGAAGATAAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2304
              ||||| |   |||    | ||||||||| || || |||||||    | || || ||    |||
Db        602 CTTGAGGGAAAAATAGGGTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACTTGAG 661

Qy       2305 GGAGATAGGATGATTGT-ATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTG 2363
              | ||||| | |||    |  ||||||| ||||||   | || ||||| || || |||| |||
Db        662 GAAGATAAGGTGAACATCTTTTGAAAGAGGAAATTTGGTATTTGTTTTCAACTTTCCCTG 721

Qy       2364 G 2364
              |
Db        722 G 722


RESULT 9
AV939010
LOCUS       AV939010               678 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV939010 K. Sato unpublished cDNA library, strain H602 adult,
            heading stage top three leaves Hordeum vulgare subsp. spontaneum
            cDNA clone bah20e24 5', mRNA sequence.
ACCESSION   AV939010
VERSION     AV939010.1  GI:18234807
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1..678
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah20e24"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT      193 a    135 c    154 g    194 t      2 others
ORIGIN

  Query Match             16.0%;  Score 424.2;  DB 10;  Length 678;
  Best Local Similarity   77.7%;  Pred. No. 4.6e-86;
  Matches  524;  Conservative    0;  Mismatches  149;  Indels    1;  Gaps    1;

Qy        697 GGTATCACTTACCGTG-AGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTT 755
              ||||||||||||| | | ||||||| ||| || || || || ||    | || || ||
Db          5 GGTATCACTTACCGAGNAATGGGCTCCTGGNGCGCATTCTGCAGCATTAGTAGGTGACTT 64

Qy        756 CAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGAT 815
              |||||||||| || ||||||| || | ||||||   |   |||| | |||||| ||||||||
Db         65 CAACAATTGGAACCCAAATGCAGATACTATGACCAGAGATGATTATGGTGTTTGGGAGAT 124

Qy        816 TTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGAT 875
              ||| || || || ||||    ||||| || ||||| |||||||||||| ||   | || |||||
Db        125 TTTCCTCCCTAACAATGCTGATGGATCCCCTGCTATTCCTCATGGCTCACGTGTAAAGAT 184
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Qy    876 ACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTT 935
Db    185 ACGGATGGATACTCCATCTGGTGTGAAGGATTCAATTTCTGCTTGGATCAAGTTCTCTGT 244

Qy    936 ACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAG 995
Db    245 GCAGGCTCCAGGTGAAATACCATTCAATGGCATATATTATGATCCACCTGAAGAGGAGAA 304

Qy    996 GTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCA 1055
Db    305 GTATGTCTTCCAACATCCTCAACCTAAACGACCAGAGTCACTAAGGATATATGAATCACA 364

Qy   1056 TATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGT 1115
Db    365 CATTGGAATGAGCAGCCCGGAACCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGT 424

Qy   1116 TCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCA 1175
Db    425 GCTGCCAAGAATTAAAAGGCTTGGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCA 484

Qy   1176 TTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTT 1235
Db    485 TTCATACTATGCGAGCTTTGGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTT 544

Qy   1236 TGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGT 1295
Db    545 TGGAACTCCAGAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGT 604

Qy   1296 TCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTT 1355
Db    605 TCTTATGGATATTGTTCATAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTT 664

Qy   1356 TGACTGCACCGATA 1369
Db    665 CGATGGCACTGATA 678
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RESULT 10
BE602527

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LOCUS       BE602527                 731 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
            mRNA sequence.
ACCESSION   BE602527
VERSION     BE602527.2  GI:13190371
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Aug 21, 2000 this sequence version replaced gi:9860088.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 322
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 680.
FEATURES             Location/Qualifiers
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                     /clone="HVSMEh0099J22f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      194 a     132 c     186 g     216 t       3 others
ORIGIN

  Query Match             15.7%;  Score 414.6;  DB 10;  Length 731;
  Best Local Similarity   74.0%;  Pred. No. 7.1e-84;
  Matches  537;  Conservative    0;  Mismatches  187;  Indels    2;  Gaps    1;

Qy   1377 CTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGG 1436
Db      7 CTTTCATGGCGGCTCACGGGGCCATCACTGGATGTGGGATTCTCGTGTGTTCAACTACGG 66

Qy   1437 AAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCGTTCAA 1496
Db     67 GAATAAGGAAGTTATAAGGGTTCTACTTTCCAATGCCAGATGGGGCTTGAGGAATATAA 126

Qy   1497 ATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATC 1556
Db    127 GTTCCATGGGTTCCCATTCGACGGGCCCACCTTCATGATGTATACCCCCCATGGATTACA 186

Qy   1557 GGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGT 1616
Db    187 AGTACCTTT--ACAGGAGCTACCATGAATATTTTGGCTTTGCCACGGATGTAGATGCAGT 244

Qy   1617 TGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCAT 1676
Db    245 TGTTTACTTGATGCTGGTGAATGATCTAATTCACGCGCTNTATCCTGAAGCCGTTACTAT 304

Qy   1677 TGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCCAAGAGGGGGGTGTTGG 1736
Db    305 TGGTGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGGTTGG 364

Qy   1737 CTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTGAGTTGCTCAAGAAACG 1796
Db    365 TTTTGACTATCGCTTACATATGGCCGTTGCCGATAAATGGATTGAACTTCTCAAAGGAAG 424

Qy   1797 GGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGA 1856
Db    425 CGATGAAGGTTGGGAGATGGGTAATATTGTGCACACACTAACAAATAGAAGGTGGTTGGA 484

Qy   1857 AAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGC 1916
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Db       485 AAAGTGTGTTACTTATGCTGAAAGTCATGATCAAGCACTTGTTGGAGACAAGACTATTGC 544

Qy      1917 ATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATC 1976
             |||||| |||||||||||||||||||||||| ||||||||| |  |||| || ||| |
Db       545 ATTCTGGTTGATGGACAAGGATATGTATGATTTCATGGCTCTGAACGGACCTTCGACACC 604

Qy      1977 ATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGG 2036
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Db       605 TAATATTGATCGCGGAATAGCACTGCATAAAATGATTAGACTTATCACAATGGCTNTAGG 664

Qy      2037 AGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTT 2096
             |||||| || || || || || |||||||||||| ||| | || ||||| ||||| || |
Db       665 AGGAGAGGGTTATCTTAACTTTATGGGAAATGAGTTCCGGCATCCTGAATGGATAGACTN 724

Qy      2097 CCCTAG 2102
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Db       725 TCCAAG 730
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RESULT 11
BU005876
LOCUS       BU005876                 717 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGG9F08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGG9F08, mRNA sequence.
ACCESSION   BU005876
VERSION     BU005876.1  GI:22440271
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGG9  row: F  column: 08.
FEATURES             Location/Qualifiers
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                     /cultivar="L.serriola"
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                     /clone="QGG9F08"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=germinating seeds
                     TAG_SEQ=TCTGTGCGGG"
BASE COUNT      233 a    122 c    155 g    206 t      1 others
ORIGIN
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  Query Match             15.4%;  Score 407;  DB 14;  Length 717;
  Best Local Similarity   74.7%;  Pred. No. 3.8e-82;
  Matches  523;  Conservative    0;  Mismatches  176;  Indels    1;  Gaps    1;

Qy       462 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 521
             ||||  |         |||  | | |||  |||     || ||| |        || ||||| ||
Db        19 TTCTTTATTTGATATTGATAAAGAAAGTGAAGAAATTAGAAAATTATCGATTCCTCCTCC 78

Qy       522 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 581
             ||||    ||   |||   || |||||||| || || ||||| |  ||   ||||| |||| ||
Db        79 TGGAAAAGGGGAGAGAATATATGAAATTGATCCACTTTTAAGCAATCATCGTGAACATCT 138

Qy       582 TGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGG 641
             ||| || ||  |||||||| ||||||||   |    | || |||||||||||| ||||| |||||
Db       139 TGAGTATAGATATTCACATTACAAGAAGATACGTGAAGCAATTGACAAATATGAAGGTGG 198

Qy       642 TTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 701
             |||||| || ||||| |||||||||||||| | |||||||||| ||      ||||||||
Db       199 TTTGGAGGCGTTTTCACGTGGTTATGAAAAATTAGGTTTCACTCGAAGCAAAACAGGTAT 258

Qy       702 CACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAA 761
             ||||||   | || ||||| | ||| ||    |||| |||  | || ||||||||||||||||
Db       259 CACTTATAGAGAATGGGCACCTGGGGCAAAGTCTGCTTCACTTATTGGAGATTTCAACAA 318

Qy       762 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 821
              ||| |    ||||||||||   |||||| |||||||||||||||| |||||||| ||| |
Db       319 CTGGAATCCAAATGCTGATGTTATGACCCGGAATGAATTTGGTGTGTGGGAGATCTTTTT 378

Qy       822 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTAT 881
             |||||| ||||| |||| ||||  |    ||||||||||| ||   |||| ||||| |||||
Db       379 GCCAAACAATGTTGATGATTCTTCACCTATTCCTCATGGTTCTCGAGTAAAGATTCGTAT 438

Qy       882 GGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 941
             ||| || |||||  ||   |||| || || ||||||||||||||||  |  ||  ||||
Db       439 GGATACGCCATCTGGCATTAAAGACTCGATTCCTGCTTGGATCAAGTTTCAGTACAAGC 498

Qy       942 TCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATAT 1001
              |||| ||| ||||| ||||||||||||  | |||||||| ||   ||||||| |  ||  |
Db       499 ACCTGGTGAGATTCCTTATAATGGAATATACTATGATCCCCCACAAGAGGAAAAATACGT 558

Qy      1002 CTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGG 1061
               || ||||| ||| |  ||||||| |  ||  | ||  || |||||   | ||| | ||
Db       559 GTTTCAACATCCAAGACCAAAGAAGCCGAAATCTCTTANGATTTATGAGGCACATGTGGG 618

Qy      1062 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1121
             |||||||||| |||| || |      | || | || |   || |||||||| || ||||| ||
Db       619 AATGAGTAGTACGGAACCAATGGATCACACGTATGCTAACTTTAGAGACGATGTTCTCCC 678

Qy      1122 TCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATG 1161
             |||||||| || || || ||||||||   | ||||| |||
Db       679 TCGCATAAAGAA-CTCGGTTACAATGCAGTTCAAATCATG 717
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RESULT 12
BM526229
LOCUS       BM526229                 573 bp    mRNA    linear   EST 19-FEB-2002
DEFINITION  sa138f02.y1 Gm-c1059 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1059-4491 5' similar to TR:Q9XIS5 Q9XIS5 BRANCHING ENZYME 1
            PRECURSOR ;, mRNA sequence.
ACCESSION   BM526229
VERSION     BM526229.1  GI:18731047
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
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            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact: ccu@resgen.com web site:
            www.resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1..573
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1059-4491"
                     /clone_lib="Gm-c1059"
                     /tissue_type="Whole seedling, 2 week old, etiolated"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from 2 week old etiolated whole seedlings of PI468916.
                     Complementary DNA was synthesized from mRNA using a primer
                     consisting of a poly(dT) sequence with a XhoI restriction
                     site. EcoRI adapters were ligated to the blunt-ended cDNA
                     fragments followed by XhoI digestion. The cDNA fragments
                     were directionally cloned into the EcoRI- XhoI restriction
                     site of the pBluescript vector. The ligated cDNA fragments
                     were transformed into DH10B host cells (Gibco BRL). This
                     library was  constructed in the laboratory of Dr. Randy
                     Shoemaker at Iowa state university."
BASE COUNT      169 a    110 c    126 g    167 t      1 others
ORIGIN

  Query Match             15.4%;  Score 406.2;  DB 13;  Length 573;
  Best Local Similarity   81.8%;  Pred. No. 5.7e-82;
  Matches  468;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy        952 ATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACAC 1011
              ||||||||  |  ||||| | ||||||||| || |||||||| |  ||| ||||| ||||
Db          1 ATTCCATACAGCGGAATATACTATGATCCCCCAGAAGAGGAAAAATATGTCTTCAAACAT 60

Qy       1012 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1071
              |||| |||||||| ||||| || || |||||||||| || || |||||||| |||
Db         61 CCACAGCCAAAGAGACCAAAATCACTTAGAATATATGAGTCACACATCGGAATGAGCAGT 120

Qy       1072 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1131
              ||||||| ||||| ||  |||| || |||||||||||||| || || |||||||| |||
Db        121 CCGGAGCCAAAAATCAATACATATGTCAATTTTAGAGATGATGTACTGCCTCGCATTAAA 180

Qy       1132 AAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGT 1191
              | |||||| || |||||  | || ||||||||||| ||||| ||||||||||| || ||
Db        181 AGGCTTGGCTATAATGCTGTCCAGATTATGGCTATCCAAGAACATTCTTATTATGCCAGC 240

Qy       1192 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGAC 1251
              ||||| || ||||| |||||||| |||||||| |||||||| |||||||| || || ||
Db        241 TTTGGGTACCATGTTACAAATTTCTTTGCACCTAGCAGCCGATTTGGAACTCCAGAGGAA 300

Qy       1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1311
              |||||||| |||| || | ||| ||||| || ||   | ||||||| ||||| |||||
Db        301 CTTAAGTCTCTGATAGACAGAGCCCATGAACTGGGTCTGCTTGTTCTGATGGATATTGTA 360

Qy       1312 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGT 1371
              ||||||||||||||||||||| || ||||| ||||||||||||||  | || ||| ||
Db        361 CACAGCCATGCATCAAATAATACATTGGATGGGCTGAACATGTTTGATGGAACTGATGGT 420

Qy       1372 TGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAAC 1431
              |||||| ||  ||||  | || ||||||||||||||||||||||| ||||| ||||||
Db        421 CATTACTTCCATCCTGGGTCACGAGGTTATCATTGGATGTGGGATTCTCGCCTTTTTAAC 480

Qy       1432 TATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGCG 1491
              ||||||| |||||| || || |||||||| || || |||||  |||||||| ||||||
Db        481 TATGGAAGCTGGGAAGTTCTAAGGTATCTACTTTCGAATGCACGATGGTGGCTGGATGAA 540

Qy       1492 TTCAAATTTGATGGATTTAGATTTGATGGTGT 1523
              | | | |||||||||||| ||||||||||||
Db        541 TACNAGTTTGATGGATTTCGATTTGATGGTGT 572


RESULT 13
BF065047
LOCUS       BF065047                 825 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  HV_CEb0022L05f Hordeum vulgare seedling green leaf EST library
            HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
            HV_CEb0022L05f, mRNA sequence.
ACCESSION   BF065047
VERSION     BF065047.1  GI:10841686
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 825)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
            Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
            ,D.W., Fenton,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Blumeria infected incompatible (Mla6) seedling
            leaf cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 594
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1..825
                     /organism="Hordeum vulgare"
                     /cultivar="CI16151 (Mla6)"
                     /db_xref="taxon:4513"
                     /clone="HV_CEb0022L05f"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0005 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16151 (Mla6) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate 5874 (AvrMla6
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids (Choi, Close). Phagemids were plated and picked
                     at the Clemson University Genomics Institute (CUGI) (Begum
                     , Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
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              , Rambo, Main). The sequence has been trimmed to remove
              vector sequence and contains a minimum of 100 bases of
              phred value 20 or above. For more details on library
              preparation and sequence analysis see
              http://www.genome.clemson.edu/projects/barley. To order
              this clone see http://www.genome.clemson.edu/orders Also
              see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
              Genetically and physically anchored EST resources for
              barley genomics. Barley Genetics Newsletter 31:29-30.
              (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      220 a    167 c    212 g    226 t
ORIGIN

  Query Match             15.0%;  Score 397.6;  DB 12;  Length 825;
  Best Local Similarity   70.4%;  Pred. No. 5.4e-80;
  Matches  532;  Conservative    0;  Mismatches  224;  Indels    0;  Gaps    0;

Qy       1886 ATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATG 1945
Db         11 ATTCGGCACGAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTATG 70

Qy       1946 ATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACA 2005
Db         71 ATTTCATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACATA 130

Qy       2006 AGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAA 2065
Db        131 AAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTAATTTCATGGGAA 190

Qy       2066 ATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATG 2125
Db        191 ATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGGGGTCCGCAAACTCTTCCAACCG 250

Qy       2126 GCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGG 2185
Db        251 GCAAAGTTCTCCCTGGCAATAACAATAGTTATGATAAATGCCGCCGTAGATTTGATCTTG 310

Qy       2186 GAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATC 2245
Db        311 GAGATGCAGATTTTCTTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATC 370

Qy       2246 TTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAG 2305
Db        371 TTGAGGAAAAATATGGGTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACATGAGG 430

Qy       2306 GAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGA 2365
Db        431 AAGATAAGGTGATCATCTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGA 490

Qy       2366 CAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCT 2425
Db        491 GCAATAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTGGCCT 550

Qy       2426 TGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATT 2485
Db        551 TAGACTCTGATGATGCACTCTTTGGTGGATTCAGCAGGCTTGATCATGATGTCGACTACT 610

Qy       2486 TCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTA 2545
Db        611 TCACAACCGAACATCCGCATGACAACAGGCCACGCTCTTTCTCGGTGTACACTCCGAGCA 670

Qy       2546 AAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 2605
Db        671 GAACTGCGGTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCTGTTTGTTACAATGCAA 730

Qy       2606 AAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAG 2641
Db        731 AAAAGAGAAACTCAATGGAGCTCGTGGATTGTGAAG 766

RESULT 14
BQ240494
LOCUS       BQ240494              695 bp    mRNA    linear   EST 03-MAY-2002
DEFINITION  TaE05016F12R TaE05 Triticum aestivum cDNA clone TaE05016F12R, mRNA
            sequence.
ACCESSION   BQ240494
VERSION     BQ240494.1  GI:20436370
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 695)
  AUTHORS   Cloutier,S.
  TITLE     Wheat functional genomics - Glenlea developing seeds cDNA libraries
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Dr. Sylvie Cloutier
            Cereal Research Centre, Agriculture and Agri-food Canada
            195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
            Tel: (204) 983-2340
            Fax: (204) 983-4604
            Email: scloutier@em.agr.ca
            was cloned directionally, not all sequences generated with reverse
            primer were from the 5' end (same with forward primer and 3' end).
            Average insert size is >2.0 kb
            Plate: 016  row: F  column: 12
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1..695
                     /organism="Triticum aestivum"
                     /cultivar="Glenlea"
                     /db_xref="taxon:4565"
                     /clone="TaE05016F12R"
                     /clone_lib="TaE05"
                     /tissue_type="developing seeds"
                     /dev_stage="5 days after anthesis"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
                     NotI; Site_2: MluI; mRNA obtained from wheat seeds of
                     cultivar Glenlea 5 days post-anthesis"
BASE COUNT      193 a    135 c    171 g    196 t
ORIGIN

  Query Match             14.9%;  Score 393.2;  DB 14;  Length 695;
  Best Local Similarity   75.3%;  Pred. No. 5.3e-79;
  Matches  503;  Conservative    0;  Mismatches  163;  Indels    2;  Gaps    1;

Qy       1822 ATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGT 1881
Db         27 ATTGTGCGGACCCTAACAAATAGAAGGTGGCTTGAGAAGTGTGTAACTTATGCAGAAAGT 86

Qy       1882 CATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATG 1941
Db         87 CATGATCAAGCACTAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGG--ATG 144

Qy       1942 TATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTG 2001
Db        145 TATGATTTCATGGCTCTGGATAGGCCTTCAACTCCTCGCATTGATCGTGGCATAGCATTA 204

Qy       2002 CACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATG 2061
Db        205 CATAAAATGATCAGGCTTGTCACCATGGGTTTAGGTGGTGAAGGCTATCTTAACTTCATG 264

Qy       2062 GGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCT 2121
Db        265 GGAAATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGAGGCCCACAAACTCTTCCA 324

Qy       2122 GATGGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGAC 2181
Db        325 ACCGGCAAAGTTCTCCCTGAAAATAACAATAGTTATGATAAATGCCGCCGTAGATTTGAT 384

Qy       2182 CTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAG 2241
Db        385 CTTGGAGATGCAGATTTTCTTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAG 444
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Qy       2242 TATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGAT 2301
Db        445 CATCTTGAGGAAAAATATGGGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACAT 504

Qy       2302 GAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCAC 2361
Db        505 GAGGAAGATAAGGTGATCATCTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCAC 564

Qy       2362 TGGACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTT 2421
Db        565 TGGAGCAATAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGAGAAGTACAAGGTG 624

Qy       2422 GCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAA 2481
Db        625 GCCTTGGACTCCGACGATGCACTCTTTGGTGGATTCAGCAGGCTTGATCATGATGTCGAC 684

Qy       2482 TATTTCAC 2489
Db        685 TACTTCAC 692
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RESULT 15
BG521671
LOCUS       BG521671                 621 bp    mRNA    linear   EST 01-FEB-2002
DEFINITION  13-3 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
            sequence.
ACCESSION   BG521671
VERSION     BG521671.1  GI:18464735
KEYWORDS    EST.
SOURCE      Stevia rebaudiana.
  ORGANISM  Stevia rebaudiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Stevia.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P.
  TITLE     Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
            diterpene synthesis
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Jim Brandle
            Genomics and Biotechnology
            Agriculture and Agri-Food Canada - SCPFRC
            1391 Sandford St., London, Ontario, CANADA, N5V 4T3
            Tel: 519 457 1470
            Fax: 519 457 3997
            Email: brandleje@em.agr.ca
            Seq primer: T3 promoter primer.
FEATURES             Location/Qualifiers
     source          1..621
                     /organism="Stevia rebaudiana"
                     /strain="751/1501"
                     /cultivar="Landrace"
                     /db_xref="taxon:55670"
                     /clone_lib="Stevia field grown leaf cDNA"
                     /tissue_type="leaf"
                     /dev_stage="field grown, mid-size"
                     /lab_host="E. coli strain XLOLR"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
                     cDNA library was constructed from polyA+ enriched mRNA
                     from field grown leaves. Mid-size actively growing leaves
                     were collected and pooled from several plants and frozen
                     immediately after harvesting in liquid nitrogen. The cDNA
                     was prepared using an XhoI-poly(dT) linker-primer. An
                     EcoRI  adapter was ligated to the blunt end cDNA and the
                     products  were digested with EcoRI and XhoI enabling
                     directional  cloning into the lambda ZAP Express vector.
                     The library was amplified using the host strain XL1-Blue
                     MRF'. Mass  excision of the library was performed to
                     obtain pBK-CMV  phagemid clones in the host strain XLOLR.
                     Single pass DNA  sequencing was performed using the T3
                     promoter primer: 5'  ATTAACCCTCACTAAAGGGA 3'. This library
                     was constructed by  Alex Richman."
BASE COUNT      169 a     91 c    162 g    198 t      1 others
ORIGIN

  Query Match             14.6%;  Score 385.4;  DB 12;  Length 621;
  Best Local Similarity   78.8%;  Pred. No. 3.1e-77;
  Matches  472;  Conservative    0;  Mismatches  126;  Indels    1;  Gaps    1;
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```
Qy       1528 TCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATAC 1587
Db          2 TCAATGATGTACACTCATCATGGTTTACAGGTAGCATTTACTGGAAACTACAACGAGTAT 61

Qy       1588 TTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATT 1647
Db         62 TTTGGTTTGGCAACGGATGTTGATGCGGTGGTTTATTTAATGATGGTTAATGATCTTATT 121

Qy       1648 CATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTT 1707
Db        122 CATGGGTTGTTTCCGGAAGCCATCACTGTTGGTGAAGATGTGAGTGGAATGCCAACGTTC 181

Qy       1708 TGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCT 1767
Db        182 TGCATTCCTGTACAAGATGGTGGTGTGGGGTTTGACTACCGGTTGCATATGGCGGTTGCT 241

Qy       1768 GATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTT 1827
Db        242 GATAAGTGGATTGAGCTTCTCAAGCTGAGGGACGAAGATTGGAAAATGGGTGATATCATT 301

Qy       1828 CATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGAT 1887
Db        302 CACACGCTTACCAACAGAAGATGGTCTGAAAAGTGCGTTTGTTATGCTGAAAGTCATGAT 361

Qy       1888 CAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGAT 1947
Db        362 CAAGCTTTAGTTGGTGATAAAACTATTGCATTTTGGCTTATGGACAAGGATATGTATGAA 421

Qy       1948 TTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAG 2007
Db        422 TTTATGGCAATTGATAGACCATCGACTCCTCTTATAGATCGCGGTATTGCATTACATAAA 481

Qy       2008 ATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTA-CCTAAATTTCATGGGAAA 2066
Db        482 ATGATCAGGCTTATTACAATGGGATTAGGTGGAGAAGGATATTTGAATTTCATGGGAAA 541

Qy       2067 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATG 2125
Db        542 TGAATTTGGCATCCTGAGTGGATAGATTTTCCAAGAGCCCGATCAACCGTCTTTCCTG 600
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Search completed: July 5, 2003, 20:10:07
Job time : 3606.65 secs

6


```
OM protein - nucleic search, using frame_plus_p2n model

Run on:         July  6, 2003, 00:19:16 ; Search time 5591 Seconds
                                          (without alignments)
                                          4341.216 Million cell updates/sec

Title:          US-10-056-454A-15_COPY_49_882
Perfect score:  4465
Sequence:       1 EKSSYNSEFRPSTVAASGKV..........EEEEEEEEVAAVEEVVVEEE 834

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:      4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10056454/runat_01072003_145459_8244/app_query.fasta_1.1031
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10056454_@CGN_1_1_3750_@runat_01072003_145459_8244 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      GenEmbl:*
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                2:  gb_htg:*
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                32:  em_htg_other:*
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                34:  em_htg_pln:*
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                36:  em_htg_mam:*
                37:  em_htg_vrt:*
                38:  em_sy:*
                39:  em_htgo_hum:*
                40:  em_htgo_mus:*
                41:  em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4465	100.0	2992	8	STU011890	AJ011890 Solanum t
2	4465	100.0	3033	6	A58164	A58164 Sequence 14
3	4372.5	97.9	2523	8	STU011889	AJ011889 Solanum t
4	4358.5	97.6	2578	6	A58169	A58169 Sequence 19
5	4339	97.2	2493	8	STSBEII	AJ000004 Solanum t
6	4334	97.1	2576	6	A58166	A58166 Sequence 16
7	4320	96.8	3074	6	AR123355	AR123355 Sequence
~~8~~	~~4297~~	~~96.2~~	~~2982~~	~~8~~	~~STU011888~~	~~AJ011888 Solanum t~~
9	4274	95.7	2563	6	AX256072	AX256072 Sequence
10	4269	95.6	3003	6	A58162	A58162 Sequence 12
11	4268.5	95.6	3231	6	A58168	A58168 Sequence 18
12	4225	94.6	2529	6	A58167	A58167 Sequence 17
13	4220.5	94.5	2955	8	STU011885	AJ011885 Solanum t
14	4161.5	93.2	2975	6	A58163	A58163 Sequence 13
15	3535.5	79.2	3123	8	AB071286	AB071286 Ipomoea b
16	3363	75.3	3090	6	A92164	A92164 Sequence 30
17	3347.5	75.0	3549	8	PSSBEIGEN	X80009 P.sativum m
18	3320	74.4	2517	8	AB042937	AB042937 Ipomoea b
19	3318.5	74.3	3360	8	AB029548	AB029548 Phaseolus
20	3309.5	74.1	2542	8	ATU22428	U22428 Arabidopsis
21	3281.5	73.5	2913	6	A92162	A92162 Sequence 28
22	3266	73.1	2577	6	AX412751	AX412751 Sequence
23	3266	73.1	2577	6	AX412752	AX412752 Sequence
24	3249	72.8	2668	8	ATU18817	U18817 Arabidopsis
25	3239	72.5	3015	6	E14723	E14723 Rice mRNA f
26	3239	72.5	3015	8	AB023498	AB023498 Oryza sat
27	3236	72.5	2364	6	E14724	E14724 Rice mRNA f
28	3184.5	71.3	2795	8	ZMU65948	U65948 Zea mays st
29	3166	70.9	2970	8	AF286319	AF286319 Triticum
30	3160	70.8	2970	8	TASBA2	Y11282 T.aestivum
31	3149	70.5	2853	8	TAU66376	U66376 Triticum ae
32	3136	70.2	2726	8	AF338432	AF338432 Triticum
33	3130.5	70.1	2554	8	AF064560	AF064560 Hordeum v
34	3096	69.3	2919	6	E08183	E08183 Gene of sta
35	3092	69.2	2918	8	RICBCE3	D16201 Rice mRNA f
36	3021.5	67.7	2725	6	AR106495	AR106495 Sequence
37	3021.5	67.7	2725	8	MZEGLUCTRN	L08065 Corn starch
38	3002	67.2	2780	8	AF064561	AF064561 Hordeum v
39	2496.5	55.9	104364	8	AC006919	AC006919 Arabidops
40	2489.5	55.8	7020	8	ATSBE21	AJ000497 Arabidops
41	2462	55.1	1393	6	AR123356	AR123356 Sequence
42	2387.5	53.5	102897	8	ATF17C15	AL162506 Arabidops
43	2165	48.5	3128	6	A46462	A46462 Sequence 1
44	2159	48.4	2493	8	STY08786	Y08786 S.tuberosum
45	2156	48.3	2843	8	MESBERNA	X77012 M.esculenta

ALIGNMENTS

RESULT 1

```
STU011890
LOCUS       STU011890              2992 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-6.
ACCESSION   AJ011890
VERSION     AJ011890.1  GI:4584512
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2992)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2992)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1. .2992
                     /organism="Solanum tuberosum"
                     /cultivar="Desiree"
                     /db_xref="taxon:4113"
                     /note="sequence SBE A-6"
     gene            140. .2788
                     /gene="SBE II"
     CDS             140. .2788
                     /gene="SBE II"
                     /EC_number="2.4.1.18"
                     /standard_name="1,4-alpha-Glucan branching enzyme"
                     /codon_start=1
                     /evidence=experimental
                     /product="starch branching enzyme II"
                     /protein_id="CAB40748.1"
                     /db_xref="GI:4584513"
                     /translation="MVYTLSGVRFPTVPSVYKSNGFSSNGDRRNANVSVFLKKHSLSR
                     KILAEKSSYNSEFRPSTVAASGKVLVPGTQSDSSSSSTDQFEFTETSPENSPASTDVD
                     SSTMEHASQIKTENDDVEPSSDLTGSVEELDFASSLQLQEGGKLEESKTLNTSEETII
                     DESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
                     SRGYEKMGFTRSATGITYREWALGAQSAALIGDFNNWDANADIMTRNEFGVWEIFLPN
                     NVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIHYDPPEEERYI
                     FQHPRPKKPKSLRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYNALQIMAIQEH
                     SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                     MFDCTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDAFKFDGFRFDGV
                     TSMMYIHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
                     PTFCIPVQEGGVGFDYRLHMAIADKRIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEG
                     YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGDAEYLRYRGLQ
                     EFDRPMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHWTKSYSDYRIA
                     CLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYAPCKTAVVYAL
                     VDKEEEEEEEEEEEVAAVEEVVVEEE"
     transit_peptide 140. .283
                     /gene="SBE II"
     mat_peptide     284. .2785
                     /gene="SBE II"
                     /product="starch branching enzyme II"
                     /EC_number="2.4.1.18"
BASE COUNT      893 a    542 c    701 g    856 t
ORIGIN

Alignment Scores:
Pred. No.:              0           Length:        2992
Score:                  4465.00     Matches:       834
Percent Similarity:     100.00%     Conservative:  0
Best Local Similarity:  100.00%     Mismatches:    0
Query Match:            100.00%     Indels:        0
DB:                     8           Gaps:          0
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US-10-056-454A-15_COPY_49_882 (1-834) x STU011890 (1-2992)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 343

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 403

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db        404 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 463

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 523

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 583

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 643

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 703

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 763

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 GACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 823

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTC 883

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 943

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1003

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Db       1004 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1063

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Db       1064 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCC 1123

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1183

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Db       1184 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1243

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCT 1303

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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Db       1304 ATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1363

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1423

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Db       1424 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1483

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
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Db       1484 CTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1543

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
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Db       1544 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1603

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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Db       1604 TCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1663

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Db       1664 ACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1723

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db       1724 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1783

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Db       1784 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1843

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Db       1844 TTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1903

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 GCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1963

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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Db       2024 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2083

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db       2084 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2143

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db       2144 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2203

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2204 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2263

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2264 GGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2323

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Db       2324 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTAT 2383

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2384 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2443

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db       2444 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2503

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2504 ACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2563

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Db       2564 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2623

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2624 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2683

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2684 AAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 2743

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
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Db       2744 GAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2785
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```
RESULT 2
A58164
LOCUS       A58164                  3033 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 14 from Patent WO9634968.
ACCESSION   A58164
VERSION     A58164.1  GI:3713889
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3033)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 14 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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                     DESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
                     SRGYEKMGFTRSATGITYREWALGAQSAALIGDFNNWDANADIMTRNEFGVWEIFLPN
                     NVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIHYDPPEEERYI
                     FQHPRPKKPKSLRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYNALQIMAIQEH
                     SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                     MFDCTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDAFKFDGFRFDGV
                     TSMMYIHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
                     PTFCIPVQEGGVGFDYRLHMAIADKRIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEG
                     YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGDAEYLRYRGLQ
                     EFDRPMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHWTKSYSDYRIA
                     CLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYAPCKTAVVYAL
                     VDKEEEEEEEEEEEVAAVEEVVVEEE"
BASE COUNT      900 a    553 c    712 g    868 t
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         3033
Score:                  4465.00        Matches:        834
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Percent Similarity:      100.00%      Conservative:  0
Best Local Similarity:   100.00%      Mismatches:    0
Query Match:             100.00%      Indels:        0
DB:                      6            Gaps:          0

US-10-056-454A-15_COPY_49_882 (1-834) x A58164 (1-3033)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 348

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 408

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db        409 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 468

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
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Db        469 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 528

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
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Db        529 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 588

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 648

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
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Db        649 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 708

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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Db        709 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 768

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
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Db        769 GACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 828

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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Db        829 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTC 888

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 948

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
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Db        949 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1008

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Db       1009 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1068

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Db       1069 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCC 1128

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Db       1129 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1188

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Db       1189 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1248

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCT 1308

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 ATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1368

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
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Db       1369 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1428

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Db       1429 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1488

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 CTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1548

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1608

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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Db       1609 TCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1668

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Db       1849 TTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1908

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
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Db       1909 GCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1968

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
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Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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Db       2029 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2088

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db       2089 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2148

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2149 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2208

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2209 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2268

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Db       2269 GGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2328

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Db       2389 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2448

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db       2449 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2508

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
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Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Db       2569 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2628

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
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Db       2629 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2688

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
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Db       2689 AAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 2748

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
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Db       2749 GAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2790
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RESULT 3
STU011889
LOCUS       STU011889             2523 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-5.
ACCESSION   AJ011889
VERSION     AJ011889.1  GI:4584510
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2523)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2523)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
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                     /note="sequence SBE A-5"
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                     HSHASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWL
                     DEFKFDGFRFDGVTSMMYTHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLF
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                     MIRLVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDDSVIPGNQFSYDKCRRRFD
                     LGDAEYLRYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFN
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     transit_peptide <2..10
                     /gene="SBE II"
     mat_peptide     11..2509
                     /gene="SBE II"
                     /product="starch branching enzyme II"
                     /EC_number="2.4.1.18"
BASE COUNT      749 a    449 c    605 g    720 t
ORIGIN

Alignment Scores:
Pred. No.:              0               Length:          2523
Score:                  4372.50         Matches:         820
Percent Similarity:     98.80%          Conservative:    4
Best Local Similarity:  98.32%          Mismatches:      9
Query Match:            97.93%          Indels:          1
DB:                     8               Gaps:            1

US-10-056-454A-15_COPY_49_882 (1-834) x STU011889 (1-2523)
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Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
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Db         11 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 70

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db         71 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATTTGAGTTCACT 130

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 190

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 250

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 310

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 370

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 430

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 490

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 550

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        551 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 610

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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Db     611 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 670

Qy     221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     671 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 730

Qy     241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Db     731 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 790

Qy     261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
           ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db     791 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 850

Qy     281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Db     851 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 910

Qy     301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Db     911 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 970

Qy     321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
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Db     971 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCT 1030

Qy     341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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Db    1031 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1090

Qy     361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
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Qy     381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Db    1151 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1210

Qy     401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
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Db    1211 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1270

Qy     421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
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Qy     441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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Qy     461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Db    1391 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1450

Qy     481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db    1451 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1510

Qy     501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Qy     521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Qy     541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
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Db    1631 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1690

Qy     561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
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Qy     581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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Qy     601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db    1811 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1870

Qy     621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db    1871 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1930

Qy     641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Qy     661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Qy     681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
           |||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db    2051 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2110

Qy     701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Db    2111 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2170

Qy     721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db    2171 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2230

Qy     741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
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Db    2231 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2290

Qy     761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Db    2291 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2350

Qy     781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
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Db    2351 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2410

Qy     801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
           :::||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db    2411 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAAGAA 2467

Qy     821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
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Db    2468 GAAGAAGTAGCAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2509
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A58169
LOCUS       A58169                  2578 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 19 from Patent WO9634968.
ACCESSION   A58169
VERSION     A58169.1  GI:3713894
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2578)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 19 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
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                    /db_xref="taxon:32644"
BASE COUNT      770 a    462 c    616 g    730 t
ORIGIN

Alignment Scores:
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Score:                  4358.50         Matches:        817
Percent Similarity:     98.56%          Conservative:   5
Best Local Similarity:  97.96%          Mismatches:     11
Query Match:            97.61%          Indels:         1
DB:                     6               Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x A58169 (1-2578)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 125

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        126 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATTTGAGTTCACT 185

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db        186 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 245

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
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Db        246 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 305

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
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Db        306 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 365

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
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Db        366 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 425

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
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Db        426 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 485

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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Db        486 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 545

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
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Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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Db        606 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 665

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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Db        666 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 725

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
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Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Db        906 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 965

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
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Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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Db       1086 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1145

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
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Db       1146 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1205

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
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Db       1266 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1325

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
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Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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Db       1386 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1445

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Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db       1506 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1565

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Db       1626 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1685

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
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Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
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Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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Db       1806 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1865

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db       1866 GATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1925

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db       1926 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1985

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Db       1986 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2045
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Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Db       2046 GACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2105

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Db       2106 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2165

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2166 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2225

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2226 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2285

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db       2286 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2345

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2346 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2405

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2406 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2465

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db       2466 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAAGAA 2522

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||   ||||||||||||||||||||||||||
Db       2523 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2564
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RESULT 5
STSBEII
LOCUS       STSBEII                 2493 bp    mRNA    linear   PLN 27-MAY-1998
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II.
ACCESSION   AJ000004
VERSION     AJ000004.1  GI:2764395
KEYWORDS    Sbe-II gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2493)
  AUTHORS   Larsson,C.T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell
            Research, Genetic Center, Swedish University of Agricultural
            Sciences, Box 7055, S-750 07 Uppsala, SWEDEN
REFERENCE   2  (bases 1 to 2493)
  AUTHORS   Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H.
  TITLE     Molecular cloning and characterization of starch-branching enzyme
            II from potato
  JOURNAL   Plant Mol. Biol. 37 (3), 505-511 (1998)
  MEDLINE   98278379
   PUBMED   9617817
FEATURES             Location/Qualifiers
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                     /cultivar="Amanda"
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                     /plasmid="pALSBE-II (#123)"
     gene            1..2493
                     /gene="Sbe-II"
     CDS             <1..2493
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                     /EC_number="2.4.1.18"
                     /function="branches 1,4-alpha glucans"
                     /codon_start=1
                     /product="starch branching enzyme II, SBE-II"
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                     /db_xref="GI:2764396"
                     /db_xref="SPTREMBL:O49953"
                     /translation="EKSSYNSESRPSTVAASGKVLVPGTQSDSSSSSTDQFEFTETSP
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                     ASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEF
                     KFDGFRFDGVTSIMYTHHGLSVGFTGNYKEYFGLATDVDAVVYLMLVNDLIHGLFPDA
                     ITIGEDVSGMPTFCIPVQDGGVGFDYRLHMAIADKWIELLKKRDEDWRVGDIVHTLTN
                     RRWSEKCVSYAESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIR
                     LVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGD
                     AEYLRYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHW
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BASE COUNT      742 a    445 c    595 g    711 t
ORIGIN

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Score:                  4339.00        Matches:        814
Percent Similarity:     98.32%         Conservative:   6
Best Local Similarity:  97.60%         Mismatches:     10
Query Match:            97.18%         Indels:         4
DB:                     8              Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x STSBEII (1-2493)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 60

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 120

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 180

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 240

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 300

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 360

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 420

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 480

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 540
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Qy   181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
Db   541 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 600

Qy   201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
Db   601 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 660

Qy   221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
Db   661 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 720

Qy   241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
Db   721 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 780

Qy   261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
Db   781 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 840

Qy   281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
Db   841 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 900

Qy   301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
Db   901 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 960

Qy   321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
Db   961 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCT 1020

Qy   341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
Db  1021 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1080

Qy   361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db  1081 AGCAGCCGTTTTGGAACTCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1140

Qy   381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db  1141 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1200

Qy   401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
Db  1201 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1260

Qy   421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
Db  1261 TGGATGTGGGATTCCCGCCTCTTTAATTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1320

Qy   441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db  1321 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTCGATGGTGTG 1380

Qy   461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db  1381 ACATCAATAATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACAAGGAA 1440

Qy   481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
Db  1441 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1500

Qy   501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db  1501 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1560

Qy   521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db  1561 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1620

Qy   541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db  1621 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1680

Qy   561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db  1681 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1740

Qy   581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
Db  1741 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1800

Qy   601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db  1801 GATTTTATGGCTCTGGATAGACCATCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1860

Qy   621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
Db  1861 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1920

Qy   641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db  1921 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 1980

Qy   661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
Db  1981 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2040

Qy   681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db  2041 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2100

Qy   701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Qy   721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
Db  2161 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2220

Qy   741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db  2221 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2280

Qy   761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db  2281 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2340

Qy   781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
Db  2341 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2400

Qy   801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
Db  2401 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA------------GAAGAAGAAGAAGAA 2448

Qy   821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
Db  2449 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2490
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RESULT 6
A58166

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LOCUS       A58166              2576 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 16 from Patent WO9634968.
ACCESSION   A58166
VERSION     A58166.1  GI:3713891
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2576)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
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  TITLE       IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL     Patent: WO 9634968-A 16 07-NOV-1996;
              NAT STARCH CHEM INVEST (US)
COMMENT       Other publication AU 5509996 961121.
FEATURES               Location/Qualifiers
     source            1. .2576
                       /organism="unidentified"
                       /db_xref="taxon:32644"
BASE COUNT       770 a     462 c     615 g     729 t
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Alignment Scores:
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Score:                    4334.00        Matches:        818
Percent Similarity:       98.56%         Conservative:   4
Best Local Similarity:    98.08%         Mismatches:     11
Query Match:              97.07%         Indels:         2
DB:                       6              Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x A58166 (1-2576)

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Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
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Db        126 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATTTGAGTTCACT 185

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db        186 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 245

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
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Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
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Db        306 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 365

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 425

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
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Db        426 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 485

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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Db        486 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 545

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
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Db        546 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 605

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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Db        606 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 665

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 845

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||   |||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        846 AACTACT--CTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 903

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Db        904 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 963

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
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Db       1024 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCT 1083

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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Db       1084 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1143

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1203

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Db       1204 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1263

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1264 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1323

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1383

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db       1384 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1443

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1444 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1503

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1504 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1563

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1564 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1623

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1624 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1683

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1684 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1743

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1744 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1803

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1804 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1863

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db       1864 GATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1923

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db       1924 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1983

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1984 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2043

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2044 GACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2103

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       2104 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2163

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2164 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2223

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2224 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2283

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db       2284 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2343

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2344 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2403

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2404 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2463

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::|||||||||||||||||||||||||||||      ||||||||||||||||||||||
Db       2464 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAAGAA 2520

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||   ||||||||||||||||||||||||||
Db       2521 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2562
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RESULT 7
AR123355

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LOCUS       AR123355                 3074 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6169226.
ACCESSION   AR123355
VERSION     AR123355.1  GI:14108321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3074)
  AUTHORS   Ek,B., Khosnoodi,J., Larsson,C.-T., Larsson,H. and Rask,L.
  TITLE     Starch branching enzyme II of potato
  JOURNAL   Patent: US 6169226-A 1 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1..3074
                     /organism="unknown"
BASE COUNT      902 a     558 c     712 g     896 t     6 others
ORIGIN

Alignment Scores:
Pred. No.:                 0               Length:          3074
Score:                     4320.00         Matches:         812
Percent Similarity:        97.96%          Conservative:    5
Best Local Similarity:     97.36%          Mismatches:      13
Query Match:               96.75%          Indels:          4
DB:                        6               Gaps:            1

US-10-056-454A-15_COPY_49_882 (1-834) x AR123355 (1-3074)
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see sean 3, res 1 — since date too late

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Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db        333 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 392

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 452

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 512

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 GCTAGGCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 572

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 632

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 692

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 752

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 812

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
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Db        813 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 872

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        873 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 932

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 992

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1052

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1112

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1113 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1172

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1232

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1292

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCT 1352

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db       1353 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCA 1412

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 AGCAGCCGTTTTGGAACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1472

Qy         381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1532

Qy         401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
               ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db        1533 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1592

Qy         421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1593 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1652

Qy         441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
               ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db        1653 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1712

Qy         461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Db        1713 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1772

Qy         481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db        1773 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1832

Qy         501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Db        1833 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1892

Qy         521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
               |||   ||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        1893 TTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1952

Qy         541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
               |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        1953 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2012

Qy         561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2013 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2072

Qy         581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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Db        2073 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGAGAAGGATATGTAT 2132

Qy         601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db        2133 GATTTTATGGCTCTGGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2192

Qy         621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2193 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2252

Qy         641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Db        2253 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2312

Qy         661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Db        2313 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2372

Qy         681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Db        2373 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2432

Qy         701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Db        2433 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2492

Qy         721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db        2493 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2552

Qy         741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
               ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        2553 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2612

Qy         761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Qy         781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
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Qy         801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
               :::|||||||||||||||||||||||||||||||            ||||||||||||||
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Qy         821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
               ||||||||||||   |||||||||||||||||||||||||||
Db        2781 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822
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RESULT 8
STU011888
LOCUS       STU011888               2982 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-4.
ACCESSION   AJ011888
VERSION     AJ011888.1  GI:4584508
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2982)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2982)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
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                     DESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
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                     SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                     MFDGTDSCYFHSGARGYHWMWDFRLFNYGNWEVLRYLLSNARWWLDEFKFDGFRFDGV
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                              YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPRNQFSYDKCRRRFDLGDAEYLRYRGLQ
                              EFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHWTKGYSDYRIG
                              CLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYAPSRTAVVYAL
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                     /gene="SBE II"
     mat_peptide     284. .2773
                     /gene="SBE II"
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                     /EC_number="2.4.1.18"
BASE COUNT      888 a    529 c    703 g    862 t
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          2982
Score:                    4297.00        Matches:         805
Percent Similarity:       97.48%         Conservative:    8
Best Local Similarity:    96.52%         Mismatches:      17
Query Match:              96.24%         Indels:          4
DB:                       8              Gaps:            1

US-10-056-454A-15_COPY_49_882 (1-834) x STU011888 (1-2982)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||     |||||||||||:::|||||||||||||||||||
Db        284 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAATTGCAGCATCGGGGAAAGTC 343

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        344 CTTGTGCCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGATCAATTTGAGTTCGCT 403

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db        404 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 463

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
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Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
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Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
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Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Db       1664 ACATCAATGATGTGTACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1723

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Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
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Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
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Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Db       2624 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2683

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
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Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
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RESULT 9
AX256072
LOCUS       AX256072                2563 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 1 from Patent WO0170942.
ACCESSION   AX256072
VERSION     AX256072.1  GI:16075112
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 2563)
  AUTHORS   Poulson,P. and s Rensen,I.S.
  TITLE     Enzyme
  JOURNAL   Patent: WO 0170942-A 1 27-SEP-2001;
            DANISCO A/S (DK)
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BASE COUNT      749 a    462 c    614 g    738 t
ORIGIN

Alignment Scores:
Pred. No.:                0               Length:          2563
Score:                    4274.00         Matches:         802
Percent Similarity:       97.58%          Conservative:    6
Best Local Similarity:    96.86%          Mismatches:      14
Query Match:              95.72%          Indels:          6
DB:                       6               Gaps:            1

US-10-056-454A-15_COPY_49_882 (1-834) x AX256072 (1-2563)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
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Db         81 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 140

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Db        321 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 380

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
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Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
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Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
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Db       1281 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1340

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
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Db       1761 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1820

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1821 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1880

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1881 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1940

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1941 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2000

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2001 AATGAATTCGGCCACCCCGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2060

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2061 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2120

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||:::|||||||||||||||||||||||||||||||||||   |||||||||
Db       2121 GGAGATGCAGATTATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2180

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2181 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2240

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2241 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2300

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db       2301 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2360

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2361 TTGGACTCGGATGATCCACTTTTTGGTGGCTTTGGGAGAATTGATCATAATGCCGAATAC 2420

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2421 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2480

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||||||||||||||                  |||   |||
Db       2481 AGGACAGCAGTGGTCTATGCACTAGTAGACAAA------------------GAAGCAGAA 2522

Qy        821 GluGluValAlaAlaValGluGlu 828
              ||||||||||||    ||||||||
Db       2523 GAAGAAGTAGCAGTAGTAGAAGAA 2546
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RESULT 10
A58162
LOCUS       A58162                  3003 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 12 from Patent WO9634968.
ACCESSION   A58162
VERSION     A58162.1  GI:3713887
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3003)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 12 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1..3003
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      895 a    535 c    706 g    867 t
ORIGIN
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Alignment Scores:
Pred. No.:              0              Length:          3003
Score:                  4269.00        Matches:         804
Percent Similarity:     97.25%         Conservative:    8
Best Local Similarity:  96.29%         Mismatches:      18
Query Match:            95.61%         Indels:          5
DB:                     6              Gaps:            1

US-10-056-454A-15_COPY_49_882 (1-834) x A58162 (1-3003)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||   ||||||||||||:::||||||||||||||||||
Db        287 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAATTGCAGCATCGGGGAAAGTC 346

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||   
Db        347 CTTGTGCCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGATCAATTTGAGTTCGCT 406

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 466

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 526

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 586

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 646

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 706

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 766

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        767 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAGAATGGGTTTCACT 826

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        827 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 886

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        887 ATTGGGGATTTCAACAATTGGGACGCAAATGCTGACTTTATGACTCGGAATGAATTTGGT 946

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        947 GTCTGAGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1006

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1007 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1066

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1067 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1126

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1127 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGGTGAGAATA 1186

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1246

Qy        321 ArgAspGluValLeuProArgIle-LysLysLeuGlyTyrAsnAlaLeuGlnIleMetAl 340
              |||||||||||||||||||||||| ||||||||||||||||||||:::||||||||||||
Db       1247 AGAGATGAAGTTCTTCCTCGCATAAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGC 1306

Qy        340 aIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 TATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACC 1366

Qy        360 oSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 AAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCT 1426

Qy        380 uGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGl 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 AGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGG 1486

Qy        400 yLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHi 420
              ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db       1487 ACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCA 1546

Qy        420 sTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLe 440
              |||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1547 TTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCT 1606

Qy        440 uSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVa 460
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db       1607 CTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGT 1666

Qy        460 lThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGl 480
              |||||||||||||      |||||||||||||||||||||||||||||||||||||||||
Db       1667 GACATCAATGATGTGTACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGA 1726

Qy        480 uTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLe 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 ATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCT 1786

Qy        500 uIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProTh 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 TATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGAC 1846

Qy        520 rPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIl 540
              ||||||:::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 ATTTGTGTTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAAT 1906

Qy        540 eAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIl 560
              ||||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 TGCTGATAAATGGATTGAGTTGCTCAAGAAACGGATGAGGATTGGAGAGTGGGTGATAT 1966

Qy        560 eValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHi 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1967 TGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCA 2026

Qy        580 sAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTy 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2027 TGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTA 2086

Qy        600 rAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHi 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 TGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTACA 2146

Qy        620 sLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGl 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 CAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGG 2206

Qy        640 yAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAs 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 AAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGA 2266

Qy        660 pGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLe 680
              ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db       2267 TGGCTCAGTAATTCCCAGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCT 2326
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Qy        680 uGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTy 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||    |||||||
Db       2327 GGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTA 2386

Qy        700 rLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGl 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2387 TCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGA 2446

Qy        720 uGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTr 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2447 AGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTG 2506

Qy        740 pThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAl 760
              ||||||   |||||||||||||||||    ||||||||||||||||||||||||||||
Db       2507 GACAAAAGGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGC 2566

Qy        760 aLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTy 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2567 CTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATA 2626

Qy        780 rPheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCy 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2627 TTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAG 2686

Qy        800 sLysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGl 820
               :::||||||||||||||||||||||||||||||             ||||||||||||
Db       2687 TAGAACAGCAGTGGTCTATGCACTAGTAGACAAA------------GAAGAAGAAGAAGA 2734

Qy        820 uGluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||    |||||||||||||||||||||||||||
Db       2735 AGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2777
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RESULT 11
A58168

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LOCUS       A58168                3231 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 18 from Patent WO9634968.
ACCESSION   A58168
VERSION     A58168.1  GI:3713893
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3231)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 18 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT     960 a    577 c    739 g    947 t     8 others
ORIGIN
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Alignment Scores:

Pred. No.:	0	Length:	3231
Score:	4268.50	Matches:	802
Percent Similarity:	97.12%	Conservative:	8
Best Local Similarity:	96.16%	Mismatches:	19
Query Match:	95.60%	Indels:	5
DB:	6	Gaps:	1

US-10-056-454A-15_COPY_49_882 (1-834) x A58168 (1-3231)

```
Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||:::||||||   ||||||||||||||||||||||||||||||||||
Db        372 GAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 431

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||    |||||||||||||||||||||||||||||||||||||||||||||
Db        432 CTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 491

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||:::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 GAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACAC 551

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 611

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 GTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 671

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 731

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 791

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db        792 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATT 851

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 911

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        912 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTC 971

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 1031

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1091

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db       1092 AGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1151

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db       1152 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1211

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db       1212 GAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1271

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1272 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1331

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||    |||||||||||||||:::||||||||||||
Db       1332 AGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCT 1391

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1392 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1451

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1452 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1511

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1512 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1571
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Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              |||||||||||||||     ||||||||||||||||||||||||||||||||||||||||
Db       1572 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1631

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1632 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1691

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              |||||||||||||||||||||||       ||||||   |||||||||||||||||||||
Db       1692 TCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTG 1751

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1752 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1811

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              |||||||||||||||||||||||||||||   |||||||||||||||   ||||||||||
Db       1812 TACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTT 1871

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1872 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1931

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1932 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1991

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1992 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGATGAGGATTGGAGAGTGGGTGATATT 2051

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2052 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2111

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2112 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2171

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2172 GATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2231

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2232 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2291

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2292 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2351

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2352 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2411

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       2412 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2471

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Db       2472 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2531

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db       2532 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2591

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||||        ||||||||||||||||||||||||||
Db       2592 ACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCC 2651
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Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2652 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGT 2711

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2712 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2771

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::|||||||||||||||||||||||||||||||               ||||||||||||
Db       2772 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---------------GAAGAAGAAGAA 2816

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||    ||||||||||||||||||||||||||
Db       2817 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2858

RESULT 12
A58167
LOCUS       A58167                  2529 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 17 from Patent WO9634968.
ACCESSION   A58167
VERSION     A58167.1  GI:3713892
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2529)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 17 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      735 a    458 c    599 g    722 t     15 others
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         2529
Score:                  4225.00        Matches:        792
Percent Similarity:     96.84%         Conservative:   4
Best Local Similarity:  96.35%         Mismatches:     26
Query Match:            94.62%         Indels:         0
DB:                     6              Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x A58167 (1-2529)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db         59 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 118

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db        119 CTTGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 178

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 238

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 298

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 358

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 418
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Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 478

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 538

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 598

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        599 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 658

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 718

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 778

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 AGAGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 838

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Db        839 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 898

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db        899 GAAGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 958

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1018

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||    ||||||||||||||:::|||||||||||||
Db       1019 AGAGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCT 1078

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1138

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1198

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1258

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db       1259 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1318

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1378

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db       1379 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1438

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Db       1439 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1498

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db       1499 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1558

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Db       1559 ATTCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1618

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db       1619 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1678

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1738

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db       1739 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCAT 1798

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db       1799 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTAT 1858

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              |||||||||||||||||||||||    |||    ||||||||||||||||||||||||||
Db       1859 GATTTTATGGCTCTGGATAGACCGYCAACAYCATTAATAGATCGTGGGATAGCATTGCAC 1918

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1919 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1978

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1979 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGAT 2038

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2039 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2098

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Db       2099 GGAGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2158

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Db       2159 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2218

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       2219 GGAGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2278

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              |||    ||||||||||||||||||||||    |||||||||||||||||||||||||||
Db       2279 ACAAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGC 2338

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2398

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||    ||||||    ||||||||||||||||||||||||||||||||||||||||
Db       2399 TTCACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2458

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::|||||||||||||||||||||||||||||    |||    |||||||||||||||||
Db       2459 AGAACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCC 2518

Qy        821 GluGlu 822
                 |||
Db       2519 GNNGAA 2524
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RESULT 13

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STU011885
LOCUS       STU011885               2955 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-1.
ACCESSION   AJ011885
VERSION     AJ011885.1  GI:4584502
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2955)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2955)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
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                     /codon_start=1
                     /evidence=experimental
                     /product="starch branching enzyme II"
                     /protein_id="CAB40743.1"
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ORIGIN

Alignment Scores:
Pred. No.:              2.02e-317      Length:         2955
Score:                  4220.50        Matches:        795
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Percent Similarity:     96.27%       Conservative:   6
Best Local Similarity:  95.55%       Mismatches:     22
Query Match:            94.52%       Indels:         9
DB:                     8            Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x STU011885 (1-2955)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
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Db        284 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 343

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
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Db        344 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 403

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db        404 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 463

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 523

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 583

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 643

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
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Db        644 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 703

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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Db        704 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 763

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
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Db        764 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 823

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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Db        824 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 883

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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Db        884 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 943

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
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Db        944 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1003

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Db       1004 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1063

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1064 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1123

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Db       1124 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1183

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Db       1184 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1243

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
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Db       1244 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCGAATTATGGCT 1303

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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Db       1304 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1363

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              |||||||||||||||||||||||||||||||||||      |||||||||||||||||||
Db       1364 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTCGATTGATAAAGCTCATGAGCTA 1423

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
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Db       1424 GGAATTGTTGTTCTCATGGACATCGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1483

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db       1484 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1543

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
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Db       1544 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1603

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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Db       1604 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTCGATGGTGTG 1663

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Db       1664 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1723

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db       1724 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1783

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Db       1784 ATTCATAGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1843

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Db       1844 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1903

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
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Db       1904 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1963

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
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Db       1964 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2023

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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Db       2024 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2083

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db       2084 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2143

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db       2144 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2203

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Db       2204 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAGCCACACCTTTCTGAT 2263

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
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Db       2264 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2323

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Db       2324 GGAGATGCAGAATATTTAAGATACCATGGGTTACAAGAATTTGACTGGGCTATGCAGTAT 2383

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Db       2384 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2443

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db       2444 GGAGATAGGATGATTGTATTTGAAAGGAGGAAACCTAGTTTTCGTCTTTAATTTTCACTGG 2503

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
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Db       2504 ACAAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGTC 2563

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Db       2564 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2623

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||    ||||||    ||||||||||||||||    ||||||||||||||||||||
Db       2624 TTCACCTCTGAAGGATCGTATGATGATCGTCCTTGTTCAATTATGGTGTATGCACCTAGT 2683

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||||||||||||||
Db       2684 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA--------------------------- 2716

Qy        821 GluGluValAlaAlaValGluGluValValValGlu 832
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Db       2717 CTAGAAGTAGCAGTAGTAGAAGAACCCATTGAAGAA 2752
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RESULT 14
A58163
LOCUS       A58163                  2975 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 13 from Patent WO9634968.
ACCESSION   A58163
VERSION     A58163.1  GI:3713888
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2975)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 13 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1..2975
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BASE COUNT      870 a    548 c    693 g    864 t
ORIGIN

Alignment Scores:
Pred. No.:              9.24e-313      Length:         2975
Score:                  4161.50        Matches:        792
Percent Similarity:     95.91%         Conservative:   6
Best Local Similarity:  95.19%         Mismatches:     25
Query Match:            93.20%         Indels:         11
DB:                     6              Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x A58163 (1-2975)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 348

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 408

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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Db      409 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 468

Qy       61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
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Db      469 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 528

Qy       81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
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Db      529 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 588

Qy      101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
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Db      589 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 648

Qy      121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
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Db      649 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 708

Qy      141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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Db      709 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 768

Qy      161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
            |||||||||||||||||||||||||      |||||||||||||||||||||||||||||
Db      769 GACAAGTATGAGGGTGGTTTGGAAGC-TTTCTCGTGGTTATGAAAAAATGGGTTTCACT 827

Qy      181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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Db      828 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 887

Qy      201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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Db      888 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 947

Qy      221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
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Db      948 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1007

Qy      241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Db     1008 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1067

Qy      261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Db     1068 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1127

Qy      281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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Db     1128 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1187

Qy      301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
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Db     1188 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1247

Qy      321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
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Db     1248 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCGAATTATGGCT 1307

Qy      341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1308 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1367

Qy      361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
            ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db     1368 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTCGATTGATAAAGCTCATGAGCTA 1427

Qy      381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1428 GGAATTGTTGTTCTCATGGACATCGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1487

Qy      401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
            ||||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db     1488 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1547

Qy      421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
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Db     1548 TGGATGTGGGATTC-CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1606

Qy      441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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Db     1607 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTCGATGGTGTG 1666

Qy      461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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Db     1667 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1726

Qy      481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
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Db     1727 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1786

Qy      501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Db     1787 ATTCATAGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1846

Qy      521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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Qy      541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
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Qy      561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
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Qy      601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Qy      621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db     2147 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2206

Qy      641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Qy      661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Qy      681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
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Qy      701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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Qy      741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
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Qy      761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
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Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
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Qy        821 GluGluValAlaAlaValGluGluValValValGlu 832
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AB071286
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DEFINITION  Ipomoea batatas SBE II mRNA for starch branching enzyme II,
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ACCESSION   AB071286
VERSION     AB071286.1  GI:15553090
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SOURCE      Ipomoea batatas (cultivar:Kokei 14) cDNA to mRNA.
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REFERENCE   1
  AUTHORS   Kimura,T. and Saito,A.
  TITLE     Ipomoea batatas mRNA for starch branching enzyme II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3123)
  AUTHORS   Kimura,T. and Saito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2001) Takashi Kimura, National Agricultural
            Research Center for Kyushu Okinawa Region; 2421 Suya, Nishigoshi,
            Kumamoto 861-1192, Japan (E-mail:tkimura@affrc.go.jp,
            Tel:81-96-242-1150)
FEATURES             Location/Qualifiers
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BASE COUNT      883 a    614 c    740 g    886 t
ORIGIN

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Query Match:            79.18%         Indels:         1
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US-10-056-454A-15_COPY_49_882 (1-834) x AB071286 (1-3123)
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Qy         23 ProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThrGluThr 42
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Qy         43 SerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSer 62
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Qy         83 GluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLys 102
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Db        505 GAGCAGGATCACACGTCTTCACTACAATTTGAAGAAGATGGTAATGTGGAAGTTTCACAA 564

Qy        103 ThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArgGly 122
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Db        565 AAACCAGAGACTTTGGATGAC---ATCAGTGCTGAATCTGAAATGGTGAAAAAGAGGGCC 621

Qy        123 IleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyr 142
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Qy        163 TyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSer 182
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Qy        183 AlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGly 202
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Qy        203 AspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrp 222
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Qy        223 GluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgVal 242
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Qy        243 LysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyr 262
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Qy        343 GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSer 362
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Qy        363 ArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIle 382
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Qy        403 MetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMet 422
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Qy        643 PheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySer 662
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Search completed: July 6, 2003, 04:49:04
Job time : 5762 secs

7

GenCore version 5.1.6


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OM protein - nucleic search, using frame_plus_p2n model

Run on:          July  6, 2003, 00:16:41 ; Search time 469 Seconds
                                            (without alignments)
                                            4004.620 Million cell updates/sec

Title:           US-10-056-454A-15_COPY_49_882
Perfect score:   4465
Sequence:        1 EKSSYNSEFRPSTVAASGKV..........EEEEEEEEVAAVEEVVVEEE 834

Scoring table:   BLOSUM62
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Searched:        2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:      4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Command line parameters:
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                 8:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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                 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4465	100.0	3033	17	AAT42630	Class A starch bra
	2	4358.5	97.6	2578	17	AAT42631	Class A starch bra
	3	4329	97.0	3074	18	AAT69587	Potato starch bran
	4	4322	96.8	2576	17	AAT42636	Class A starch bra
	5	4274	95.7	2563	23	ABK50301	Potato cDNA encodi
	6	4269	95.6	3003	17	AAT42634	Class A starch bra
	7	4268.5	95.6	3231	17	AAT42632	Class A starch bra
	8	4229	94.7	2531	17	AAT17267	Class A starch bra
	9	4218	94.5	2529	17	AAT42637	Class A starch bra
	10	4155.5	93.1	2975	17	AAT42635	Class A starch bra
	11	3363	75.3	3090	19	AAV38720	Full length cassav
	12	3281.5	73.5	2913	19	AAV38719	Full length cassav
	13	3269	73.2	2715	21	AAC45939	Arabidopsis thalia
	14	3239	72.5	3015	19	AAV05639	Rice type IV starc
	15	3136	70.2	2726	22	AAH78337	Nucleotide sequenc
	16	3096	69.3	2919	15	AAQ73750	Rice starch branch
	17	3037	68.0	3039	24	ABK15494	Wheat starch branc
	18	3030.5	67.9	2640	19	AAV70961	DNA encoding maize
	19	3026.5	67.8	2665	18	AAT69729	Plasmid pBE240 ins
	20	3026	67.8	2968	22	AAH78342	Nucleotide sequenc
	21	3021.5	67.7	2725	19	AAV29757	Zea mays starch br
	22	2676.5	59.9	2087	18	AAT69737	Corn starch branch
c	23	2669.5	59.8	2165	18	AAT69736	Corn starch branch
	24	2628	58.9	2307	21	AAZ99938	DNA encoding part
	25	2221.5	49.8	1919	19	AAV38722	cDNA encoding star
	26	2165	48.5	3128	16	AAT00774	Potato starch bran
	27	2147	48.1	4563	22	AAF30910	Wheat starch branc
	28	2139.5	47.9	2733	15	AAQ62135	Rice starch branch
	29	2130.5	47.7	2733	15	AAQ54674	Rice starch branch
	30	2107	47.2	2565	18	AAT69752	Corn starch branch
	31	2107	47.2	2763	19	AAV29758	Zea mays starch br
c	32	2104	47.1	2487	18	AAT69747	Corn starch branch
	33	2104	47.1	2771	13	AAQ24257	Branching enzyme D
	34	2104	47.1	2772	18	AAT69740	Plasmid pBE65 inse
	35	2100	47.0	2687	20	AAX34646	wSBE I-D4 cDNA seq
	36	2098.5	47.0	2909	13	AAQ27778	Potato amylose-amy
	37	2058	46.1	2899	22	AAH02926	Human shear stress
	38	2058	46.1	2955	24	ABN95650	Gene #2148 used to
	39	2058	46.1	3075	24	AAS94880	Human DNA sequence
	40	2052	46.0	2713	19	AAV70962	DNA encoding maize
	41	1914.5	42.9	3753	23	ABK50305	Red alga DNA encod
	42	1899	42.5	2598	23	ABL07067	Drosophila melanog
	43	1866	41.8	1452	21	AAC36957	Arabidopsis thalia
	44	1828.5	41.0	4147	21	AAC83166	Glycogen branching
c	45	1805	40.4	6556	23	ABL07066	Drosophila melanog

ALIGNMENTS

```
RESULT 1
AAT42630
ID   AAT42630 standard; DNA; 3033 BP.
XX
AC   AAT42630;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (19con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             145..2793
FT                   /*tag= a
```

```
FT   sig_peptide     145..288
FT                   /*tag=  b
FT   mat_peptide     289..2790
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;    96WO-GB01075.
XX
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAW06399.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 28-30; Page 42-46; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;

Alignment Scores:
Pred. No.:               0            Length:        3033
Score:                   4465.00      Matches:       834
Percent Similarity:      100.00%      Conservative:  0
Best Local Similarity:   100.00%      Mismatches:    0
Query Match:             100.00%      Indels:        0
DB:                      17           Gaps:          0

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42630 (1-3033)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 348

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 408

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 468

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 528

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 588

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 648

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 708

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 768

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 GACAAGTATGAGGGTGGTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 828

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTC 888

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 948

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1008

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1068

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCC 1128

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1188

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1248

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCT 1308

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 ATTCAAGAGCATTCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1368

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1428

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1488

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 CTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1548

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1608

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1609 TCAAATGCGAGATGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1668

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1669 ACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1728

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1729 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1788

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1789 ATTCATGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1848

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1849 TTTTGTATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1908

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1909 GCTGATAAACGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1968

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1969 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2028

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2029 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2088

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2089 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2148

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2149 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2208

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2209 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2268

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2269 GGCTCAGTAATCCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2328

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2329 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTAT 2388

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2389 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2448

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2449 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2508

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2509 ACAAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2568

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2569 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2628

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2629 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2688

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2689 AAAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 2748

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||||||||||||||||||||||||||||||||
Db       2749 GAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2790
```

RESULT 2
AAT42631

```
ID   AAT42631 standard; DNA; 2578 BP.
XX
AC   AAT42631;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (psbe2con.seq - clone pSJ90).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             24..2567
FT                   /*tag=  a
FT   sig_peptide     24..56
FT                   /*tag=  b
FT   mat_peptide     57..2564
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAW06400.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 32; Page 55-56; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;

Alignment Scores:
Pred. No.:              0             Length:        2578
Score:                  4358.50       Matches:       817
Percent Similarity:     98.56%        Conservative:  5
Best Local Similarity:  97.96%        Mismatches:    11
Query Match:            97.61%        Indels:        1
DB:                     17            Gaps:          1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42631 (1-2578)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 125

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        126 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATTTGAGTTCACT 185

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 245

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 305

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      306 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 365

Qy      101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      366 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 425

Qy      121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      426 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 485

Qy      141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      486 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 545

Qy      161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      546 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 605

Qy      181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
            |||||||||||||||||||||||||||||||||||     ||||||||||||||||||||
Db      606 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 665

Qy      201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      666 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 725

Qy      221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      726 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 785

Qy      241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      786 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 845

Qy      261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
            |||||||||   ||||||||||||||||||||||||||||||||||||:::|||||||||
Db      846 AACTACTCTTCACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 905

Qy      281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      906 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 965

Qy      301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      966 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1025

Qy      321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
            |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db     1026 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCT 1085

Qy      341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1086 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1145

Qy      361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1146 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1205

Qy      381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1206 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1265

Qy      401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
            |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db     1266 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1325

Qy      421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1326 TGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1385

Qy      441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
            ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db     1386 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1445

Qy      461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
            |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db     1446 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1505

Qy      481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1506 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1565

Qy      501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1566 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1625

Qy      521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
            |||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db     1626 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1685

Qy      541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
            |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1686 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1745

Qy      561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1746 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1805

Qy      581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1806 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1865

Qy      601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
            |||||||||||||||||||||      |||||||||||||||||||||||||||||||||
Db     1866 GATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1925

Qy      621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1926 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1985

Qy      641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1986 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2045

Qy      661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2046 GACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2105

Qy      681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
            ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db     2106 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2165

Qy      701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2166 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2225

Qy      721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2226 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2285

Qy      741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
            |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db     2286 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2345

Qy      761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2346 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2405

Qy      781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2406 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2465

Qy      801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
            :::||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     2466 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAAGAA 2522
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Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              |||||||||||   |||||||||||||||||||||||||||
Db       2523 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2564

RESULT 3
AAT69587
ID   AAT69587 standard; cDNA; 3074 BP.
XX
AC   AAT69587;
XX
DT   26-AUG-1997  (first entry)
XX
DE   Potato starch branching enzyme II gene (beII).
XX
KW   Starch branching enzyme II; beII gene; potato; transgenic plant;
KW   amylopectin; amylose; starch; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             189..2825
FT                   /*tag=  a
FT   sig_peptide     189..332
FT                   /*tag=  b
FT   mat_peptide     333..2822
FT                   /*tag=  c
XX
PN   WO9720040-A1.
XX
PD   05-JUN-1997.
XX
PF   28-NOV-1996;   96WO-SE01558.
XX
PR   19-APR-1996;   96SE-0001506.
PR   29-NOV-1995;   95SE-0004272.
XX
PA   (EKBB/) EK B.
PA   (KHOS/) KHOSNOODI J.
PA   (LARS/) LARSSON C.
PA   (LARS/) LARSSON H.
PA   (RASK/) RASK L.
PA   (AMYL-) AMYLOGENE HB.
XX
PI   Ek B,  Khosnoodi J,  Larsson C,  Larsson H,  Rask L;
XX
DR   WPI; 1997-310596/28.
DR   P-PSDB; AAW19113.
XX
PT   Isolated potato starch branching enzyme II - useful for altering
PT   degree of amylopectin branching and amylopectin/amylose ratio in
PT   potato starch
XX
PS   Claim 4; Page 12-15; 24pp; English.
XX
CC   A cDNA clone (AAT69587) codes for potato starch branching enzyme II
CC   (BEII) (AAW19113).  It was isolated from potato tuber cDNA by PCR
CC   amplification using primers (AAT69588-89) based on tryptic peptides
CC   of isolated BEII; the 5' and 3' ends of the sequence were detd. by
CC   RACE.  A vector comprising the whole or a functional active part of
CC   the isolated sequence (sense or antisense), plus regulatory
CC   sequences active in potato, can be used to produce transgenic
CC   potatoes.  The starch obtd. from such plants will show a changed
CC   pattern of amylopectin branching and an altered amylopectin/amylose
CC   ratio.
XX
SQ   Sequence 3074 BP; 902 A; 560 C; 710 G; 896 T; 6 other;

Alignment Scores:
Pred. No.:               0             Length:          3074
Score:                   4329.00       Matches:         814
Percent Similarity:      98.08%        Conservative:    4
Best Local Similarity:   97.60%        Mismatches:      12
Query Match:             96.95%        Indels:          4
DB:                      18            Gaps:            1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT69587 (1-3074)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db        333 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 392

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 452

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 512

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 572

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 632

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 692

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 752

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 812

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 872

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        873 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 932

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 992

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1052

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1112

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1113 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1172

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1232

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1292

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1293 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCT 1352

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db      1353 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCA 1412

Qy       361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 AGCAGCCGTTTTGGAACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1472

Qy       381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1532

Qy       401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
             |||||||||||||||    |||||||||||||||||||||||||||||||||||||||||
Db      1533 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1592

Qy       421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1593 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1652

Qy       441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
             ||||||||||||||||||||||||     |||||||||||||||||||||||||||||||
Db      1653 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1712

Qy       461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
             |||||||||||||||     ||||||||||||||||||||||||||||||||||||||||
Db      1713 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1772

Qy       481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1773 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1832

Qy       501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1833 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1892

Qy       521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
             |||   |||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db      1893 TTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1952

Qy       541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
             |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1953 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2012

Qy       561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2013 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2072

Qy       581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2073 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2132

Qy       601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2133 GATTTTATGGCTCTGGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2192

Qy       621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2193 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2252

Qy       641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2253 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2312

Qy       661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2313 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2372

Qy       681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
             ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db      2373 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2432

Qy       701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2433 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2492

Qy       721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2493 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2552

Qy       741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
             ||||||||||||||||||||||||||     |||||||||||||||||||||||||||||
Db      2553 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2612

Qy       761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2613 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2672

Qy       781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2673 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2732

Qy       801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
             :::||||||||||||||||||||||||||||||            ||||||||||||||
Db      2733 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA------------GAAGAAGAAGAAGAA 2780

Qy       821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
             ||||||||||||    ||||||||||||||||||||||||||
Db      2781 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822
```

```
RESULT 4
AAT42636
ID   AAT42636 standard; DNA; 2576 BP.
XX
AC   AAT42636;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (86con.seq) cloned in QE32.
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 49-51; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:        2576
Score:                  4322.00        Matches:       816
Percent Similarity:     98.44%         Conservative:  5
```

```
Best Local Similarity:   97.84%     Mismatches:   12
Query Match:             96.80%     Indels:        2
DB:                      17         Gaps:          1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42636 (1-2576)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 125

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        126 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATTTGAGTTCACT 185

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 245

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 305

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 365

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 425

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 485

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 545

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 605

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        606 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 665

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 725

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 785

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 845

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||   ||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        846 AACTACT--CTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 903

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 963

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1023

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCT 1083

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1143

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1203

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1263

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1264 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1323

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1383

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              |||||||||||||||            ||||||||||||||||:::   |||||||||||
Db       1384 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATATTGATTTGATGGTGTG 1443

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1444 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1503

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1504 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1563

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1564 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1623

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1624 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1683

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1684 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1743

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1744 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1803

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1804 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1863

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db       1864 GATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1923

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1924 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1983

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1984 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2043

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2044 GACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2103

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       2104 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2163
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Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2164 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2223

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2224 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2283

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db       2284 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2343

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2344 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2403

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2404 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGT 2463

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       2464 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAAGAA 2520

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||   |||||||||||||||||||||||||||
Db       2521 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2562
```

RESULT 5
ABK50301
ID   ABK50301 standard; cDNA; 2563 BP.
XX
AC   ABK50301;
XX
DT   15-JUL-2002 (first entry)
XX
DE   Potato cDNA encoding starch branching enzyme, SBE II.
XX
KW   Potato; starch branching enzyme; SBE II; glucan branching enzyme;
KW   GBE; ss; gene; plant; transgenic; antisense; food industry;
KW   paper industry; chemical industry.
XX
OS   Solanum tuberosum.
XX
FH   Key   Location/Qualifiers
FT   CDS   3..2552
FT   /*tag= a
FT   /product= "SBE II"
FT   /partial
FT   /note= "No start codon shown"
XX
PN   GB2360521-A.
XX
PD   26-SEP-2001.
XX
PF   20-MAR-2000; 2000GB-0006733.
XX
PR   20-MAR-2000; 2000GB-0006733.
XX
PA   (DANI-) DANISCO AS.
XX
PI   Poulsen P, Sorensen IS;
XX
DR   WPI; 2001-650142/75.
DR   P-PSDB; AAU80169.
XX
PT   New transformed plants with reduced endogenous starch branching enzyme
PT   and heterologous glucan branching enzyme activities, useful for
PT   producing starch with improved properties, which is in the food, paper
PT   and chemical industries -
XX
PS   Example 1; Page 31-35; 61pp; English.
XX
CC   The invention relates to a transformed organism, preferably a transformed
CC   plant, having a reduced endogenous starch branching enzyme (SBE)
CC   activity, and having a heterologous glucan branching enzyme (GBE)
CC   activity. The reduced SBE activity is effected via expression of a
CC   nucleotide sequence that is antisense to at least part of a SBE exon.
CC   Also included are a method of producing starch with altered
CC   characteristics comprising (a) providing a plant having reduced
CC   endogenous SBE activity, and having heterologous GBE activity
CC   (b) propagating the plant of (a) and optionally (c) obtaining starch
CC   from the plant; starch obtainable from the transformed plant; and
CC   a nucleic acid construct system capable of directing the expression
CC   of all or part of one or more antisense SBE exons and optionally one or
CC   more heterologous GBE. The transformed plants are useful for producing
CC   starch with modified and improved properties, which is an important raw
CC   material and used in the food, paper and chemical industries. The
CC   present sequence encodes Potato SBE II, used to make transgenic plants of
CC   the invention.
XX
SQ   Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;

```
Alignment Scores:
Pred. No.:               0              Length:          2563
Score:                   4274.00        Matches:         802
Percent Similarity:      97.58%         Conservative:    6
Best Local Similarity:   96.86%         Mismatches:      14
Query Match:             95.72%         Indels:          6
DB:                      23             Gaps:            1
```

US-10-056-454A-15_COPY_49_882 (1-834) x ABK50301 (1-2563)

```
Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||
Db         81 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 140

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 200

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 260

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 320

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 380

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        381 TCTAAAACATTAAATACTTTTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 440

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 500

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 560

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 620

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        621 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 680

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 740
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Qy    221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
Db    741 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 800

Qy    241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
Db    801 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 860

Qy    261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
Db    861 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGGATATATTATGATCCACCC 920

Qy    281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
Db    921 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 980

Qy    301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
Db    981 TATGAATCTCATATTGGAATGAGTAGTCCGGAACCTAAAATTAACTCATACGTGAATTTT 1040

Qy    321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
Db   1041 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACGATGCGGTGCAAATTATGGCT 1100

Qy    341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
Db   1101 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1160

Qy    361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db   1161 AGCAGCCGTTTTGGAACTCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1220

Qy    381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db   1221 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1280

Qy    401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
Db   1281 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1340

Qy    421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
Db   1341 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1400

Qy    441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db   1401 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1460

Qy    461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db   1461 ACATCAATGATGTGTACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1520

Qy    481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
Db   1521 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1580

Qy    501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db   1581 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1640

Qy    521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db   1641 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1700

Qy    541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db   1701 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGAGTGATATT 1760

Qy    561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db   1761 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1820

Qy    581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
Db   1821 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 1880

Qy    601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db   1881 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1940

Qy    621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
Db   1941 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2000

Qy    641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db   2001 AATGAATTCGGCCACCCCGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2060

Qy    661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
Db   2061 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2120

Qy    681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db   2121 GGAGATGCAGATTATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2180

Qy    701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db   2181 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2240

Qy    721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
Db   2241 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2300

Qy    741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db   2301 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2360

Qy    761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db   2361 TTGGACTCGGATGATCCACTTTTTGGTGGCTTTGGGAGAATTGATCATAATGCCGAATAC 2420

Qy    781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
Db   2421 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2480

Qy    801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
Db   2481 AGGACAGCAGTGGTCTATGCACTAGTAGACAAA------------------GAAGCAGAA 2522

Qy    821 GluGluValAlaAlaValGluGlu 828
Db   2523 GAAGAAGTAGCAGTAGTAGAAGAA 2546
```

RESULT 6
AAT42634
ID   AAT42634 standard; DNA; 3003 BP.
XX
AC   AAT42634;
XX
DT   03-MAR-1997 (first entry)
XX
DE   Class A starch branching enzyme (10con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX

```
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 38-39; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;

Alignment Scores:
Pred. No.:              0             Length:         3003
Score:                  4269.00       Matches:        804
Percent Similarity:     97.25%        Conservative:   8
Best Local Similarity:  96.29%        Mismatches:     18
Query Match:            95.61%        Indels:         5
DB:                     17            Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42634 (1-3003)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              |||||||||||||||||||||||     ||||||||||:::|||||||||||||||||||
Db        287 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAATTGCAGCATCGGGGAAAGTC 346

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db        347 CTTGTGCCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGATCAATTTGAGTTCGCT 406

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 466

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 526

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 586

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 646

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 706

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 766

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db        767 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAGAATGGGTTTCACT 826

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db        827 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 886

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||   |||||||||||||||||
Db        887 ATTGGGGATTTCAACAATTGGGACGCAAATGCTGACTTTATGACTCGGAATGAATTTGGT 946

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        947 GTCTGAGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1006

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1007 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1066

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1067 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1126

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db       1127 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGGTGAGAATA 1186

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1246

Qy        321 ArgAspGluValLeuProArgIle-LysLysLeuGlyTyrAsnAlaLeuGlnIleMetAl 340
              ||||||||||||||||||||||| |||||||||||||||||||||:::||||||||||||
Db       1247 AGAGATGAAGTTCTTCCTCGCATAAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGC 1306

Qy        340 aIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 TATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACC 1366

Qy        360 oSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLe 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 AAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCT 1426

Qy        380 uGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGl 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 AGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGG 1486

Qy        400 yLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHi 420
              |||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db       1487 ACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCA 1546

Qy        420 sTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLe 440
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1547 TTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCT 1606

Qy        440 uSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVa 460
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db       1607 CTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGT 1666

Qy        460 lThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGl 480
              ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db       1667 GACATCAATGATGTGTACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGA 1726

Qy        480 uTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLe 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 ATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCT 1786

Qy        500 uIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProTh 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 TATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGAC 1846

Qy        520 rPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIl 540
              ||||||:::|||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1847 ATTTGTGTTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAAT 1906

Qy        540 eAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIl 560
              ||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 TGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATAT 1966

Qy        560 eValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHi 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1967 TGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCA 2026

Qy        580 sAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTy 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2027 TGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTA 2086

Qy        600 rAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHi 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 TGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTACA 2146

Qy        620 sLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGl 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 CAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGG 2206

Qy        640 yAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAs 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 AAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGA 2266

Qy        660 pGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLe 680
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db       2267 TGGCTCAGTAATTCCCAGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCT 2326

Qy        680 uGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTy 700
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db       2327 GGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTA 2386

Qy        700 rLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGl 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2387 TCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGA 2446

Qy        720 uGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTr 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2447 AGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTG 2506

Qy        740 pThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAl 760
              ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||||||
Db       2507 GACAAAAGGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGC 2566

Qy        760 aLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTy 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2567 CTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATA 2626

Qy        780 rPheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCy 800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2627 TTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAG 2686

Qy        800 sLysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGl 820
               :::|||||||||||||||||||||||||||||||||            |||||||||||
Db       2687 TAGAACAGCAGTGGTCTATGCACTAGTAGACAAA------------GAAGAAGAAGAAGA 2734

Qy        820 uGluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||   ||||||||||||||||||||||||||
Db       2735 AGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2777

RESULT 7
AAT42632
ID   AAT42632 standard; DNA; 3231 BP.
XX
AC   AAT42632;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (psbe2con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        45..3200
FT                   /*tag=  a
FT                   /note= "claim 34"
FT   CDS             228..2855
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 31, 34; Page 53-55; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
CC   The same sequence is given in Figure 8, however, nucleotides
CC   1-44 omitted.
XX
SQ   Sequence 3231 BP; 960 A; 577 C; 739 G; 947 T; 8 other;

Alignment Scores:
Pred. No.:              0            Length:        3231
Score:                  4268.50      Matches:       802
Percent Similarity:     97.12%       Conservative:  8
Best Local Similarity:  96.16%       Mismatches:    19
Query Match:            95.60%       Indels:        5
DB:                     17           Gaps:          1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42632 (1-3231)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||:::||||||   ||||||||||||||||||||||||||||||||||
Db        372 GAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 431

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db        432 CTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 491

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||:::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 GAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACAC 551

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 611

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 GTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 671

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 731

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 791

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
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Db        792 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATT 851

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 911

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        912 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTC 971

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 1031

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1091

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       1092 AGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1151

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db       1152 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1211

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||||
Db       1212 GAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1271

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1272 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1331

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              |||||||||||||||||||||||||||    ||||||||||||||||:::||||||||||
Db       1332 AGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCT 1391

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1392 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1451

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1452 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1511

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1512 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1571

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              |||||||||||||||    |||||||||||||||||||||||||||||||||||||||||
Db       1572 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1631

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1632 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1691

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||        ||||||   |||||||||||||||||||||
Db       1692 TCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTG 1751

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              |||||||||||||||    |||||||||||||||||||||||||||||||||||||||||
Db       1752 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1811

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||    |||||||||||||||    |||||||||
Db       1812 TACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTT 1871

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1872 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1931

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1932 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1991

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db       1992 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2051

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2052 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2111

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2112 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2171

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2172 GATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2231

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2232 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2291

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2292 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2351

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2352 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2411

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              |||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db       2412 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2471

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2472 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2531

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2532 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2591

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       2592 ACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCC 2651

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2652 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGT 2711

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2712 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2771

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||||||||||||||               ||||||||||||
Db       2772 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA---------------GAAGAAGAAGAA 2816

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||  ||||||||||||||||||||||||||||
Db       2817 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2858
```

RESULT 8
AAT17267
ID   AAT17267 standard; DNA; 2531 BP.
XX
AC   AAT17267;
XX
DT   03-MAR-1997 (first entry)
XX

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DE   Class A starch branching enzyme (direct sequencing).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAR93804.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Fig 9; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
CC   This sequence was obtained by direct sequencing of PCR fragments
CC   amplified from first strand cDNA.  Nucleotides which could not
CC   be unambiguously assigned are indicated using standard IUPAC
CC   notation.
XX
SQ   Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;

Alignment Scores:
Pred. No.:              0              Length:         2531
Score:                  4229.00        Matches:        793
Percent Similarity:     96.96%         Conservative:   4
Best Local Similarity:  96.47%         Mismatches:     25
Query Match:            94.71%         Indels:         0
DB:                     17             Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x AAT17267 (1-2531)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
                ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db         59 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 118

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
                ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db        119 CTTGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 178

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 238

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 298

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 358

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 418

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 478

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 538

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 598

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
                ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        599 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 658

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 718

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 778

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 AGAGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 838

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
                ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        839 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 898

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
                ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db        899 GAAGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 958

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1018

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
                |||||||||||||||||||||||||   |||||||||||||||||||||:::||||||||
Db       1019 AGAGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCT 1078

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1138

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1198

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1258

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
                ||||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db       1259 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1318

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1378

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
                |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db       1379 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1438

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
                ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db       1439 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1498
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Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1558

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 ATTCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1618

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db       1619 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1678

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1738

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db       1739 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCAT 1798

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||      ||||||||||||||||||||
Db       1799 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTAT 1858

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1859 GATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 1918

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1919 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1978

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1979 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGAT 2038

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2039 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2098

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||||    ||||||||||||||||||||    ||||||||
Db       2099 GGAGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2158

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2159 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2218

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       2219 GGAGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2278

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              |||   ||||||||||||||||||||     |||||||||||||||||||||||||||||
Db       2279 ACAAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGC 2338

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2398

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||   ||||||   ||||||||||||||||||   |||||||||||||||||||
Db       2399 TTCACCTCTGAAGGATCGTATGATGATCGTCCYCGYYCAATTATGGTGTATGCACCTAGT 2458

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::|||||||||||||||||||||||||||||||||    |||    ||||||||||||||
Db       2459 AGAACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCC 2518

Qy        821 GluGlu 822
                 |||
Db       2519 GNNGAA 2524
```

RESULT 9

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AAT42637
ID   AAT42637 standard; DNA; 2529 BP.
XX
AC   AAT42637;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 51-53; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;

Alignment Scores:
Pred. No.:              0            Length:         2529
Score:                  4218.00      Matches:        790
Percent Similarity:     96.72%       Conservative:   5
Best Local Similarity:  96.11%       Mismatches:     27
Query Match:            94.47%       Indels:         0
DB:                     17           Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42637 (1-2529)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              |||||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db         59 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 118

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CTTGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 178

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 238

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 298

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 358

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 418

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 478

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 538

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||   :::||||||||||||||||||||||||||||||||||||
Db        539 GACAAGTATGAGGGTGGTTTTCAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 598

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        599 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 658

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 718

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 778

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 AGAGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 838

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              |||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        839 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 898

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db        899 GAAGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 958

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1018

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||   ||||||||||||||||||:::||||||||||||
Db       1019 AGAGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCT 1078

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1138

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1198

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1258

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db       1259 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1318

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1378

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db       1379 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1438

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db       1439 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1498

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1558

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 ATTCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1618

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1619 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1678

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1738

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db       1739 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCAT 1798

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db       1799 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTAT 1858

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              |||||||||||||||||||||   |||   ||||||||||||||||||||||||||||||
Db       1859 GATTTTATGGCTCTGGATAGACCGYCAACAYCATTAATAGATCGTGGGATAGCATTGCAC 1918

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1919 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 1978

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1979 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGAT 2038

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2039 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2098

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||   ||||||||||||||||||||   ||||||||||||
Db       2099 GGAGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2158

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2159 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2218

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db       2219 GGAGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2278

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              |||   ||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db       2279 ACAAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGC 2338

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2398

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||   ||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       2399 TTCACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2458

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||||||||||||||   |||   ||||||||||||||||||
Db       2459 AGAACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCC 2518

Qy        821 GluGlu 822
                 |||
Db       2519 GNNGAA 2524
```

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RESULT 10
AAT42635
ID   AAT42635 standard; DNA; 2975 BP.
XX
AC   AAT42635;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (11con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 40-41; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2975 BP; 871 A; 548 C; 693 G; 863 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:         2975
Score:                  4155.50        Matches:        791
Percent Similarity:     95.79%         Conservative:   6
Best Local Similarity:  95.07%         Mismatches:     26
Query Match:            93.07%         Indels:         11
DB:                     17             Gaps:           1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42635 (1-2975)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 348

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 408

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db        409 GAGACATCTCCAGAAAAATCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 468

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 528

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 588

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 648

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 708

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 768

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        769 GACAAGTATGAGGGTGGTTTGGAAGC-TTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 827

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        828 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 887

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        888 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 947

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        948 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1007

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1008 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1067

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1068 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1127

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1128 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1187

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1188 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1247

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db       1248 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCGAATTATGGCT 1307

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1308 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCA 1367

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db       1368 AGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTCGATTGATAAAGCTCATGAGCTA 1427

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1428 GGAATTGTTGTTCTCATGGACATCGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1487

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db       1488 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1547

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db       1548 TGGATGTGGGATTC-CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1606

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db       1607 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTCGATGGTGTG 1666
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Qy      461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
            ||||||||||||||     ||||||||||||||||||||||||||||||||||||||||||
Db     1667 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1726

Qy      481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1727 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1786

Qy      501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
            |||||    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1787 ATTCATAGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1846

Qy      521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
            ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db     1847 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1906

Qy      541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
            |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db     1907 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 1966

Qy      561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1967 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2026

Qy      581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2027 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2086

Qy      601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
            |||||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db     2087 GATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2146

Qy      621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2147 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2206

Qy      641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
            ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db     2207 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAGCCACACCTTTCTGAT 2266

Qy      661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2267 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2326

Qy      681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
            ||||||||||||||||||||||||    ||||||||||||||||||      ||||||||
Db     2327 GGAGATGCAGAATATTTAAGATACCATGGGTTACAAGAATTTGACTGGGCTATGCAGTAT 2386

Qy      701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2387 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2446

Qy      721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
            |||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db     2447 GGAGATAGGATGATTGTATTTGAAAGAGGAAACCTAGTTTTCGTCTTTAATTTTCACTGG 2506

Qy      741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
            |||   ||||||||||||||||||||||    ||||||||||||||||||||||||||
Db     2507 ACAAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGTC 2566

Qy      761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2567 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2626

Qy      781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
            ||||||   ||||||   ||||||||||||||||   |||||||||||||||||||
Db     2627 TTCACCTCTGAAGGATCGTATGATGATCGTCCTTGTTCAATTATGGTGTATGCACCTAGT 2686

Qy      801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
            :::|||||||||||||||||||||||||||||||
Db     2687 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA--------------------------- 2719

Qy      821 GluGluValAlaAlaValGluGluValValValGlu 832

            |||||||||    |||||||||    :::    |||
Db     2720 CTAGAAGTAGCAGTAGTAGAAGAACCCATTGAAGAA 2755
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RESULT 11
AAV38720
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ID   AAV38720 standard; DNA; 3090 BP.
XX
AC   AAV38720;
XX
DT   21-SEP-1998  (first entry)
XX
DE   Full length cassava tuber cDNA in pSJ146.
XX
KW   Starch branching enzyme; SBE; cassava; ss.
XX
OS   Manihot esculenta.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    35..2760
FT                   /*tag= a
FT                   /note= "these nycleotides are SBE II sequence, the
FT                          reminder are derived from the plamsid"
FT   CDS             131..2677
FT                   /*tag= b
FT                   /product= SBE II
XX
PN   WO9820145-A2.
XX
PD   14-MAY-1998.
XX
PF   04-NOV-1997;   97WO-GB03032.
XX
PR   05-NOV-1996;   96GB-0023095.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Jobling SA,  Safford R;
XX
DR   WPI; 1998-286958/25.
DR   P-PSDB; AAW62600.
XX
PT   Starch branching gene from cassava - useful for producing altered
PT   plants giving modified starch
XX
PS   Claim 2; Fig 13; 67pp; English.
XX
CC   The present sequence encodes starch branching enzyme (SBE) II. It
CC   was isolated from cassava tubers. The products can be used for
CC   producing plants having altered starch quantities and qualities.
CC   They can also be used for producing altered plants such as cassava,
CC   banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
CC   and rice plants.
XX
SQ   Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;

Alignment Scores:
Pred. No.:              3.27e-315      Length:         3090
Score:                  3363.00        Matches:        618
Percent Similarity:     84.20%         Conservative:   75
Best Local Similarity:  75.09%         Mismatches:     98
Query Match:            75.32%         Indels:         32
DB:                     19             Gaps:           4

US-10-056-454A-15_COPY_49_882 (1-834) x AAV38720 (1-3090)

Qy        2 LysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeu 21
            ||||||||||||    |||:::                ||||||:::||||||    |||||||||
Db      284 AAGTCCTCTTATGAATCTGACTCCTCAAATTTAACTGTCTCTGCATCTGAGAAGGTCCTT 343

Qy       22 ValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThrGlu 41
            ||||||    |||    |||    |||||||||||||||    |||    |||    |||
Db      344 GTTCCTGATGATCAGATTGATGGCTCTTCTTCTTCAACATATCAATTAGAAACCACTGGC 403
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Qy     42 ThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAla 61
Db    404 ACAGTTTTGGAGGAATCCCAGGTTCTTGGTGATGCAGAGAGTCTTGTGATGGAAGATGAT 463

Qy     62 SerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerVal 81
Db    464 AAGAATGTT------GAGGAGGATGAAGTAAAA-------------------------- 490

Qy     82 GluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSer 101
Db    491 ---------------------------------AAAGAGTCGGTTCCATTGCATGAGACA 517

Qy    102 LysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArg 121
Db    518 ATTAGCATTGGAAAAAGTGAATCT--------------------------AAACCAAGG 550

Qy    122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db    551 TCCATTCCTCCACCTGGCAGTGGGCAGAGAATATATGACATAGATCCAAGCTTGGCAGGT 610

Qy    142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db    611 TTCCGTCAGCATCTTGACTACCGATATTCACAGTACAAAAGGCTGCGTGAGGAAATTGAC 670

Qy    162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db    671 AAGTATGAAGGTGGTTTGGATGCATTCTCTCGTGGATTTGAAAAGTTTGGTTTCTTACGC 730

Qy    182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db    731 AGTGAAACAGGAATAACTTATAGGGAATGGGCACCTGGAGCTACGTGGGCTGCACTTATT 790

Qy    202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db    791 GGAGATTTCAACAATTGGAATCCTAATGCAGATGTCATGACTCGGAATGAGTTTGGTGTC 850

Qy    222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db    851 TGGGAGATTTTTTTGCCAAATAACGCAGATGGTTCACCACCAATTCCTCATGGTTCTCGA 910

Qy    242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db    911 GTAAAGATACGCATGGATACTCCATCTGGCATCAAAGATTCAATTCCTGCTTGGATCAAG 970

Qy    262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
Db    971 TTCTCAGTTCAGGCACCTGGTGAAATCCCATACAATGCCATATACTATGATCCACCAAAG 1030

Qy    282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db   1031 GAGGAGAAGTATGTGTTCAAACATCCTCAGCCAAAGAGACCAAAATCACTTAGGATTTAT 1090

Qy    302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db   1091 GAATCTCATGTTGGGATGAGTAGTATGGAGCCAATAATTAACACATATGCCAACTTTAGA 1150

Qy    322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db   1151 GATGATATGCTTCCTCGCATCAAAAAGCTTGGCTACAATGCTGTTCAGATCATGGCTATT 1210

Qy    342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
Db   1211 CAAGAGCATTCCTATTATGCTAGTTTTGGGTACCATGTCACAAACTTTTTTGCACCTAGC 1270

Qy    362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db   1271 AGCCGATTTGGAACTCCTGATGATTTGAAGTCTTTAATAGATAAAGCTCATGAGTTAGGG 1330

Qy    382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db   1331 CTGCTTGTTCTCATGGATATTGTTCATAGCCATGCGTCAAATAATACGTTGGATGGGCTG 1390

Qy    402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db   1391 AACATGTTTGATGGTACGGATAGTCACTACTTCCACTCCGGATCACGGGGTCATCATTGG 1450

Qy    422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
Db   1451 TTGTGGGACTCTCGCCTTTTCAACTATGGAAGCTGGGAGGTGCTAAGATTTCTTCTTTCA 1510

Qy    442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db   1511 AATGCAAGATGGTGGTTGGAAGAGTACAGGTTTGATGGTTTTAGATTTGATGGGGTGACT 1570

Qy    462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db   1571 TCCATGATGTACACTCCCCATGGGTTGCAGGTAGCTTTTACTGGCAACTACAATGAGTAC 1630

Qy    482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db   1631 TTTGGATATGCAACTGATGTAGATGCTGTGATTTATTTGATGCTTGTGAATGATATGATT 1690

Qy    502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db   1691 CACGGTCTTTTCCCTGAGGCTGTTACCATTGGTGAAGATGTTAGCGGAAAGCCAACATTT 1750

Qy    522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db   1751 TGCATTCCAGTGGAAGATGGTGGTGTTGGATTTGATTACCGTCTCCACATGGCCATTGCC 1810

Qy    542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
Db   1811 GATAAATGGATTGAGATTCTTAAGAAGAGAGATGAGGACTGGAAAATGGGTGACATTGTG 1870

Qy    562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db   1871 CATACACTCACCAACAGAAGGTGGTTGGAAAAATGTGTTGCTTATGCTGAAAGTCATGAC 1930

Qy    582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db   1931 CAAGCTCTTGTTGGTGACAAAACTATTGCATTTTGGCTGATGGACAAGGACATGTACGAC 1990

Qy    602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db   1991 TTCATGGCTCGTGACAGACCATCTACTCCTCTTATAGATCGTGGAATAGCATTGCACAAA 2050

Qy    622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
Db   2051 ATGATCAGGCTTATTACCATGGGCTTAGGCGGAGAAGGATATTTGAATTTTATGGGAAAT 2110

Qy    642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db   2111 GAATTTGGACATCCTGAGTGGATTGATTTTCCAAGAGGGGATCGACATCTGCCCAATGGT 2170

Qy    662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db   2171 AAAGTAATTCCAGGGAACAACCACAGTTATGATAAATGCCGTCGTAGATTTGATCTAGGT 2230

Qy    682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db   2231 GATGCAGACTATCTAAGATATCATGGAATGCAAGAGTTTGATCAGGCAATGCAACATCTT 2290

Qy    702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
Db   2291 GAAGAAGCCTATGGTTTCATGACTTCTGAGCACCAGTATATATCACGGAAGGATGAAGGA 2350

Qy    722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
Db   2351 GATCGGATCATTGTCTTTGAGAGGGGAAACCTTGTTTTTGTATTCAACTTTCATTGGACT 2410

Qy    742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
Db   2411 AACAGCTATTCAGATTACCGAGTTGGCTGCTTCAAGTCAGGAAAGTACAAGATTGTTTTG 2470

Qy    762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
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Db       2471 GACTCGGATGATGGCTTGTTTGGAGGCTTCAACAGGCTTAGTCATGATGCCGAGCACTTC 2530

Qy        782 ThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLys 801
Db       2531 ACCTTTGACGGGTGGTATGATAACCGGCCTCGGTCCTTCATGGTATATGCACCATCTAGG 2590

Qy        802 ThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu---Glu 820
Db       2591 ACAGCAGTGGTCTATGCTTTAGTAGAAGATGAAGAGAATGAAGCAGAGAATGAAGTAGAA 2650

Qy        821 GluGluVal 823
Db       2651 AGTGAAGTG 2659

RESULT 12
AAV38719
ID   AAV38719 standard; cDNA; 2913 BP.
XX
AC   AAV38719;
XX
DT   21-SEP-1998  (first entry)
XX
DE   Full length cassava tuber cDNA in pSJ107.
XX
KW   Starch branching enzyme; SBE; cassava; ss.
XX
OS   Manihot esculenta.
XX
FH   Key             Location/Qualifiers
FT   CDS             21..2531
FT                   /*tag=  a
FT                   /product= SBE II
XX
PN   WO9820145-A2.
XX
PD   14-MAY-1998.
XX
PF   04-NOV-1997;    97WO-GB03032.
XX
PR   05-NOV-1996;    96GB-0023095.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Jobling SA,  Safford R;
XX
DR   WPI; 1998-286958/25.
DR   P-PSDB; AAW62599.
XX
PT   Starch branching gene from cassava - useful for producing altered
PT   plants giving modified starch
XX
PS   Claim 2; Fig 4; 67pp; English.
XX
CC   The present sequence encodes starch branching enzyme (SBE) II. It
CC   was isolated from cassava tubers. The products can be used for
CC   producing plants having altered starch quantities and qualities.
CC   They can also be used for producing altered plants such as cassava,
CC   banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
CC   and rice plants.
XX
SQ   Sequence 2913 BP; 818 A; 549 C; 680 G; 866 T; 0 other;

Alignment Scores:
Pred. No.:              2.34e-307     Length:          2913
Score:                  3281.50       Matches:         600
Percent Similarity:     83.35%        Conservative:    86
Best Local Similarity:  72.90%        Mismatches:      100
Query Match:            73.49%        Indels:          37
DB:                     19            Gaps:            5

US-10-056-454A-15_COPY_49_882 (1-834) x AAV38719 (1-2913)

Qy          2 LysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeu 21
Db        168 AAGTCATCTCATGAATCTGACTCCTCAAATGTAATGGTCACTGCTTCTAAAAGAGTCCTT 227

Qy         22 ValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThrGlu 41
Db        228 ---CCTGATGGTCGGATTGAATGCTATTCTTCTTCAACAGATCAATTGGAAGCCCCTGGC 284

Qy         42 ThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAla 61
Db        285 ACAGTTTCAGAAGAATCCCAGGTGCTTACTGATGTTGAGAGTCTCATTATGGATGAT--- 341

Qy         62 SerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerVal 81
Db        342 ---------AAGATTGTTGAAGATGAAGTA-----------------------AATAAA 368

Qy         82 GluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSer 101
Db        369 GAATCTGTTCCAATGCGGGAGACAGTTAGCATCAGAAAAATTGGATCT------------ 416

Qy        102 LysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArg 121
Db        417 ---------------------------------------------------AAACCAAGG 425

Qy        122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db        426 TCCATTCCTCCACCCGGCAGAGGGCAAAGAATATATGACATAGATCCAAGCTTGACAGGC 485

Qy        142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db        486 TTTCGTCAACACCTAGATTACCGGTATTCACAGTACAAAAGACTCCGAGAAGAAATTGAC 545

Qy        162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db        546 AAGTATGAAGGTAGTCTGGATGCATTTTCTCGTGGCTATGAAAAGTTTGGTTTCTCACGC 605

Qy        182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db        606 AGTGAAACAGGAATAACTTATAGAGAGTGGGCACCAGGAGCTACGTGGGCTGCATTGATT 665

Qy        202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db        666 GGAGATTTCAATAACTGGAATCCTAATGCAGATGTCATGACTCAGAATGAGTGTGGTGTC 725

Qy        222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db        726 TGGGAGATCTTTTTGCCGAATAATGCAGATGGTTCACCACCAATTCCCCATGGTTCTCGA 785

Qy        242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db        786 GTAAAGATACGCATGGATACTCCATCTGGCAACAAAGATTCTATTCCTGCTTGGATCAAG 845

Qy        262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
Db        846 TTCTCAGTTCAAGCACCAGGTGAACTCCCATATAATGGCATATACTATGATCCTCCCGAG 905

Qy        282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db        906 GAGGAGAAGTATGTGTTCAAAAATCCTCAGCCAAAGAGACCAAAATCACTTCGGATTTAT 965

Qy        302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db        966 GAGTCGCACGTTGGAATGAGTAGTACGGAGCCAGTAATTAACACATATGCCAACTTTAGA 1025

Qy        322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db       1026 GATGATGTGCTTCCTCGCATCAAAAAGCTTGGCTACAATGCTGTTCAGCTCATGGCTATT 1085

Qy        342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
Db       1086 CAAGAGCATTCATATTATGCTAGTTTTGGGTATCACGTCACAAACTTTTATGCAGCTAGC 1145

Qy        362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
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Db       1146 AGCCGATTTGGAACTCCTGATGATTTAAAGTCTCTAATAGATAAAGCTCACGAGTTAGGT 1205

Qy        382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
              :::::|||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db       1206 CTTCTTGTTCTCATGGATATTGTTCATAGCCATGCATCAACTAATACGTTGGATGGGCTG 1265

Qy        402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
              |||||||||||  ||||||          ||||||||||||||  ||||||:::||||||
Db       1266 AATATGTTTGATGGTACGGATGGTCACTACTTTCACTCTGGACCACGGGGTCATCATTGG 1325

Qy        422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
              |||||||||||||||||||||||||||:::|||||||||||||||:::|||||||||
Db       1326 ATGTGGGACTCTCGCCTTTTCAACTATGGAGCTGGGAGGTTCTAAGGTTTCTTCTTTCA 1385

Qy        442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
              ||||||||||||||||||||    :::|||||||||||||||||||||||||||||||||
Db       1386 AATGCAAGGTGGTGGTTGGATGAGTACAAGTTTGATGGTTCAGATTTGATGGGGTGACT 1445

Qy        462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
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Qy        482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
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Db       1566 CATGGTCTCTTCCCAGAGGCTGTCACCATTGGTGAAGATGTTAGTGGAATGCCAACAGTT 1625

Qy        522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
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Qy        542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
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Qy        562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
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Qy        582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
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Qy        602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
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Qy        622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
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Qy        662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
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Qy        682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
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Qy        722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
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Qy        742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
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Qy        762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
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Qy        802 ThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGluGlu 821
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RESULT 13
AAC45939

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KW   Hybridisation assay; genetic mapping; gene expression control;
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Score:                    3269.00       Matches:        603
Percent Similarity:       83.19%        Conservative:   90
Best Local Similarity:    72.39%        Mismatches:     114
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DB:                       21            Gaps:           6

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Qy     221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
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Qy     241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Qy     641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              |||  ||||||||||||||||||||  |||     ||||||||||||||||:::
Db       2305 ACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAAGTACAAAATCGTT 2364

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||:::   ||||||||||||||   |||:::|||   :::||||||:::
Db       2365 TTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGACTCCGCGGAGTTT 2424

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||   :::|||   :::||||||||||||   |||   |||||||||||||||||
Db       2425 TTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGTGTATGCACCGTGC 2484

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||    ||||||   ::::::::::::|||
Db       2485 AGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGAACGTTCTTCTCTT 2544

Qy        821 GluGluValAlaAlaValGluGluValValValGluGlu 833
                    :::    :::   |||   |||   |||:::
Db       2545 GTCCCCATAGGCCTGTTACCCGAAGATGTTTAGGAGCAA 2583
```

RESULT 14
AAV05639
ID   AAV05639 standard; cDNA to mRNA; 3015 BP.
XX
AC   AAV05639;
XX
DT   01-MAY-1998 (first entry)
XX
DE   Rice type IV starch branching enzyme cDNA.
XX
KW   Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
XX
OS   Oryza sativa.
XX
FH   Key   Location/Qualifiers
FT   CDS   129..2654
FT   /*tag= a
FT   sig_peptide   129..287
FT   /*tag= b
FT   mat_peptide   288..2651
FT   /*tag= c
FT   /product= type_IV_starch_branching_enzyme
XX
PN   JP10004970-A.
XX
PD   13-JAN-1998.
XX
PF   24-JUN-1996;   96JP-0162983.
XX
PR   24-JUN-1996;   96JP-0162983.
XX
PA   (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA   (MITK) MITSUI TOATSU CHEN INC.
XX
DR   WPI; 1998-133625/13.
DR   P-PSDB; AAW41763.
XX
PT   Rice starch branching enzyme gene - synthesises amylopectin to yield
PT   high quality starch
XX
PS   Claim 4; Pages 5-8; 13pp; Japanese.
XX
CC   The present sequence encodes the rice type IV starch branching
CC   enzyme, which has the ability to synthesise amylopectin. The
CC   quality of starch is improved by the use of the protein.
XX
SQ   Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;

Alignment Scores:

Pred. No.:	3.21e-303	Length:	3015
Score:	3239.00	Matches:	594
Percent Similarity:	83.52%	Conservative:	80
Best Local Similarity:	73.61%	Mismatches:	107
Query Match:	72.54%	Indels:	26
DB:	19	Gaps:	4

US-10-056-454A-15_COPY_49_882 (1-834) x AAV05639 (1-3015)

```
Qy         12 SerThrValAlaAlaSerGlyLysValLeuValProGlyThrGlnSerAspSerSerSer 31
              |||     |||  ||||||||||||||||||||||            ||||||
Db        282 AGCTGCGCGGGTGCTCCTGGGAAGGTGCTGGTGCCTGGCGGTGGGAGCGACGACTTGCTG 341

Qy         32 SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr 51
              ||||||   :::              |||:::        ||||||   |||
Db        342 TCCTCTGCGGAACCAGACGTGGAAACTCAAGAGCAACCTGAAGAATCTCAGATACCTGAT 401

Qy         52 AspValAspSerSerThrMetGluHisAlaSerGln----------------------- 63
              |||                  |||       :::
Db        402 GATAATAAAGTAAAACCTTTTGAGGAGGAGGAAGAGATTCCAGCAGTGGCAGAAGCAAGC 461

Qy         64 IleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGlu 83
              ||||||           :::|||            ||||||:::::         :::||||||
Db        462 ATAAAGGTTGTGGCTGAAGACAAACTTGAATCTTCAGAAGTGATTCAAGACATTGAGGAA 521

Qy         84 LeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThr 103
                                    :::   ||||||
Db        522 --------------------AATGTGACTGAGGGT---------------------GTG 539

Qy        104 LeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArgGlyIle 123
              :::      ::::::|||       ::::::::       |||:::               |||
Db        540 ATCAAAGATGCTGATGAACCAACTGTGGAGGATAAACCACGAGTT------------ATC 587

Qy        124 ProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg 143
              ||||||||||||   ||||||||||||||||:::|||||||||:::|||      :::|||
Db        588 CCACCACCAGGAGATGGGCAGAAGATATACCAAATTGACCCAATGCTGGAAGGATTTCGG 647

Qy        144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyr 163
                 ||||||||||||||||||||:::||||||:::::|||    ||||||||:::::
Db        648 AACCATCTTGACTACCGATACAGTGAATACAAGAGAATGCGTGCAGCTATTGACCAACAT 707

Qy        164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
              ||||||||||||:::|||||||||||||||||||||||||:::|||||||||||||||||
Db        708 GAAGGTGGCTTGGATGCATTTTCTCGTGGTTACGAAAAGCTTGGATTCACCCGCAGCGCT 767

Qy        184 ThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAsp 203
                 |||||||||||||||||||||   |||||||||||||||||||||:::||||||
Db        768 GAAGGCATTACCTACCGAGAATGGGCACCTGGAGCACAGTCTGCAGCATTAGTAGGTGAC 827

Qy        204 PheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 223
              ||||||||||||:::   |||||||||   ||||||||||||||:::||||||||||||
Db        828 TTCAACAATTGGAACCCAAATGCAGATACTATGACCAGAAATGAGTATGGTGTTTGGGAG 887

Qy        224 IlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLys 243
              |||   ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        888 ATTTCCCTGCCTAACAATGCTGATGGATCCCCTGCTATTCCTCATGGCTCACGTGTAAAG 947

Qy        244 IleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSer 263
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::::
Db        948 ATTCGGATGGATACACCATCTGGCGTAAAGGATTCAATTCCTGCCTGGATTAAGTTTGCT 1007
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Qy        264 LeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGlu 283
              ::::|||    |||    ||||||||||||||||||||:::|||||||||||||||||||||
Db       1008 GTGCAGGCTCCAGGTGAAATACCGTACAACGGTATATATTATGATCCACCTGAAGAAGAA 1067

Qy        284 ArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSer 303
              :::|||:::|||||||||||||||:::||||||:::|||   |||||||||||||||||||
Db       1068 AAATATGTATTCCAACATCCTCAACCTAAACGACCAAATTCGCTGCGGATATATGAATCA 1127

Qy        304 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu 323
              ||||||||||||||||||||||||||||||||||||:::|||   |||||||||||||||
Db       1128 CATATTGGAATGAGTAGCCCGGAACCGAAGATAAACACATATGCTAATTTTAGGGATGAG 1187

Qy        324 ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 343
              ||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db       1188 GTGCTACCAAGAATTAAAAAGCTTGGGTACAATGCTGTACAGATAATGGCAATCCAGGAG 1247

Qy        344 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1248 CACTCTTATTACGCAAGCTTTGGGTATCATGTTACTAACTTCTTTGCGCCAAGTAGCCGT 1307

Qy        364 PheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 383
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||::::::
Db       1308 TTCGGAACCCCAGAAGACTTGAAATCTCTGATTGATAAAGCTCACGAGCTTGGTTTGCTT 1367

Qy        384 ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 403
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1368 GTACTTATGGATATTGTTCACAGTCATGCATCAAACAATACCCTGGATGGTTTGAATGGT 1427

Qy        404 PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrp 423
              ||||||   ||||||:::   |||||||||   |||   ||||||:::||||||||||||
Db       1428 TTTGATGGTACTGATACACATTACTTCCATGGTGGACCACGGGGTCATCACTGGATGTGG 1487

Qy        424 AspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAla 443
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db       1488 GATTCTCGCCTGTTCAACTATGGAGTTGGGAAGTTTTAAGATATTTACTGTCGAATGCA 1547

Qy        444 ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet 463
              ||||||||||||:::      :::||||||||||||||||||||||||||||||||||||
Db       1548 AGGTGGTGGCTTGAAGAATACAAGTTTGATGGGTTTCGATTTGATGGGGTGACCTCCATG 1607

Qy        464 MetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGly 483
              ||||||   ||||||||||||      |||   |||||||||||||||   ||||||||||||
Db       1608 ATGTATACTCATCATGGTTTACAGGTGGCATTTACTGGCAACTATGGCGAATATTTTGGA 1667

Qy        484 LeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 503
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1668 TTTGCTACTGATGTTGATGCAGTAGTTTACTTGATGCTGGTGAACGATCTAATTCATGGG 1727

Qy        504 LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle 523
              |||:::|||:::|||:::   ||||||||||||||||||||||||||||||||||||||
Db       1728 CTTTATCCTGAGGCTGTAGCCATTGGTGAAGATGTCAGCGGGATGCCCACATTTTGTATT 1787

Qy        524 ProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys 543
              |||||||||:::||||||||||||||||||||||||||||||||||:::    ||||||
Db       1788 CCTGTTCAAGATGGTGGTGTTGGTTTTGACTATCGTTTGCATATGGCTGTACCGGACAAA 1847

Qy        544 ArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
                 |||||||||||||||:::    ||||||   |||:::::::||||||||||||||||||
Db       1848 TGGATCGAACTCCTCAAGCAAAGTGACGAATATTGGAAAATGGGTGATATCGTGCACACC 1907

Qy        564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db       1908 CTAACGAATAGAAGGTGGTCAGAGAAGTGTGTTACTTATGCAGAAAGTCATGACCAAGCA 1967

Qy        584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1968 CTAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTATGATTTTATG 2027

Qy        604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
              ||||||||||||||||||||||         |||||||||||||||||||||||||||||
Db       2028 GCTCTAGACAGACCTTCAACACCTCGCATTGATCGTGGGATAGCATTACATAAAATGATT 2087

Qy        624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2088 AGGCTTGTCACCATGGGCTTAGGAGGCGAAGGCTATCTTAATTTCATGGGAAATGAGTTT 2147

Qy        644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
              |||||||||||||||||||||||||||||||       |||   |||   :::|||||||||
Db       2148 GGGCATCCTGAATGGATAGATTTCCCAAGAGGCCCGCAAAGTCTTCCAAATGGCTCGGTC 2207

Qy        664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
              :::|||||||||   :::|||:::||||||||||||||||||||||||||||||||||
Db       2208 CTCCCAGGAAACAACTACAGTTTTGATAAATGCCGTCGTAGATTTGACCTTGGAGATGCA 2267

Qy        684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
              :::||||||||||||   |||:::||||||||||||:::   ||||||:::||||||:::
Db       2268 GATTATCTTAGATATCATGGTATGCAAGAGTTTGATCAGGCCATGCAGCATCTTGAGGAA 2327

Qy        704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
              ||||||   ||||||||||||||||||||||||:::||||||||||||   |||   |||:::
Db       2328 AAATATGGATTCATGACATCTGAGCACCAGTATATATCGCGCAAACACGAGGAGGATAAG 2387

Qy        724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
              :::|||:::||||||:::|||:::||||||||||||||||||||||||||||:::   |||
Db       2388 GTGATCATCTTCGAGAGAGGAGATTTGGTATTCGTGTTCAACTTCCACTGGAGTAATAGC 2447

Qy        744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
              |||   |||||||||:::   ||||||||||||||||||||||||:::   |||||||||
Db       2448 TATTTTGACTATCGCGTCGGTTGTTTAAAGCCTGGAAAGTACAAGATTGTGTTGGACTCA 2507

Qy        764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
              ||||||      ||||||||||||||   |||:::||||||:::|||||||||||||:::
Db       2508 GACGATGGCCTCTTTGGTGGATTCAGTCGGCTTGATCATGATGCTGAGTACTTCACTGCT 2567

Qy        784 GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
              :::      :::|||:::||||||   |||      ||||||   |||   :::||||||
Db       2568 GACTGGCCGCATGACAACAGACCATGTTCATTCTCGGTGTACACCCCAAGCAGAACCGCC 2627

Qy        804 ValValTyrAlaLeuValAsp 810
              |||||||||||||||   :::
Db       2628 GTCGTGTATGCACTTACAGAG 2648
```

RESULT 15
AAH78337

```
ID   AAH78337 standard; cDNA; 2726 BP.
XX
AC   AAH78337;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of wheat starch branching enzyme 9 (BEIIa).
XX
KW   Wheat; starch branching enzyme; BEIIa; BEIIb; SBE; transgenic plant;
KW   starch biosynthetic pathway; amylopectin; amylose; ss.
XX
OS   Triticum sp.
XX
PN   WO200162934-A1.
XX
PD   30-AUG-2001.
XX
PF   21-FEB-2001; 2001WO-AU00175.
XX
PR   21-FEB-2000; 2000AU-0005742.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA   (GOOD-) GOODMAN FIELDER LTD.
PA   (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
PI   Morell M,  Rahman S;
XX
DR   WPI; 2001-570635/64.
XX
PT   Nucleic acids encoding wheat starch branching enzyme IIb, useful for
PT   altering the amylose and amylopectin content of cereal plants, e.g.
```

```
PT   wheat and barley -
XX
PS   Example 1; Fig 1; 103pp; English.
XX
CC   The present sequence encodes wheat starch branching enzyme 9,
CC   designated BEIIa. The specification describes BEIIb. BEIIb is a
CC   type II starch branching enzyme (SBE). The BEIIb nucleic acids may
CC   be used to genetically transform cereal plants such as wheat or
CC   barley and for altering their nutritional content by modulating
CC   the starch biosynthetic pathway to vary levels of amylopectin and/or
CC   amylose produced in the plant.
XX
SQ   Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 other;

Alignment Scores:
Pred. No.:               2.62e-293     Length:         2726
Score:                   3136.00       Matches:        577
Percent Similarity:      81.95%        Conservative:   86
Best Local Similarity:   71.32%        Mismatches:     98
Query Match:             70.24%        Indels:         48
DB:                      22            Gaps:           6

US-10-056-454A-15_COPY_49_882 (1-834) x AAH78337 (1-2726)

Qy     12 SerThrValAlaAlaSerGlyLysValLeuValProGlyThrGlnSerAspSerSerSer 31
Db    127 GCGACGTTCGCGGTGTCCGGCGCGACCCTC------GGTGTGGCGCGGCCGCCGGCGGCG 180

Qy     32 SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr 51
Db    181 GCGCAACCTGAAGAATTACAGATACCTGAA------------------------------ 210

Qy     52 AspValAspSerSerThrMetGluHisAlaSerGlnIleLysThrGluAsnAspAspVal 71
Db    211 GACATCGAGGAGCAAACGGCTGAA------------------------------------ 234

Qy     72 GluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeuGln 91
Db    235 ---------GTAAACATGACAGGGGGGACTGCAGAA------------------------ 261

Qy     92 LeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIle 111
Db    262 ---------------AAACTTGAATCTTCAGAACCGACTCAAGGCATTGTGGAAACAATC 306

Qy    112 IleAspGluSerAspArg---IleArgGlu--------------------ArgGlyIle 123
Db    307 ACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTC 366

Qy    124 ProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg 143
Db    367 CCAAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACGCTGAAAGATTTTCGG 426

Qy    144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyr 163
Db    427 AGCCATCTTGACTACCGATACAGCGAATACAGGAGAATTCGTGCTGCTATTGACCAACAT 486

Qy    164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
Db    487 GAAGGTGGATTGGAAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAGTGCT 546

Qy    184 ThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAsp 203
Db    547 GAAGGTATCACTTACCGAGAATGGGCTCCTGGAGCGCATTCTGCAGCATTAGTAGGTGAC 606

Qy    204 PheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 223
Db    607 TTCAACAATTGGAATCCGAATGCAGATACTATGACCAGAGATGATTATGGTGTTTGGGAG 666

Qy    224 IlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLys 243
Db    667 ATTTTCCTCCCTAACAATGCTGATGGATCCCCAGCTATTCCTCATGGCTCACGTGTAAAG 726

Qy    244 IleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSer 263
Db    727 ATACGGATGGATACTCCATCTGGTGTGAAGGATTCAATTTCTGCTTGGATCAAGTTCTCT 786

Qy    264 LeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGlu 283
Db    787 GTGCAGGCTCCAGGTGAAATACCATTCAATGGCATATATTATGATCCACCTGAAGAGGAG 846

Qy    284 ArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSer 303
Db    847 AAGTATGTCTTCCAACATCCTCAACCTAAACGACCAGAGTCACTGAGGATTTATGAATCA 906

Qy    304 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu 323
Db    907 CACATTGGAATGAGCAGCCCAGAACCGAAGATAAATTCATATGCTAATTTTAGGGATGAG 966

Qy    324 ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 343
Db    967 GTGCTGCCAAGAATTAAAAGGCTTGGATACAATGCAGTGCAGATAATGGCAATCCAGGAG 1026

Qy    344 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 363
Db   1027 CATTCATACTATGCGAGCTTTGGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGT 1086

Qy    364 PheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 383
Db   1087 TTTGGAACTCCAGAGGACTTAAAATCCCTGATCGATAGAGCACATGAGCTTGGTTTGCTT 1146

Qy    384 ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 403
Db   1147 GTTCTTATGGATATTGTTCATAGTCATTCATCAAATAATACCCTTGACGGCTTGAATGGT 1206

Qy    404 PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrp 423
Db   1207 TTCGATGGCACTGATACACATTACTTCCACGGTGGTCCACGTGGCCATCATTGGATGTGG 1266

Qy    424 AspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAla 443
Db   1267 GATTCTCGTCTATTCAACTATGGGAGTTGGGAAGTATTGAGATTCTTACTGTCAAACGCG 1326

Qy    444 ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet 463
Db   1327 AGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATG 1386

Qy    464 MetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGly 483
Db   1387 ATGTATACTCACCATGGATTACAAATGACATTTACTGGGAACTATGGCGAGTATTTTGGA 1446

Qy    484 LeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 503
Db   1447 TTTGCTACTGATGTTGATGCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGA 1506

Qy    504 LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle 523
Db   1507 CTTCATCCTGATGCTGTATCCATTGGTGAAGATGTCAGTGGAATGCCCACATTTTGCATC 1566

Qy    524 ProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys 543
Db   1567 CCTGTTCCAGATGGTGGTGTTGGTTTTGACTATCGCTTGCATATGGCTGTAGCAGATAAA 1626

Qy    544 ArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
Db   1627 TGGATTGAACTCCTCAAGCAAAGTGACGAATCTTGGAAAATGGGTGATATTGTGCACACC 1686

Qy    564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
Db   1687 CTAACAAATAGAAGGTGGCTTGAGAAGTGTGTAACTTATGCAGAAAGTCATGATCAAGCA 1746

Qy    584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db   1747 CTAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTATGATTTCATG 1806

Qy    604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
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Db      1807 GCTCTGGATAGGCCTTCAACTCCTCGCATTGATCGTGGCATAGCATTACATAAAATGATC 1866

Qy       624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1867 AGGCTTGTCACCATGGGTTTAGGTGGTGAAGGCTATCTTAACTTCATGGGAAATGAGTTT 1926

Qy       644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
             |||||||||||||||||||||||||||         |||   |||      |||   |||
Db      1927 GGGCATCCTGAATGGATAGATTTTCCAAGAGGTCCGCAAACTCTTCCAACCGGCAAAGTT 1986

Qy       664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
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Qy       684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
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Db      2047 GATTTTCTTAGATATCATGGTATGCAAGAGTTCGATCAGGCAATGCAGCATCTTGAGGAA 2106

Qy       704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
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Db      2107 AAATATGGGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAG 2166

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Db      2167 GTGATCATCTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGC 2226

Qy       744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
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Qy       764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
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Db      2287 GACGATGCACTCTTTGGTGGATTCAGCAGGCTTGATCATGATGTCGACTACTTCACAACC 2346

Qy       784 GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
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Qy       804 ValValTyrAlaLeuValAspLysGlu 812
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Search completed: July 6, 2003, 03:15:45
Job time : 646 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

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Run on:          July  6, 2003, 02:55:51 ; Search time 100 Seconds
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Perfect score:   4465
Sequence:        1 EKSSYNSEFRPSTVAASGKV..........EEEEEEEEVAAVEEVVVEEE 834

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Searched:        441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Database :       Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4320	96.8	3074	4	US-09-087-277-1	Sequence 1, Appli
	2	4320	96.8	3074	4	US-09-658-499-1	Sequence 1, Appli
	3	3026.5	67.8	2665	4	US-09-257-894-1	Sequence 1, Appli
	4	3021.5	67.7	2725	3	US-08-941-445A-14	Sequence 14, Appl
	5	2676.5	59.9	2087	4	US-09-257-894-9	Sequence 9, Appli
c	6	2669.5	59.8	2165	4	US-09-257-894-8	Sequence 8, Appli
	7	2462	55.1	1393	4	US-09-087-277-3	Sequence 3, Appli
	8	2462	55.1	1393	4	US-09-658-499-3	Sequence 3, Appli
	9	2165	48.5	3128	3	US-08-716-449-1	Sequence 1, Appli
	10	2107	47.2	2565	4	US-09-257-894-24	Sequence 24, Appl
	11	2107	47.2	2763	3	US-08-941-445A-16	Sequence 16, Appl
c	12	2104	47.1	2487	4	US-09-257-894-19	Sequence 19, Appl
	13	2104	47.1	2772	4	US-09-257-894-12	Sequence 12, Appl
	14	2098.5	47.0	2909	4	US-08-104-158-1	Sequence 1, Appli
	15	1699.5	38.1	1809	4	US-09-257-894-25	Sequence 25, Appl
	16	1696.5	38.0	1865	4	US-09-257-894-20	Sequence 20, Appl
	17	1524.5	34.1	11478	3	US-08-981-803-29	Sequence 29, Appl
	18	1524.5	34.1	11478	4	US-08-983-440-29	Sequence 29, Appl
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c	22	507.5	11.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c	23	455.5	10.2	11384	4	US-08-961-527-45	Sequence 45, Appl
	24	261.5	5.9	1680	4	US-09-242-690A-14	Sequence 14, Appl
	25	261.5	5.9	2691	4	US-09-298-924-5	Sequence 5, Appli
	26	241.5	5.4	2712	2	US-08-410-784A-1	Sequence 1, Appli
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	29	233	5.2	1791	1	US-08-607-321-3	Sequence 3, Appli
	30	233	5.2	1791	2	US-08-961-240-3	Sequence 3, Appli
	31	233	5.2	1791	2	US-08-605-501-3	Sequence 3, Appli
	32	233	5.2	2056	1	US-08-399-646-13	Sequence 13, Appl
	33	233	5.2	2056	1	US-08-607-321-13	Sequence 13, Appl
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	37	226	5.1	661	3	US-08-961-083-77	Sequence 77, Appl
	38	226	5.1	6142	4	US-09-514-302-1	Sequence 1, Appli
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	45	222.5	5.0	2161	2	US-08-961-240-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-09-087-277-1
; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT: KHOSNOODI, Jamshid
;  APPLICANT: LARSSON, Clas-Tomas
;  APPLICANT: LARSSON, Hakan
;  APPLICANT: RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/09/087,277B
;  CURRENT FILING DATE: 1998-05-29
;  EARLIER APPLICATION NUMBER: PCT/SE96/01558
;  EARLIER FILING DATE: 1996-11-28
;  EARLIER APPLICATION NUMBER: SE 9504272-7
;  EARLIER FILING DATE: 1995-11-29
;  EARLIER APPLICATION NUMBER: SE 9601506-0
;  EARLIER FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (189)..(2825)
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (189)..(332)
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;    NAME/KEY: mat_peptide
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;    OTHER INFORMATION: n wherein n = A, C, G or T.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (285)..(287)
;    OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
;    OTHER INFORMATION: or Phe.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1404)..(1406)
;    OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1428)..(1430)
;    OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1896)..(1898)
;    OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;    OTHER INFORMATION: or Phe.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (2154)..(2156)
;    OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Alignment Scores:
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Percent Similarity:     97.96%       Conservative:   5
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Qy       41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
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RESULT 2
US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beII gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

Alignment Scores:			
Pred. No.:	0	Length:	3074
Score:	4320.00	Matches:	812
Percent Similarity:	97.96%	Conservative:	5
Best Local Similarity:	97.36%	Mismatches:	13
Query Match:	96.75%	Indels:	4
DB:	4	Gaps:	1

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-658-499-1 (1-3074)

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Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        333 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 392

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 452

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 512
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Qy        61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
             |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       513 GCTAGGCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 572

Qy        81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       573 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 632

Qy       101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 692

Qy       121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 752

Qy       141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 812

Qy       161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 872

Qy       181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
             ||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db       873 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 932

Qy       201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 992

Qy       221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1052

Qy       241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1112

Qy       261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
             ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db      1113 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1172

Qy       281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1232

Qy       301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1292

Qy       321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
             ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db      1293 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCT 1352

Qy       341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db      1353 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCA 1412

Qy       361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 AGCAGCCGTTTTGGAACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1472

Qy       381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1532

Qy       401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
             ||||||||||||||       ||||||||||||||||||||||||||||||||||||||
Db      1533 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1592

Qy       421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1593 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1652

Qy       441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
             ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db      1653 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1712

Qy       461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
             ||||||||||||||     ||||||||||||||||||||||||||||||||||||||||
Db      1713 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1772

Qy       481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1773 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1832

Qy       501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1833 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1892

Qy       521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
             |||   ||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db      1893 TTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1952

Qy       541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
             ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1953 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2012

Qy       561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2013 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2072

Qy       581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
             ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db      2073 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGAGAAGGATATGTAT 2132

Qy       601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2133 GATTTTATGGCTCTGGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2192

Qy       621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2193 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2252

Qy       641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
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Db      2253 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2312

Qy       661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
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Db      2313 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2372

Qy       681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
             ||||||||||||||||||||||||||||||||||||||||||||||     ||||||||
Db      2373 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2432

Qy       701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2433 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2492

Qy       721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
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Db      2493 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2552

Qy       741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
             ||||||||||||||||||||||||     ||||||||||||||||||||||||||||||
Db      2553 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2612

Qy       761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2613 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2672

Qy       781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2673 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2732

Qy         801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
               :::|||||||||||||||||||||||||||||             ||||||||||||||
Db        2733 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA------------GAAGAAGAAGAAGAA 2780

Qy         821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
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Db        2781 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822

RESULT 3
US-09-257-894-1
; Sequence 1, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:     2665 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..2476
US-09-257-894-1

Alignment Scores:
Pred. No.:              0              Length:         2665
Score:                  3026.50        Matches:        553
Percent Similarity:     83.85%         Conservative:   75
Best Local Similarity:  73.83%         Mismatches:     100
Query Match:            67.78%         Indels:         21
DB:                     4              Gaps:           3

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-1 (1-2665)

Qy          67 GluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86
               ||||||||   :::            :::|||
Db         277 GAGAATGATGGCCTCGCATCAAGGGCTGAC------------------------------ 306

Qy          87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
                     |||  |||  |||                 :::|||  :::   :::
Db         307 ------TCGGCTCAATTCCAGTCG------------GATGAACTGGAGGTACCAGACATT 348

Qy         107 SerGluGluThr---------------IleIleAspGluSerAspArgIleArgGluArg 121
               ||||||||||||                :::  |||              |||  |||
Db         349 TCTGAAGAGACAACGTGCGGTGCTGGTGTGGCTGATGCTCAAGCCTTGAACAGAGTTCGA 408

Qy         122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
                  :::|||||||||      ||||||||||||:::::|||||||||:::|||
Db         409 GTGGTCCCCCCACCAAGCGATGGACAAAAAATATTCCAGATTGACCCCATGTTGCAAGGC 468

Qy         142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
               |||:::   ||||||:::||||||||||||   |||:::::::::|||       ||||||
Db         469 TATAAGTACCATCTTGAGTATCGGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGAT 528

Qy         162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
               ::::::||||||||||||||||||||||||||||   |||||||||   ||||||
Db         529 GAACATGAAGGAGGCTTGGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCC 588

Qy         182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
               ||||||   ||||||||||||||||||||||||   ||||||   ||||||||||||:::
Db         589 AGCGCGGAAGGTATCACATATCGAGAATGGGCTCCTGGAGCATTTTCTGCAGCATTGGTG 648

Qy         202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
               ||||||||||||||||||||||   |||||||||   |||::::::||||||||||||||
Db         649 GGTGACTTCAACAACTGGGATCCAAATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTT 708

Qy         222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
               |||||||||||||||||||||||||||   ||||||:::      ||||||||||||||||
Db         709 TGGGAAATTTTTCTGCCTAACAATGCAGATGGTACATCACCTATTCCTCATGGATCTCGT 768

Qy         242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
               ||||||:::||||||||||||||||||||||:::|||||||||||||||||||||||||
Db         769 GTAAAGGTGAGAATGGATACTCCATCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAG 828

Qy         262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
               ||||||:::|||   |||   ||||||||||||:::||||||:::||||||||||||||
Db         829 TACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAA 888

Qy         282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
               |||   :::|||:::|||:::|||   :::||||||:::||||||||||||||||||||||
Db         889 GAGGTAAAGTATGTGTTCAGGCATGCGCAACCTAAACGACCAAAATCATTGCGGATATAT 948

Qy         302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
               |||:::|||:::||||||||||||||||||||||||||||||:::||||||||||||||
Db         949 GAAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAAACACATATGTAAACTTTAGG 1008

Qy         322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
               |||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        1009 GATGAAGTCCTCCCAAGAATAAAAAAACTTGGATACAATGCAGTGCAAATAATGGCAATC 1068

Qy         342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
               ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        1069 CAAGAGCACTCATATTATGGAAGCTTTGGATACCATGTAACTAATTTTTTTGCGCCAAGT 1128

Qy         362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
               ||||||||||||||||||:::||||||||||||||||||||||:::|||||||||||||||
Db        1129 AGTCGTTTTGGTACCCCAGAAGATTTGAAGTCTTTGATTGATAGAGCACATGAGCTTGGT 1188

Qy         382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
               ::::::||||||||||||:::|||||||||||||||||||:::||||||||||||||||||
Db        1189 TTGCTAGTTCTCATGGATGTGGTTCATAGTCATGCGTCAAGTAATACTCTGGATGGGTTG 1248

Qy         402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
               |||   ||||||   |||||||:::   |||||||||||||||   ||||||:::||||||
Db        1249 AATGGTTTTGATGGTACAGATACACATTACTTTCACAGTGGTCCACGTGGCCATCACTGG 1308

Qy         422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
               ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
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Db       1309 ATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTTTTAAGATTTCTTCTCTCC 1368

Qy        442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
              ||||||||||||||||||:::    :::||||||||||||||||||||||||||||||||
Db       1369 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTGATGGTTTCCGTTTTGATGGTGTGACC 1428

Qy        462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
              |||||||||||   |||||||||||   |||   ||||||||||||:::   ||||||
Db       1429 TCCATGATGTACACTCACCACGGATTACAAGTAACATTTACGGGGAACTTCAATGAGTAT 1488

Qy        482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TTTGGCTTTGCCACCGATGTAGATGCAGTGGTTTACTTGATGCTGGTAAATGATCTAATT 1548

Qy        502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
              ||||||||:::|||:::|||:::||||||||||||||||||||||||||||||||||||||
Db       1549 CATGGACTTTATCCTGAGGCTGTAACCATTGGTGAAGATGTTAGTGGAATGCCTACATTT 1608

Qy        522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
                :::||||||   :::|||||||||||||||||||||||:::|||||||||:::|||
Db       1609 GCCCTTCCTGTTCACGATGGTGGGGTAGGTTTTGACTATCGGATGCATATGGCTGTGGCT 1668

Qy        542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
              ||||||   |||:::||||||||||:::   ||||||   |||:::::::||||||||||||
Db       1669 GACAAATGGATTGACCTTCTCAAGCAAAGTGATGAAACTTGGAAGATGGGTGATATTGTG 1728

Qy        562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
              ||||||||||||||||||||||||   ||||||||||||:::||||||||||||||||||
Db       1729 CACACACTGACAAATAGGAGGTGGTTAGAGAAGTGTGTAACTTATGCTGAAAGTCATGAT 1788

Qy        582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1789 CAAGCATTAGTCGGCGACAAGACTATTGCGTTTTGGTTGATGGACAAGGATATGTATGAT 1848

Qy        602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
              |||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db       1849 TTCATGGCCCTCGATAGACCTTCAACTCCTACCATTGATCGTGGGATAGCATTACATAAG 1908

Qy        622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db       1909 ATGATTAGACTTATCACAATGGGTTTAGGAGGAGAGGGCTATCTTAATTTCATGGGAAAT 1968

Qy        642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
              |||||||||||||||||||||||||||||||||||||      |||    |||    |||
Db       1969 GAGTTTGGACATCCTGAATGGATAGATTTTCCAAGAGGTCCGCAAAGACTTCCAAGTGGT 2028

Qy        662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
                     ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db       2029 AAGTTTATTCCAGGGAATAACAACAGTTATGACAAATGTCGTCGAAGATTTGACCTGGGT 2088

Qy        682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
              ||||||:::||||||||||||   |||:::|||||||||||||:::   ||||||:::|||
Db       2089 GATGCAGACTATCTTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCAACATCTT 2148

Qy        702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
              |||   ||||||||||||||||||||||:::|||||||:::|||||||||||   |||
Db       2149 GAGCAAAAAATATGAATTCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAG 2208

Qy        722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
              |||::::::||||||||||||||||||:::|||||||||||||||||||||||||
Db       2209 GATAAGGTGATTGTGTTCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAAC 2268

Qy        742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
                ||||||   |||||||||||   |||   |||||||||   |||||||||   |||
Db       2269 AACAGCTATTTTGACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG 2328

Qy        762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
              ||||||||   ||||||||||||||   ||||||   |||   |||||||:::|||
Db       2329 GACTCCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCACGCAGCCGAGCACTTC 2388

Qy        782 ThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLys 801
              |||   :::      :::|||:::||||||   |||      ||||||   |||   :::
Db       2389 ACCGCCGACTGTTCGCATGATAATAGGCCATATTCATCCTCGGTTTATACACCAAGCAGA 2448

Qy        802 ThrAlaValValTyrAlaLeuValAsp 810
              |||   ||||||||||||   |||:::
Db       2449 ACATGTGTCGTCTATGCTCCAGTGGAG 2475
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RESULT 4

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US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
;  GENERAL INFORMATION:
;    APPLICANT:  Keeling, Peter
;    APPLICANT:  Guan, Hanping
;    TITLE OF INVENTION:  Starch Encapsulation
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Greenlee, Winner and Sullivan, P.C.
;      STREET:  5370 Manhattan Circle
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/941,445A
;      FILING DATE:  30-SEP-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,855
;      FILING DATE:  30-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winner, Ellen P
;      REGISTRATION NUMBER:  28,547
;      REFERENCE/DOCKET NUMBER:  89-97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2725 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  mRNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Zea mays
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  91..264
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  265..2487
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  91..2490
US-08-941-445A-14
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Alignment Scores:

Pred. No.:	0	Length:	2725
Score:	3021.50	Matches:	552
Percent Similarity:	83.71%	Conservative:	75
Best Local Similarity:	73.70%	Mismatches:	101
Query Match:	67.67%	Indels:	21
DB:	3	Gaps:	3

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-941-445A-14 (1-2725)

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Qy         67 GluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86
              |||||||||   :::            :::|||
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Db   289 GAGAATGATGGCCTCGCATCAAGGGCTGAC------------------------------ 318
Qy    87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db   319 ------TCGGCTCAATTCCAGTCG------------GATGAACTGGAGGTACCAGACATT 360
Qy   107 SerGluGluThr---------------IleIleAspGluSerAspArgIleArgGluArg 121
Db   361 TCTGAAGAGACAACGTGCGGTGCTGGTGTGGCTGATGCTCAAGCCTTGAACAGAGTTCGA 420
Qy   122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db   421 GTGGTCCCCCCACCAAGCGATGGACAAAAAATATTCCAGATTGACCCCATGTTGCAAGGC 480
Qy   142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db   481 TATAAGTACCATCTTGAGTATCGGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGAT 540
Qy   162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db   541 GAACATGAAGGAGGCTTGGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCC 600
Qy   182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db   601 AGCGCGGAAGGTATCACATATCGAGAATGGGCTCCTGGAGCATTTTCTGCAGCATTGGTG 660
Qy   202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db   661 GGTGACGTCAACAACTGGGATCCAAATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTT 720
Qy   222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db   721 TGGGAAATTTTTCTGCCTAACAATGCAGATGGTACATCACCTATTCCTCATGGATCTCGT 780
Qy   242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db   781 GTAAAGGTGAGAATGGATACTCCATCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAG 840
Qy   262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
Db   841 TACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAA 900
Qy   282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db   901 GAGGTAAAGTATGTGTTCAGGCATGCGCAACCTAAACGACCAAAATCATTGCGGATATAT 960
Qy   302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db   961 GAAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAAACACATATGTAAACTTTAGG 1020
Qy   322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db  1021 GATGAAGTCCTCCCAAGAATAAAAAAACTTGGATACAATGCAGTGCAAATAATGGCAATC 1080
Qy   342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
Db  1081 CAAGAGCACTCATATTATGGAAGCTTTGGATACCATGTAACTAATTTTTTGCGCCAAGT 1140
Qy   362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db  1141 AGTCGTTTTGGTACCCCAGAAGATTTGAAGTCTTTGATTGATAGAGCACATGAGCTTGGT 1200
Qy   382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db  1201 TTGCTAGTTCTCATGGATGTGGTTCATAGTCATGCGTCAAGTAATACTCTGGATGGGTTG 1260
Qy   402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db  1261 AATGGTTTTGATGGTACAGATACACATTACTTTCACAGTGGTCCACGTGGCCATCACTGG 1320
Qy   422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
Db  1321 ATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTTTTAAGATTTCTTCTCTCC 1380
Qy   442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db  1381 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTGATGGTTTCCGTTTTGATGGTGTGACC 1440
Qy   462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db  1441 TCCATGATGTACACTCACCACGGATTACAAGTAACATTTACGGGGAACTTCAATGAGTAT 1500
Qy   482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db  1501 TTTGGCTTTGCCACCGATGTAGATGCAGTGGTTTACTTGATGCTGGTAAATGATCTAATT 1560
Qy   502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db  1561 CATGGACTTTATCCTGAGGCTGTAACCATTGGTGAAGATGTTAGTGGAATGCCTACATTT 1620
Qy   522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db  1621 GCCCTTCCTGTTCACGATGGTGGGGTAGGTTTTGACTATCGGATGCATATGGCTGTGGCT 1680
Qy   542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
Db  1681 GACAAATGGATTGACCTTCTCAAGCAAAGTGATGAAACTTGGAAGATGGGTGATATTGTG 1740
Qy   562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db  1741 CACACACTGACAAATAGGAGGTGGTTAGAGAAGTGTGTAACTTATGCTGAAAGTCATGAT 1800
Qy   582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db  1801 CAAGCATTAGTCGGCGACAAGACTATTGCGTTTTGGTTGATGGACAAGGATATGTATGAT 1860
Qy   602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db  1861 TTCATGGCCCTCGATAGACCTTCAACTCCTACCATTGATCGTGGGATAGCATTACATAAG 1920
Qy   622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
Db  1921 ATGATTAGACTTATCACAATGGGTTTAGGAGGAGAGGGCTATCTTAATTTCATGGGAAAT 1980
Qy   642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db  1981 GAGTTTGGACATCCTGAATGGATAGATTTCCAAGAGGTCCGCAAAGACTTCCAAGTGGT 2040
Qy   662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db  2041 AAGTTTATTCCAGGGAATAACAACAGTTATGACAAATGTCGTCGAAGATTTGACCTGGGT 2100
Qy   682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db  2101 GATGCAGACTATCTTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCAACATCTT 2160
Qy   702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
Db  2161 GAGCAAAAAATATGAATTCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAG 2220
Qy   722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
Db  2221 GATAAGGTGATTGTGTTCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAAC 2280
Qy   742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
Db  2281 AACAGCTATTTGACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG 2340
Qy   762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
Db  2341 GACTCCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCACGCAGCCGAGCACTTC 2400
Qy   782 ThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLys 801
Db  2401 ACCGCCGACTGTTCGCATGATAATAGGCCATATTCATTCTCGGTTTATACACCAAGCAGA 2460
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Qy        802 ThrAlaValValTyrAlaLeuValAsp 810
Db       2461 ACATGTGTCGTCTATGCTCCAGTGGAG 2487

RESULT 5
US-09-257-894-9
; Sequence 9, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2087 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-257-894-9

Alignment Scores:
Pred. No.:              2.8e-289        Length:         2087
Score:                  2676.50         Matches:        485
Percent Similarity:     85.12%          Conservative:   64
Best Local Similarity:  75.19%          Mismatches:     75
Query Match:            59.94%          Indels:         21
DB:                     4               Gaps:           3

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-9 (1-2087)

Qy         67 GluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86
Db        199 GAGAATGATGGCCTCGCATCAAGGGCTGAC------------------------------ 228

Qy         87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db        229 ------TCGGCTCAATTCCAGTCG------------GATGAACTGGAGGTACCAGACATT 270

Qy        107 SerGluGluThr---------------IleIleAspGluSerAspArgIleArgGluArg 121
Db        271 TCTGAAGAGACAACGTGCGGTGCTGGTGTGGCTGATGCTCAAGCCTTGAACAGAGTTCGA 330

Qy        122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db        331 GTGGTCCCCCCACCAAGCGATGGACAAAAAATATTCCAGATTGACCCCATGTTGCAAGGC 390

Qy        142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db        391 TATAAGTACCATCTTGAGTATCGGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGAT 450

Qy        162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db        451 GAACATGAAGGAGGCTTGGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCC 510

Qy        182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db        511 AGCGCGGAAGGTATCACATATCGAGAATGGGCTCCTGGAGCATTTTCTGCAGCATTGGTG 570

Qy        202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db        571 GGTGACTTCAACAACTGGGATCCAAATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTT 630

Qy        222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db        631 TGGGAAATTTTTCTGCCTAACAATGCAGATGGTACATCACCTATTCCTCATGGATCTCGT 690

Qy        242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db        691 GTAAAGGTGAGAATGGATACTCCATCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAG 750

Qy        262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
Db        751 TACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAA 810

Qy        282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
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Qy        302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db        871 GAAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAAACACATATGTAAACTTTAGG 930

Qy        322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db        931 GATGAAGTCCTCCCAAGAATAAAAAAACTTGGATACAATGCAGTGCAAATAATGGCAATC 990

Qy        342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
Db        991 CAAGAGCACTCATATTATGGAAGCTTTGGATACCATGTAACTAATTTTTTTGCGCCAAGT 1050

Qy        362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db       1051 AGTCGTTTTGGTACCCCAGAAGATTTGAAGTCTTTGATTGATAGAGCACATGAGCTTGGT 1110

Qy        382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db       1111 TTGCTAGTTCTCATGGATGTGGTTCATAGTCATGCGTCAAGTAATACTCTGGATGGGTTG 1170

Qy        402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db       1171 AATGGTTTTGATGGTACAGATACACATTACTTTCACAGTGGTCCACGTGGCCATCACTGG 1230

Qy        422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
Db       1231 ATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTTTTAAGATTTCTTCTCTCC 1290

Qy        442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db       1291 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTGATGGTTTCCGTTTTGATGGTGTGACC 1350

Qy        462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db       1351 TCCATGATGTACACTCACCACGGATTACAAGTAACATTTACGGGGAACTTCAATGAGTAT 1410
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Qy      482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db     1411 TTTGGCTTTGCCACCGATGTAGATGCAGTGGTTTACTTGATGCTGGTAAATGATCTAATT 1470

Qy      502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db     1471 CATGGACTTTATCCTGAGGCTGTAACCATTGGTGAAGATGTTAGTGGAATGCCTACATTT 1530

Qy      522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db     1531 GCCCTTCCTGTTCACGATGGTGGGGTAGGTTTTGACTATCGGATGCATATGGCTGTGGCT 1590

Qy      542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
Db     1591 GACAAATGGATTGACCTTCTCAAGCAAAGTGATGAAACTTGGAAGATGGGTGATATTGTG 1650

Qy      562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db     1651 CACACACTGACAAATAGGAGGTGGTTAGAGAAGTGTGTAACTTATGCTGAAAGTCATGAT 1710

Qy      582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db     1711 CAAGCATTAGTCGGCGACAAGACTATTGCGTTTTGGTTGATGGACAAGGATATGTATGAT 1770

Qy      602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db     1771 TTCATGGCCCTCGATAGACCTTCAACTCCTACCATTGATCGTGGGATAGCATTACATAAG 1830

Qy      622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
Db     1831 ATGATTAGACTTATCACAATGGGTTTAGGAGGAGAGGGCTATCTTAATTTCATGGGAAAT 1890

Qy      642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db     1891 GAGTTTGGACATCCTGAATGGATAGATTTTCCAAGAGGTCCGCAAAGACTTCCAAGTGGT 1950

Qy      662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db     1951 AAGTTTATTCCAGGGAATAACAACAGTTATGACAAATGTCGTCGAAGATTTGACCTGGGT 2010

Qy      682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db     2011 GATGCAGACTATCTTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCAACATCTT 2070

Qy      702 GluAspLysTyrGlu 706
Db     2071 GAGCAAAAATATGAA 2085
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```
RESULT 6
US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2165 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-257-894-8

Alignment Scores:
Pred. No.:               1.81e-288    Length:          2165
Score:                   2669.50      Matches:         484
Percent Similarity:      84.96%       Conservative:    64
Best Local Similarity:   75.04%       Mismatches:      76
Query Match:             59.79%       Indels:          21
DB:                      4            Gaps:            3

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-8 (1-2165)

Qy       67 GluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86
Db     1889 GAGAATGATGGCCTCGCATCAAGGGCTGAC------------------------------ 1860

Qy       87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db     1859 ------TCGGCTCAATTCCAGTCG------------GATGAACTGGAGGTACCAGACATT 1818

Qy      107 SerGluGluThr---------------IleIleAspGluSerAspArgIleArgGluArg 121
Db     1817 TCTGAAGAGACAACGTGCGGTGCTGGTGTGGCTGATGCTCAAGCCTTGAACAGAGTTCGA 1758

Qy      122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db     1757 GTGGTCCCCCCACCAAGCGATGGACAAAAAATATTCCAGATTGACCCCATGTTGCAAGGC 1698

Qy      142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db     1697 TATAAGTACCATCTTGAGTATCGGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGAT 1638

Qy      162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db     1637 GAACATGAAGGAGGCTTGGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCC 1578

Qy      182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db     1577 AGCGCGGAAGGTATCACATATCGAGAATGGGCTCCTGGAGCATTTTCTGCAGCATTGGTG 1518

Qy      202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db     1517 GGTGACGTCAACAACTGGGATCCAAATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTT 1458

Qy      222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db     1457 TGGGAAATTTTTCTGCCTAACAATGCAGATGGTACATCACCTATTCCTCATGGATCTCGT 1398

Qy      242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db     1397 GTAAAGGTGAGAATGGATACTCCATCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAG 1338
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Qy        262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
              ||||||:::|||   |||   ||||||||||||:::||||||:::||||||||||||||
Db       1337 TACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAA 1278

Qy        282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
              |||   :::|||:::|||:::|||   :::|||||||:::||||||||||||||||||||
Db       1277 GAGGTAAAGTATGTGTTCAGGCATGCGCAACCTAAACGACCAAAATCATTGCGGATATAT 1218

Qy        302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
              |||:::|||:::|||||||||||||||||||||||||||||||:::||||||||||||||
Db       1217 GAAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAAACACATATGTAAACTTTAGG 1158

Qy        322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db       1157 GATGAAGTCCTCCCAAGAATAAAAAAACTTGGATACAATGCAGTGCAAATAATGGCAATC 1098

Qy        342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
              ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db       1097 CAAGAGCACTCATATTATGGAAGCTTTGGATACCATGTAACTAATTTTTTTGCGCCAAGT 1038

Qy        362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
              ||||||||||||||||||||||:::|||||||||||||||:::|||||||||||||||||
Db       1037 AGTCGTTTTGGTACCCCAGAAGATTTGAAGTCTTTGATTGATAGAGCACATGAGCTTGGT 978

Qy        382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
              ::::::|||||||||||||:::|||||||||||||||||||:::||||||||||||||||
Db        977 TTGCTAGTTCTCATGGATGTGGTTCATAGTCATGCGTCAAGTAATACTCTGGATGGGTTG 918

Qy        402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
              |||   ||||||   ||||||:::   |||||||||||||||   |||||||:::||||||
Db        917 AATGGTTTTGATGGTACAGATACACATTACTTTCACAGTGGTCCACGTGGCCATCACTGG 858

Qy        422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        857 ATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTTTTAAGATTTCTTCTCTCC 798

Qy        442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
              |||||||||||||||||||:::   :::||||||||||||||||||||||||||||||||
Db        797 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTGATGGTTTCCGTTTTGATGGTGTGACC 738

Qy        462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
              ||||||||||||   ||||||||||||   |||   ||||||||||||:::   ||||||
Db        737 TCCATGATGTACACTCACCACGGATTACAAGTAACATTTACGGGGAACTTCAATGAGTAT 678

Qy        482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
              ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 TTTGGCTTTGCCACCGATGTAGATGCAGTGGTTTACTTGATGCTGGTAAATGATCTAATT 618

Qy        502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
              |||||||||:::|||:::|||:::||||||||||||||||||||||||||||||||||||
Db        617 CATGGACTTTATCCTGAGGCTGTAACCATTGGTGAAGATGTTAGTGGAATGCCTACATTT 558

Qy        522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
                 :::||||||   :::||||||||||||||||||||||||:::|||||||||:::|||
Db        557 GCCCTTCCTGTTCACGATGGTGGGGTAGGTTTTGACTATCGGATGCATATGGCTGTGGCT 498

Qy        542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
              ||||||   |||:::||||||||||||:::   ||||||   |||:::::::||||||||||
Db        497 GACAAATGGATTGACCTTCTCAAGCAAAGTGATGAAACTTGGAAGATGGGTGATATTGTG 438

Qy        562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
              ||||||||||||||||||||||||   ||||||||||||:::||||||||||||||||||
Db        437 CACACACTGACAAATAGGAGGTGGTTAGAGAAGTGTGTAACTTATGCTGAAAGTCATGAT 378

Qy        582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 CAAGCATTAGTCGGCGACAAGACTATTGCGTTTTGGTTGATGGACAAGGATATGTATGAT 318

Qy        602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
              |||||||||||||||||||||||||||         |||||||||||||||||||||||||
Db        317 TTCATGGCCCTCGATAGACCTTCAACTCCTACCATTGATCGTGGGATAGCATTACATAAG 258

Qy        622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
              |||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        257 ATGATTAGACTTATCACAATGGGTTTAGGAGGAGAGGGCTATCTTAATTTCATGGGAAAT 198

Qy        642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
              |||||||||||||||||||||||||||||||||||         |||   |||      |||
Db        197 GAGTTTGGACATCCTGAATGGATAGATTTTCCAAGAGGTCCGCAAAGACTTCCAAGTGGT 138

Qy        662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
                       ||||||||||||      |||||||||||||||||||||||||||||||||
Db        137 AAGTTTATTCCAGGGAATAACAACAGTTATGACAAATGTCGTCGAAGATTTGACCTGGGT 78

Qy        682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
              ||||||:::||||||||||||   |||:::|||||||||||||:::   ||||||:::|||
Db         77 GATGCAGACTATCTTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCAACATCTT 18

Qy        702 GluAspLysTyrGlu 706
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Db         17 GAGCAAAAATATGAA 3
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RESULT 7
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-087-277-3

Alignment Scores:

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Pred. No.:                 1.44e-265      Length:          1393
Score:                     2462.00        Matches:         454
Percent Similarity:        98.49%         Conservative:    3
Best Local Similarity:     97.84%         Mismatches:      7
Query Match:               55.14%         Indels:          0
DB:                        4              Gaps:            0

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-087-277-3 (1-1393)

Qy        226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGT 61

Qy        246 MetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAG 121

Qy        266 LeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyr 285
              |||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db        122 CTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTAT 181

Qy        286 IlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIle 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATT 241

Qy        306 GlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeu 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTT 301

Qy        326 ProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSer 345
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db        302 CCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 361

Qy        346 TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly 365
              ||||||||||||||||||||||||||||||||||||     |||||||||||||||||||
Db        362 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGAA 421

Qy        366 ThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeu 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 481

Qy        386 MetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 541

Qy        406 CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSer 425
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCC 601

Qy        426 ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrp 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 661

Qy        446 TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 465
              ||||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 TGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTAT 721

Qy        466 IleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla 485
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 781

Qy        486 ThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 ACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTC 841

Qy        506 ProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 525
              |||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db        842 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTT 901

Qy        526 GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIle 545
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        902 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 961

Qy        546 GluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThr 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1021

Qy        566 AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1081

Qy        586 GlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeu 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1141

Qy        606 AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeu 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 GATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 1201

Qy        626 ValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHis 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 1261

Qy        646 ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIlePro 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 1321

Qy        666 GlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyr 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 1381

Qy        686 LeuArgTyrArg 689
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Db       1382 TTAAGATACCGT 1393
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RESULT 8
US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.

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;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-658-499-3

Alignment Scores:
Pred. No.:              1.44e-265      Length:         1393
Score:                  2462.00        Matches:        454
Percent Similarity:     98.49%         Conservative:   3
Best Local Similarity:  97.84%         Mismatches:     7
Query Match:            55.14%         Indels:         0
DB:                     4              Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-658-499-3 (1-1393)

Qy        226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGT 61

Qy        246 MetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAG 121

Qy        266 LeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyr 285
              |||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db        122 CTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTAT 181

Qy        286 IlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIle 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATT 241

Qy        306 GlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeu 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTT 301

Qy        326 ProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSer 345
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db        302 CCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 361

Qy        346 TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly 365
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        362 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTNGCACCAAGCAGCCGTTTTGAA 421

Qy        366 ThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeu 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 481

Qy        386 MetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 541

Qy        406 CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSer 425
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCC 601

Qy        426 ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrp 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 661

Qy        446 TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 465
              ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 TGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTAT 721

Qy        466 IleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla 485
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 781

Qy        486 ThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 ACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTC 841

Qy        506 ProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 525
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db        842 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTT 901

Qy        526 GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIle 545
              |||:::||||||||||||||||||||||||||||||||||||||||||||    |||
Db        902 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 961

Qy        546 GluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThr 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1021

Qy        566 AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1081

Qy        586 GlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeu 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1141

Qy        606 AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeu 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 GATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 1201

Qy        626 ValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHis 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 1261

Qy        646 ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIlePro 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 1321

Qy        666 GlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyr 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 1381

Qy        686 LeuArgTyrArg 689
              ||||||||||||
Db       1382 TTAAGATACCGT 1393

RESULT 9
US-08-716-449-1
; Sequence 1, Application US/08716449
; Patent No. 6103893
;  GENERAL INFORMATION:
;    APPLICANT:  National Starch and Chemical Investment
;    APPLICANT:  Holding Corporation
;    TITLE OF INVENTION:  Method for Producing Altered Starch
;    TITLE OF INVENTION:  from Potato Plants
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scott & Aylen
;      STREET:  Box 194, 24th Floor, Toronto-Dominion Bank Tower
;      CITY:  Toronto
;      STATE:  Canada M5K 1H6
;      COUNTRY:  Canada
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  IMB 1.44 MB High Density Diskette
;      COMPUTER:  COMPAQ Deskpro 590 (IBM PC compatible)
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  Word 7.0 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/716,449
;      FILING DATE:  FILED CONCURRENTLY HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/00634
;      FILING DATE:  22.03.95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Anita E.Nador
;      REGISTRATION NUMBER:
```

```
;      REFERENCE/DOCKET NUMBER:  1552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 368-2400
;      TELEFAX:  (416) 363-7246
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3128 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  cDNA encoding starch branching enzyme
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:  clone 1.2.1 and E2
;      ORGANISM:  Solanum tuberosum
;      STRAIN:  cv desiree
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:  mature tuber
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:  lambda Zap tuber cDNA
;      CLONE:  1.2.1 and E2
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:  open reading frame
;      NAME/KEY:  starch branching enzyme
;      LOCATION:  44-2788
;      IDENTIFICATION METHOD:  lone ORF with homology to other starch
;      IDENTIFICATION METHOD:  branching enzymes
;      OTHER INFORMATION:  complements KV832 E. coli glycogen
;      OTHER INFORMATION:  branching enzyme mutant
US-08-716-449-1

Alignment Scores:
Pred. No.:              9.74e-232     Length:         3128
Score:                  2165.00       Matches:        423
Percent Similarity:     64.73%        Conservative:   124
Best Local Similarity:  50.06%        Mismatches:     218
Query Match:            48.49%        Indels:         80
DB:                     3             Gaps:           12

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-716-449-1 (1-3128)

Qy          6 AsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeuValProGlyThr 25
Db         95 TCTTCCTCACCTAAAGTTTCTTCAGGGGCTTCTAGAAATAAGATATGTTTTCCTTCTCAA 154

Qy         26 GlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThrGluThrSerProGlu 45
Db        155 CATAGTACTGGACTGAAGTTTGGATCTCAGGAACGGTCTTGGGATATTTCTTCCACCCCA 214

Qy         46 AsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGlnIleLys 65
Db        215 AAATCAAGAGTTAGAAAAGAT---------GAAAGGATGAAGCACAGTTCAGCTATT--- 262

Qy         66 ThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAsp 85
Db        263 -----------------------TCCGCTGTTTTGACCGAT---------------GAC 283

Qy         86 PheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsn 105
Db        284 AATTCGACAATGGCACCCCTAGAGGAAGATGTCAAGACTGAAAATATTGACCTCCTAAAT 343

Qy        106 ThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProPro 125
Db        343 ------------------------------------------------------------ 343

Qy        126 ProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHis 145
Db        344 --------------------------TTGGATCCAACTTTGGAACCTTATCTAGATCAC 376

Qy        146 LeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGly 165
Db        377 TTCAGACACAGAATGAAGAGATATGTGGATCAGAAAATGCTCATTGAAAAATATGAGGGA 436

Qy        166 GlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGly 185
Db        437 CCCCTTGAGGAATTTGCTCAAGGTTATTTAAAATTTGGATTCAACAGGGAAGATGGTTGC 496

Qy        186 IleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsn 205
Db        497 ATAGTCTATCGTGAATGGGCTCCTGCTGCTCAGGAAGCAGAAGTTATTGGCGATTTCAAT 556

Qy        206 AsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePhe 225
Db        557 GGATGGAACGGTTCTAACCACATGATGGAGAAGGACCAGTTTGGTGTTTGGAGTATTAGA 616

Qy        226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
Db        617 ATTCCT---GATGTTGACAGTAAGCCAGTCATTCCACACAACTCCAGAGTTAAGTTTCGT 673

Qy        246 MetAspThrProSerGlyVal---LysAspSerIleProAlaTrpIleAsnTyrSerLeu 264
Db        674 TTCAAACATGGTAATGGAGTGTGGGTAGATCGTATCCCTGCTTGGATAAAGTATGCCACT 733

Qy        265 GlnLeuProAspGluIle------ProTyrAsnGlyIleHisTyrAspProProGluGlu 282
Db        734 GCAGACGCCACAAAGTTTGCAGCACCATATGATGGTGTCTACTGGGACCCACCACCTTCA 793

Qy        283 GluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGlu 302
Db        794 GAAAGGTACCACTTCAAATACCCTCGCCCTCCCAAACCCCGAGCCCCACGAATCTACGAA 853

Qy        303 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAsp 322
Db        854 GCACATGTCGGCATGAGCAGCTCTGAGCCACGTGTAAATTCGTATCGTGAGTTTGCAGAT 913

Qy        323 GluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGln 342
Db        914 GATGTTTTACCTCGGATTAAGGCAAATAACTATAATACTGTCCAGTTGATGGCCATAATG 973

Qy        343 GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSer 362
Db        974 GAACATTCTTACTATGGATCATTTGGATATCATGTTACAAACTTTTTTGCTGTGAGCAAT 1033

Qy        363 ArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIle 382
Db       1034 AGATATGGAAACCCGGAGGACCTAAAGTATCTGATAGATAAAGCACATAGCTTGGGTTTA 1093

Qy        383 ValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsn 402
Db       1094 CAGGTTCTGGTGGATGTAGTTCACAGTCATGCAAGCAATAATGTCACTGATGGCCTCAAT 1153

Qy        403 MetPheAspCys---------ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyr 419
Db       1154 GGCTTTGATATTGGCCAAGGTTCTCAAGAATCCTACTTTCATGCTGGAGAGCGAGGGTAC 1213

Qy        420 HisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeu 439
Db       1214 CATAAGTTGTGGGATAGCAGGCTGTTCAACTATGCCAATTGGGAGGTTCTTCGTTTCCTT 1273

Qy        440 LeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGly 459
Db       1274 CTTTCCAACTTGAGGTGGTGGCTAGAAGAGTATAACTTTGACGGATTTCGATTTGATGGA 1333

Qy        460 ValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGlu 479
Db       1334 ATAACTTCTATGCTGTATGTTCATCATGGAATCAATATGGGATTTACAGGAAACTATAAT 1393
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Qy        480 GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAsp 499
              |||||||||        |||||||||||||||||||||||||||||||||||  |||:::
Db       1394 GAGTATTTCAGCGAGGCTACAGATGTTGATGCTGTGGTCTATTTAATGTTGGCCAATAAT 1453

Qy        500 LeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetPro 519
              ||||||||    :::||||||||||||      |||    |||||||||||||||||||
Db       1454 CTGATTCACAAGATTTTCCCAGACGCAACTGTTATTGCCGAAGATGTTTCTGGTATGCCG 1513

Qy        520 ThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAla 539
                            ||||||   |||||||||:::||||||||||||||||  ||||||
Db       1514 GGCCTTAGCCGGCCTGTTTCTGAGGGAGGAATTGGTTTTGATTACCGCCTGGCAATGGCA 1573

Qy        540 IleAlaAspLysArgIleGluLeuLeuLys---LysArgAspGluAspTrpArgValGly 558
              |||   ||||||   |||:::   ||||||   |||   |||||||||||    :::
Db       1574 ATCCCAGATAAGTGGATAGATTATTTAAAGAATAAGAATGATGAAGATTGGTCCATGAAG 1633

Qy        559 AspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGlu 578
              :::::       :::|||||||||||||||:::::||||||||||:::::|||||||||
Db       1634 GAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGAAGTGTATAGCATATGCGGAG 1693

Qy        579 SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAsp 598
              ||||||||||||:::::|||||||||||||||||||||||||    ||||||||||||:::
Db       1694 AGCCATGATCAGTCTATTGTCGGTGACAAGACCATTGCATTTCTCCTAATGGACAAAGAG 1753

Qy        599 MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla 618
              ||||||      |||:::                ::::::   ::::::||||||||||||||
Db       1754 ATGTATTCTGGCATGTCTTGCTTGACAGATGCTTCTCCTGTTGTTGATCGAGGAATTGCG 1813

Qy        619 LeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPhe 638
              |||||||||||||||         ||||||   ||||||||||||||||||||||||||
Db       1814 CTTCACAAGATGATCCATTTTTTCACAATGGCCTTGGGAGGAGAGGGGTACCTCAATTTC 1873

Qy        639 MetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeu 658
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1874 ATGGGTAACGAGTTTGGCCATCCTGAGTGGATTGACTTCCCTAGA--------------- 1918

Qy        659 SerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPhe 678
                                   ||||||    :::|||||||||||||||||||||::::::
Db       1919 ------------------GAGGGCAATAATTGGAGTTATGACAAATGTAGACGCCAGTGG 1960

Qy        679 AspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMet 698
              :::|||   |||:::|||:::||||||||||:::      :::         ||||||||   |||
Db       1961 AACCTCGCAGATAGCGAACACTTGAGATACAAGTTTATGAATGCATTTGATAGAGCTATG 2020

Qy        699 GlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLys 718
                    |||::::::|||:::   |||:::   |||         |||      :::|||
Db       2021 AATTCGCTCGATGAAAAGTTCTCATTCCTCGCATCAGGAAAACAGATAGTAAGCAGCATG 2080

Qy        719 AspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPhe 738
              |||:::   ::::::::::::||||||||||:::|||:::|||||||||||||||||||||
Db       2081 GATGATGATAATAAGGTTGTTGTGTTTGAACGTGGTGACCTGGTATTTGTATTCAACTTC 2140

Qy        739 HisTrpThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLys 758
              |||         :::|||      |||::::::   |||      ||||||||||||:::
Db       2141 CACCCAAATAACACATACGAAGGGTATAAAGTTGGATGTGACTTGCCAGGGAAGTACAGA 2200

Qy        759 ValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAla 778
              |||||||||   ||||||               |||||||||   ||||||      |||:::
Db       2201 GTTGCACTGGGCAGTGATGCTTGGGAATTTGGTGGCCATGGAAGAGCTGGTCATGATGTT 2260

Qy        779 GluTyrPheThrPhe---------------------GluGlyTrpTyrAspAspArg 790
              ::::::||||||                        |||      ::::::   |||
Db       2261 GACCATTTCACATCACCAGAAGGAATACCTGGAGTTCCAGAAACAAATTTCAATGGTCGT 2320

Qy        791 ProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAsp 810
              |||   |||         |||   :::|||   :::|||   |||   |||      ||||||
Db       2321 CCAAATTCCTTCAAAGTGCTGTCTCCTGCGCGAACATGTGTGGCTTATTACAGAGTTGAT 2380

Qy        811 LysGluGluGluGluGluGluGluGluGluGluVal--------------------- 823
              :::         |||   |||:::   :::   ::::::
Db       2381 GAACGCATGTCAGAAACTGAAGATTACCAGACAGACATTTGTAGTGAGCTACTACCAACA 2440
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Qy        824 AlaAlaValGluGlu 828
              |||   :::||||||
Db       2441 GCCAATATCGAGGAA 2455
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RESULT 10
US-09-257-894-24
; Sequence 24, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-257-894-24

Alignment Scores:

Pred. No.:	2.16e-225	Length:	2565
Score:	2107.00	Matches:	404
Percent Similarity:	66.33%	Conservative:	124
Best Local Similarity:	50.75%	Mismatches:	206
Query Match:	47.19%	Indels:	62
DB:	4	Gaps:	10

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-24 (1-2565)

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Qy         43 SerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSer 62
                 ||||||   :::||||||                     :::      ||||||
Db         16 TCGCCCTCTTCCTCGCCGACTCCGCTTCCGCCGCCGCGGCGCTCTCGCTCGCATGCT--- 72

Qy         63 GlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGlu 82
                                |||         |||               |||
Db         73 ------------------GATCGGGCGGCACCGCCGGGGATCGCGGGTGGCGGCAATGTG 114

Qy         83 GluLeuAspPheAlaSer------------------------------------Ser 89
                 |||      |||
Db        115 CGCCTGAGTGTGTTGTCTGTCCAGTGCAAGGCTCGCCGGTCAGGGGTGCGGAAGGTCAAG 174
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Qy      90 LeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGlu 109
Db     175 AGCAAATTCGCCACTGCAGCTACTGTGCAAGAAGATAAAACTATGGCAACTGCCAAAGGC 234

Qy     110 ThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProProProGlyLeuGly 129
Db     235 GATGTC------------GACCATCTC------------------------------- 249

Qy     130 GlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArg 149
Db     250 ---CCCATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGG 306

Qy     150 TyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAla 169
Db     307 ATGAAAAGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCT 366

Qy     170 PheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArg 189
Db     367 TTTTCTAAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGT 426

Qy     190 GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAla 209
Db     427 GAATGGGCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGT 486

Qy     210 AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn 229
Db     487 GCAAACCATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAATT---GACCAT 543

Qy     230 ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro 249
Db     544 GTCAAAGGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGT 603

Qy     250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
Db     604 GGAGTATGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAA 663

Qy     270 Ile------ProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePhe 287
Db     664 TTTGGAGCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTT 723

Qy     288 GlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMet 307
Db     724 AAGCATCCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATG 783

Qy     308 SerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArg 327
Db     784 AGTGGTGAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGC 843

Qy     328 IleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyr 347
Db     844 ATACGAGCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTAT 903

Qy     348 AlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrPro 367
Db     904 GCTTCTTTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCA 963

Qy     368 AspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAsp 387
Db     964 GAGGACCTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGAT 1023

Qy     388 IleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp------ 405
Db    1024 GTTGTCCATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGA 1083

Qy     406 ---CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
Db    1084 CAAAGCACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGAT 1143

Qy     425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArg 444
Db    1144 AGTCGGCTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGA 1203

Qy     445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
Db    1204 TATTGGTTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTG 1263

Qy     465 TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeu 484
Db    1264 TATCATCACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTG 1323

Qy     485 AlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeu 504
Db    1324 GACACAGCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTC 1383

Qy     505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
Db    1384 TTGCCAGAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCA 1443

Qy     525 ValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
Db    1444 GTTGATGAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGG 1503

Qy     545 IleGluLeuLeuLysLysArgAspGlu---AspTrpArgValGlyAspIleValHisThr 563
Db    1504 ATTGACTACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACT 1563

Qy     564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
Db    1564 TTGACTAACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCT 1623

Qy     584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db    1624 ATTGTTGGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATG 1683

Qy     604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db    1684 TCAGACTTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATT 1743

Qy     624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
Db    1744 CACTTCATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTT 1803

Qy     644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db    1804 GGTCACCCAGAATGGATTGACTTTCCAAGA----------------------------- 1833

Qy     664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
Db    1834 ---GAAGGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACT 1890

Qy     684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
Db    1891 GATCACTTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAG 1950

Qy     704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db    1951 AGATTTTCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAG 2010

Qy     724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db    2011 GTTATTGTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACT 2070

Qy     744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
Db    2071 TACGAGGGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCT 2130

Qy     764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
Db    2131 GATGCTCTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGTCG 2190

Qy     784 -----------------------GluGlyTrpTyrAspAspArgProArgSerIleMet 795
Db    2191 CCTGAAGGGGTGCCAGGGGTGCCCGAAACGAACTTCAACAACCGGCCGAACTCGTTCAAA 2250

Qy     796 ValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAspLys 811
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                 |||   :::|||   :::|||   |||   |||      ||||||:::
Db       2251 GTCCTTTCTCCGCCCCGCACCTGTGTGGCTTATTACCGTGTAGACGAA 2298

RESULT 11
US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060
;  GENERAL INFORMATION:
;    APPLICANT:  Keeling, Peter
;    APPLICANT:  Guan, Hanping
;    TITLE OF INVENTION:  Starch Encapsulation
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Greenlee, Winner and Sullivan, P.C.
;      STREET:  5370 Manhattan Circle
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/941,445A
;      FILING DATE:  30-SEP-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,855
;      FILING DATE:  30-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winner, Ellen P
;      REGISTRATION NUMBER:  28,547
;      REFERENCE/DOCKET NUMBER:  89-97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  mRNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Zea mays
;    FEATURE:
;      NAME/KEY:  transit_peptide
;      LOCATION:  2..190
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  191..2467
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..2470
US-08-941-445A-16

Alignment Scores:
Pred. No.:              2.45e-225      Length:        2763
Score:                  2107.00        Matches:       404
Percent Similarity:     66.33%         Conservative:  124
Best Local Similarity:  50.75%         Mismatches:    206
Query Match:            47.19%         Indels:        62
DB:                     3              Gaps:          10

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-941-445A-16 (1-2763)

Qy         43 SerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSer 62
              ||||||   :::||||||                              :::      ||||||
Db         14 TCGCCCTCTTCCTCGCCGACTCCGCTTCCGCCGCCGCGGCGCTCTCGCTCGCATGCT--- 70

Qy         63 GlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGlu 82
                                   |||         |||                  |||
Db         71 -----------------GATCGGGCGGCACCGCCGGGGATCGCGGGTGGCGGCAATGTG 112

Qy         83 GluLeuAspPheAlaSer------------------------------------Ser 89
                 |||         |||
Db        113 CGCCTGAGTGTGTTGTCTGTCCAGTGCAAGGCTCGCCGGTCAGGGGTGCGGAAGGTCAAG 172

Qy         90 LeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGlu 109
                 :::                       ::::::|||   ||||||:::   |||::::::
Db        173 AGCAAATTCGCCACTGCAGCTACTGTGCAAGAAGATAAAACTATGGCAACTGCCAAAGGC 232

Qy        110 ThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProProProGlyLeuGly 129
                 :::            |||   :::
Db        233 GATGTC-----------GACCATCTC------------------------------- 247

Qy        130 GlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArg 149
                    ||||||::::::||||||   |||         ::::::   |||      ||||||
Db        248 ---CCCATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGG 304

Qy        150 TyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAla 169
                 ::::::   :::   :::   :::|||::::::         ||||||   |||||||:::
Db        305 ATGAAAAGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCT 364

Qy        170 PheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArg 189
              ||||||:::||||||   |||   |||            :::      |||      ||||||
Db        365 TTTTCTAAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGT 424

Qy        190 GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAla 209
              |||||||||      ||||||   |||   |||||||||||||||||||:::|||:::
Db        425 GAATGGGCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGT 484

Qy        210 AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn 229
                       |||   :::::::::||||||||||||   |||      :::   ::::::
Db        485 GCAAACCATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAATT---GACCAT 541

Qy        230 ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro 249
              |||   |||   |||||||||||||||   |||:::||||||   |||
Db        542 GTCAAAGGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGT 601

Qy        250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
                       |||   |||||||||   |||   |||:::                  :::
Db        602 GGAGTATGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAA 661

Qy        270 Ile------ProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePhe 287
                       ||||||:::|||:::|||:::|||||||||      |||||||||   |||
Db        662 TTTGGAGCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTT 721

Qy        288 GlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMet 307
              :::||||||||||||   ||||||   :::   |||||||||:::|||:::||||||
Db        722 AAGCATCCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATG 781

Qy        308 SerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArg 327
              |||      :::|||   :::::::::|||      |||   |||   ||||||||||||
Db        782 AGTGGTGAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGC 841

Qy        328 IleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyr 347
              |||:::         ||||||   :::|||:::|||||||:::   ||||||||||||||
Db        842 ATACGAGCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTAT 901

Qy        348 AlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrPro 367
              ||||||||||||||||||||||||||||||||||   |||||||||   |||||||||
Db        902 GCTTCTTTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCA 961

Qy        368 AspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAsp 387
              :::|||||||||   |||:::||||||||||||   ||||||:::   ||||||||||||
Db        962 GAGGACCTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGAT 1021

Qy        388 IleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp------ 405
              :::||||||||||||||||||||||||||||      ||||||||||||   :::|||
Db       1022 GTTGTCCATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGA 1081

Qy        406 ---CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
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Db     1082 CAAAGCACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGAT 1141

Qy      425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArg 444
Db     1142 AGTCGGCTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGA 1201

Qy      445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
Db     1202 TATTGGTTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTG 1261

Qy      465 TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeu 484
Db     1262 TATCATCACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTG 1321

Qy      485 AlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeu 504
Db     1322 GACACAGCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTC 1381

Qy      505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
Db     1382 TTGCCAGAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCA 1441

Qy      525 ValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
Db     1442 GTTGATGAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGG 1501

Qy      545 IleGluLeuLeuLysLysArgAspGlu---AspTrpArgValGlyAspIleValHisThr 563
Db     1502 ATTGACTACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACT 1561

Qy      564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
Db     1562 TTGACTAACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCT 1621

Qy      584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db     1622 ATTGTTGGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATG 1681

Qy      604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db     1682 TCAGACTTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATT 1741

Qy      624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
Db     1742 CACTTCATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTT 1801

Qy      644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db     1802 GGTCACCCAGAATGGATTGACTTTCCAAGA----------------------------- 1831

Qy      664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
Db     1832 ---GAAGGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACT 1888

Qy      684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
Db     1889 GATCACTTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAG 1948

Qy      704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db     1949 AGATTTTCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAG 2008

Qy      724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db     2009 GTTATTGTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACT 2068

Qy      744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
Db     2069 TACGAGGGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCT 2128

Qy      764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783

Db     2129 GATGCTCTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGTCG 2188

Qy      784 -----------------------GluGlyTrpTyrAspAspArgProArgSerIleMet 795
Db     2189 CCTGAAGGGGTGCCAGGGGTGCCCGAAACGAACTTCAACAACCGGCCGAACTCGTTCAAA 2248

Qy      796 ValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAspLys 811
Db     2249 GTCCTTTCTCCGCCCCGCACCTGTGTGGCTTATTACCGTGTAGACGAA 2296
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RESULT 12
US-09-257-894-19/c
; Sequence 19, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
;   APPLICANT: Broglie, Karen E.
;   APPLICANT: Klein, Theodore M.
;   APPLICANT: Hubbard, Natalie L.
;   APPLICANT: Lightner, Jonathan E.
;   TITLE OF INVENTION: No. 6376749el Starches via Modification of
;   TITLE OF INVENTION: Expression of Starch Biosynthesis
;   TITLE OF INVENTION: Enzyme Genes
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: E. I. du Pont de Nemours and Company
;   STREET: 1007 Market Street
;   CITY: Wilmington
;   STATE: Delaware
;   COUNTRY: USA
;   ZIP: 19898
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: Microsoft Windows 95
;   SOFTWARE: Version 7.0A
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/257,894
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/091,052
;   FILING DATE: JUNE 10, 1998
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Majarian, William R.
;   REGISTRATION NUMBER: 41,173
;   REFERENCE/DOCKET NUMBER: BB-1066-A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 302-992-4926
;   TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 19:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2487 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-09-257-894-19

Alignment Scores:

Pred. No.:	4.45e-225	Length:	2487
Score:	2104.00	Matches:	393
Percent Similarity:	70.60%	Conservative:	121
Best Local Similarity:	53.98%	Mismatches:	172
Query Match:	47.12%	Indels:	42
DB:	4	Gaps:	8

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-19 (1-2487)

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Qy       98 LeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArg 117
Db     2178 GTGCAAGAAGATAAAACTATGGCAACTGCCAAAGGCGATGTC-----------GACCAT 2131

Qy      118 IleArgGluArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspPro 137
```

```
                   :::                                               ||||||:::::::||||||
Db       2130 CTC---------------------------------CCCATATACGACCTGGACCCC 2107

Qy        138 LeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArg 157
                 |||      ::::::   |||       ||||||      ::::::   :::   :::
Db       2106 AAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAAAGATTCCTAGAGCAGAAA 2047

Qy        158 GluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMet 177
              :::|||:::::    ||||||    ||||||:::||||||:::||||||      |||
Db       2046 GGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCTAAAGGCTATTTGAAATTT 1987

Qy        178 GlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSer 197
              |||         :::      |||      ||||||||||||||||      ||||||
Db       1986 GGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGGGCACCTGCTGCGCAGGAG 1927

Qy        198 AlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsn 217
              |||   ||||||||||||||||||:::|||:::               |||   ::::::
Db       1926 GCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAACCATAAGATGGAGAAGGAT 1867

Qy        218 GluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIlePro 237
              :::||||||||||||      |||   :::   :::::::|||   |||   ||||||||||||
Db       1866 AAATTTGGTGTTTGGTCGATCAAAATT---GACCATGTCAAAGGGAAACCTGCCATCCCT 1810

Qy        238 HisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIlePro 257
              |||   |||:::||||||   |||                  |||   ||||||
Db       1809 CACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTATGGGTTGATCGTATTCCA 1750

Qy        258 AlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIle------ProTyrAsnGlyIle 275
              |||   |||   |||:::               :::         ||||||:::|||:::
Db       1749 GCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGAGCTCCCTATGATGGTGTT 1690

Qy        276 HisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysPro 295
              |||:::|||||||||         |||||||||   |||:::||||||||||||   ||||||
Db       1689 CATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCATCCTCGGCCTTCAAAGCCT 1630

Qy        296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
                 :::   ||||||||||||:::|||:::|||||||||         :::|||   ::::::
Db       1629 GCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGTGAAAAGCCAGCAGTAAGC 1570

Qy        316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
              :::|||         |||   |||   |||||||||||||||:::      ||||||
Db       1569 ACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGAGCAAATAACTACAACACA 1510

Qy        336 LeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
              :::|||:::||||||:::   ||||||||||||||||||||||||||||||||||||||||
Db       1509 GTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCTTTCGGGTACCATGTGACA 1450

Qy        356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAsp 375
              ||||||||||||   |||||||||   |||||||||:::|||||||||   |||:::|||
Db       1449 AATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGACCTCAAATATCTTGTTGAT 1390

Qy        376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
              |||||||||   ||||||:::   ||||||||||||:::||||||||||||||||||||||
Db       1389 AAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTCCATAGCCATGCAAGTAAT 1330

Qy        396 AsnThrLeuAspGlyLeuAsnMetPheAsp---------CysThrAspSerCysTyrPhe 412
              |||   ||||||||||||   :::|||            |||         ||||||
Db       1329 AATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGCACCCAAGAGTCCTATTTT 1270

Qy        413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
              |||:::|||   ||||||||||||   :::||||||||||||||||||||||   |||
Db       1269 CATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGGCTGTTCAACTATGCTAAC 1210

Qy        433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPhe 452
              |||||||||||||||:::||||||||||||   |||:::||||||||||||   |||   |||
Db       1209 TGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGGTTGGATGAATTCATGTTT 1150

Qy        453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
              ||||||||||||||||||||||||||||||||:::|||   ||||||||||:::::::|||
Db       1149 GATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCATCACCATGGTATCAATGTG 1090

Qy        473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
              ||||||||||||||||||:::|||||||||   |||   |||   |||||||||||||||

Db       1089 GGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACAGCTGTGGATGCAGTTGTT 1030

Qy        493 TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly 512
              |||:::||||||   |||   |||:::|||   |||   |||:::|||         :::
Db       1029 TACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCAGAAGCAACTGTTGTTGCT 970

Qy        513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPhe 532
              ||||||||||||||||||               |||   ||||||   ||||||||||||||||
Db        969 GAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGATGAAGGTGGGGTTGGGTTT 910

Qy        533 AspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAsp 552
              ||||||||||||      |||||||||      |||:::   |||:::   ||||||   :::|||
Db        909 GACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGACTACCTGAAGAATAAAGAT 850

Qy        553 Glu---AspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
              :::   :::|||   :::|||:::|||   ||||||||||||||||||||||:::::::|||
Db        849 GACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACTAACAGGAGATATACTGAA 790

Qy        572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
              |||||:::::::||||||||||||||||||||||:::::::||||||||||||||||||
Db        789 AAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTTGGCGACAAAACTATTGCA 730

Qy        592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
              |||   |||||||||||||:::||||||         |||:::         :::|||:::::
Db        729 TTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGACTTGCAGCCTGCTTCACCT 670

Qy        612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
                 ||||||||||||||||||||||   |||||||||         :::||||||   ||||||
Db        669 ACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTCATCACAATGGCCCTTGGA 610

Qy        632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPhe 651
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCACCCAGAATGGATTGACTTT 550

Qy        652 ProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyr 671
              ||||||                                      ||||||   :::||||||
Db        549 CCAAGA--------------------------------GAAGGGAACAACTGGAGCTAT 523

Qy        672 AspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeu 691
              ||||||||||||||||:::::   |||   |||      ::::::||||||||:::   :::
Db        522 GATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCACTTGCGGTACAAGTACATG 463

Qy        692 GlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGlu 711
                 ||||||:::   |||         |||:::::::::         |||:::::::|||
Db        462 AATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTTTCCTTCCTTTCGTCGTCA 403

Qy        712 HisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsn 731
                 |||   :::|||      ::::::   :::::::::||||||||||||:::|||:::
Db        402 AAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATTGTCTTTGAACGTGGAGAT 343

Qy        732 LeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCys 751
              |||||||||||||||||||||||         |||:::|||      |||::::::   |||
Db        342 TTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAGGGCTACAAAGTGGGATGC 283

Qy        752 LeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGlyGlyPhe 771
                 ||||||||||||:::|||||||||||||||||         :::||||||||||
Db        282 GATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCTCTGGTCTTCGGTGGACAT 223

Qy        772 GlyArgIleAspHisAsnAlaGluTyrPheThrPhe------------------------ 783
              ||||||:::      |||:::      :::::||||||
Db        222 GGAAGAGTTGGCCACGACGTGGATCACTTCACGTCGCCTGAAGGGGTGCCAGGGGTGCCC 163

Qy        784 GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
              |||         :::::::::||||||   |||         |||   :::|||   :::|||
Db        162 GAAACGAACTTCAACAACCGGCCGAACTCGTTCAAAGTCCTTTCTCCGCCCCGCACCTGT 103

Qy        804 ValValTyrAlaLeuValAspLys 811
              |||   |||      ||||||:::
Db        102 GTGGCTTATTACCGTGTAGACGAA 79
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RESULT 13
US-09-257-894-12
; Sequence 12, Application US/09257894

```
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2772 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  49..2580
US-09-257-894-12

Alignment Scores:
Pred. No.:              5.34e-225     Length:          2772
Score:                  2104.00       Matches:         393
Percent Similarity:     70.60%        Conservative:    121
Best Local Similarity:  53.98%        Mismatches:      172
Query Match:            47.12%        Indels:          42
DB:                     4             Gaps:            8

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-12 (1-2772)

Qy         98 LeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArg 117
              :::::|||   ||||||:::   |||::::::      :::            |||
Db        310 GTGCAAGAAGATAAAACTATGGCAACTGCCAAAGGCGATGTC------------GACCAT 357

Qy        118 IleArgGluArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspPro 137
              :::                                        |||||::::::|||||
Db        358 CTC-----------------------------------CCCATATACGACCTGGACCCC 381

Qy        138 LeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArg 157
                 |||      :::::   |||      ||||||      ::::::   :::   :::
Db        382 AAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAAAGATTCCTAGAGCAGAAA 441

Qy        158 GluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMet 177
                 :::|||::::::   ||||||   |||||:::||||||:::||||||   |||
Db        442 GGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCTAAAGGCTATTTGAAATTT 501

Qy        178 GlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSer 197
              |||         :::      |||      |||||||||||||         ||||||
Db        502 GGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGGGCACCTGCTGCGCAGGAG 561

Qy        198 AlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsn 217
              |||   ||||||||||||||||||:::|||:::                |||   ::::::
Db        562 GCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAACCATAAGATGGAGAAGGAT 621

Qy        218 GluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIlePro 237
              :::||||||||||||   |||   :::   ::::::|||   |||   ||||||||||||
Db        622 AAATTTGGTGTTTGGTCGATCAAAATT---GACCATGTCAAAGGGAAACCTGCCATCCCT 678

Qy        238 HisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIlePro 257
              |||   |||:::||||||   |||                        |||   ||||||
Db        679 CACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTATGGGTTGATCGTATTCCA 738

Qy        258 AlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIle------ProTyrAsnGlyIle 275
              |||   |||   |||:::                  :::      ||||||:::|||:::
Db        739 GCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGAGCTCCCTATGATGGTGTT 798

Qy        276 HisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysPro 295
              |||:::|||||||||         |||||||||   |||:::||||||||||||   ||||||
Db        799 CATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCATCCTCGGCCTTCAAAGCCT 858

Qy        296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
                 :::   ||||||||||||:::|||:::|||||||||         :::|||   ::::::
Db        859 GCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGTGAAAAGCCAGCAGTAAGC 918

Qy        316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
              :::|||      |||   |||   |||||||||||||||:::               ||||||
Db        919 ACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGAGCAAATAACTACAACACA 978

Qy        336 LeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
              :::|||:::||||||:::   ||||||||||||||||||||||||||||||||||||||||
Db        979 GTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCTTTCGGGTACCATGTGACA 1038

Qy        356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAsp 375
              ||||||||||||   |||||||||   ||||||||||:::||||||||   |||:::|||
Db       1039 AATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGACCTCAAATATCTTGTTGAT 1098

Qy        376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
              |||||||||   ||||||:::   ||||||||||||:::||||||||||||||||||||||
Db       1099 AAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTCCATAGCCATGCAAGTAAT 1158

Qy        396 AsnThrLeuAspGlyLeuAsnMetPheAsp---------CysThrAspSerCysTyrPhe 412
              |||      ||||||||||||   :::|||               |||         ||||||
Db       1159 AATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGCACCCAAGAGTCCTATTTT 1218

Qy        413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
              |||:::|||   ||||||||||||   :::|||||||||||||||||||||||||   |||
Db       1219 CATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGGCTGTTCAACTATGCTAAC 1278

Qy        433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPhe 452
              ||||||||||||||||:::||||||||||||   |||:::|||||||||   |||   |||
Db       1279 TGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGGTTGGATGAATTCATGTTT 1338

Qy        453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
              |||||||||||||||||||||||||||||||:::|||      |||||||||::::::|||
Db       1339 GATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCATCACCATGGTATCAATGTG 1398

Qy        473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
              ||||||||||||||||||:::|||||||||   |||   |||   |||||||||||||||
Db       1399 GGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACAGCTGTGGATGCAGTTGTT 1458

Qy        493 TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly 512
              |||:::||||||   |||   |||:::|||   |||   |||:::|||         :::
Db       1459 TACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCAGAAGCAACTGTTGTTGCT 1518

Qy        513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPhe 532
              ||||||||||||||||||||         |||   ||||||   ||||||||||||||||||
Db       1519 GAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGATGAAGGTGGGGTTGGGTTT 1578
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```
Qy        533 AspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAsp 552
              |||||||||||  |||||||||  |||:::  |||:::  ||||||  :::|||
Db       1579 GACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGACTACCTGAAGAATAAAGAT 1638

Qy        553 Glu---AspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
              :::   :::|||   :::|||:::|||  |||||||||||||||||||||||::::::|||
Db       1639 GACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACTAACAGGAGATATACTGAA 1698

Qy        572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
              ||||||::::::||||||||||||||||||||||:::::::||||||||||||||||||||
Db       1699 AAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTTGGCGACAAAACTATTGCA 1758

Qy        592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
              |||   ||||||||||||:::||||||        |||:::      :::|||::::::
Db       1759 TTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGACTTGCAGCCTGCTTCACCT 1818

Qy        612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
                 |||||||||||||||||||   |||||||||        :::||||||   ||||||
Db       1819 ACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTCATCACAATGGCCCTTGGA 1878

Qy        632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPhe 651
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCACCCAGAATGGATTGACTTT 1938

Qy        652 ProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyr 671
              ||||||                                   ||||||   :::||||||
Db       1939 CCAAGA-------------------------------GAAGGGAACAACTGGAGCTAT 1965

Qy        672 AspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeu 691
              |||||||||||||||||::::::   |||   |||   ::::::||||||||||:::   :::
Db       1966 GATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCACTTGCGGTACAAGTACATG 2025

Qy        692 GlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGlu 711
                    ||||||:::   |||      |||::::::::::::   |||::::::|||
Db       2026 AATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTTTCCTTCCTTTCGTCGTCA 2085

Qy        712 HisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsn 731
                 |||   :::|||      ::::::   :::::::||||||||||||||:::|||:::
Db       2086 AAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATTGTCTTTGAACGTGGAGAT 2145

Qy        732 LeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCys 751
              ||||||||||||||||||||||||      |||:::|||      |||::::::   |||
Db       2146 TTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAGGGCTACAAAGTGGGATGC 2205

Qy        752 LeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGlyGlyPhe 771
                    ||||||||||||:::||||||||||||||||||      :::|||||||||
Db       2206 GATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCTCTGGTCTTCGGTGGACAT 2265

Qy        772 GlyArgIleAspHisAsnAlaGluTyrPheThrPhe----------------------- 783
              ||||||:::   |||:::   ::::::||||||
Db       2266 GGAAGAGTTGGCCACGACGTGGATCACTTCACGTCGCCTGAAGGGGTGCCAGGGGTGCCC 2325

Qy        784 GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
              |||      :::::::::||||||   |||      |||   :::|||   :::|||
Db       2326 GAAACGAACTTCAACAACCGGCCGAACTCGTTCAAAGTCCTTTCTCCGCCCCGCACCTGT 2385

Qy        804 ValValTyrAlaLeuValAspLys 811
              |||   |||   ||||||:::
Db       2386 GTGGCTTATTACCGTGTAGACGAA 2409
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RESULT 14
US-08-104-158-1
; Sequence 1, Application US/08104158
; Patent No. 6215042
; GENERAL INFORMATION:
;   APPLICANT: Willmitzer, Lothar
;   APPLICANT: Sonnewald, Uwe
;   APPLICANT: Kossmann, Jens
;   APPLICANT: Mueller-Roeber, Bernd
;   APPLICANT: Visser, Richard Gerardus Francisus
;   APPLICANT: Jacobsen, Evert
;   TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
;   TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
;   TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
;   TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
;   STREET: 1180 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10036-8403
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/104,158
;   FILING DATE: 13-AUG-1993
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP PCT/EP92/00302
;   FILING DATE: 11-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE P 41 04 782.6
;   FILING DATE: 13-FEB-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Meilman, Edward A.
;   REGISTRATION NUMBER: 24,735
;   REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-382-0700
;   TELEFAX: 212-382-0888
;   TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2909 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Solanum tuberosum cv. Desiree
;   STRAIN: Desiree
;   DEVELOPMENTAL STAGE: growing tuber
;   TISSUE TYPE: tuber
;   CELL TYPE: total tuber
;   IMMEDIATE SOURCE:
;   LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 2..1699
;   OTHER INFORMATION: /note= "for Branching enzyme I
;   OTHER INFORMATION: (partial) truncated protein; 97,11 % identity to
;   OTHER INFORMATION: active potato branching enzyme"
US-08-104-158-1

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Alignment Scores:
Pred. No.:               2.39e-224      Length:         2909
Score:                   2098.50        Matches:        409
Percent Similarity:      66.00%         Conservative:   123
Best Local Similarity:   50.74%         Mismatches:     196
Query Match:             47.00%         Indels:         78
DB:                      4              Gaps:           12

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-104-158-1 (1-2909)

Qy         46 AsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGlnIleLys 65
              :::::::|||   |||                  |||:::|||:::|||   |||
Db         26 TCCACCCCAAAATCAAGAGTTAGAAAAGATGAAGGATGAAGCACAGTTCAGCTATT--- 82

Qy         66 ThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAsp 85
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Db     83 -----------------------TCCGCTGTTTGACC-------------------- 97

Qy     86 PheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsn 105
Db     98 ---------------------------------------GATGACAATTCGACAATGGCA 118

Qy    106 ThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProPro 125
Db    119 CCCCTAGAGGAAGATGTCAACACTGAAAAT------------------------------ 148

Qy    126 ProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHis 145
Db    149 ------ATTGGC------CTCCTAAATTTGGATCCAACTTTGGAACCTTATCTAGATCAC 196

Qy    146 LeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGly 165
Db    197 TTCAGACACAGAATGAAGAGATATGTGGATCAGAAAATGCTCATTGAAAAATATGAGGGA 256

Qy    166 GlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGly 185
Db    257 CCCCTTGAGGAATTTGCTCAAGGTTATTTAAAATTTGGATTCAACAGGGAAGATGGTTGC 316

Qy    186 IleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsn 205
Db    317 ATAGTCTATCGTGAATGGGCTCCTGCTGCTCAGGAAGCAGAAGTATTGGCGATTTCAAT 376

Qy    206 AsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePhe 225
Db    377 GGTAGGAACGGTTCTAACCACATGATGGAGAAGGACCAGTTTGGTGTTTGGAGTATTAGA 436

Qy    226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
Db    437 ATTCCT---GATGTTGACAGTAAGCCAGTCATTCCACACAACTCCAGAGTTAAGTTTCGT 493

Qy    246 MetAspThrProSerGlyVal---LysAspSerIleProAlaTrpIleAsnTyrSerLeu 264
Db    494 TTCAAACATGGTAATGGAGTGTGGGTAGATCGTATCCCTGCTTGGATAAAGTATGCCACT 553

Qy    265 GlnLeuProAspGluIle------ProTyrAsnGlyIleHisTyrAspProProGluGlu 282
Db    554 GCAGACGCCACAAAGTTTGCAGCACCATATGATGGTGTCTACTGGGACCCACCACCTTCA 613

Qy    283 GluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGlu 302
Db    614 GAAAGGTACCACTTCAAATACCCTCGCCCTCCCAAACCCCGAGCCCCACGAATCTACGAA 673

Qy    303 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAsp 322
Db    674 GCACATGTCGGCATGAGCAGCTCTGAGCCACGTGTAAATTCGTATCGTGAGTTTGCAGAT 733

Qy    323 GluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGln 342
Db    734 GATGTTTTACCTCGGATTAAGGCAAATAACTATAATACTGTCCAGTTGATGGCCATAATG 793

Qy    343 GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSer 362
Db    794 GAACATTCTTACTATGGATCATTTGGATATCATGTTACAAACTTTTTTGCTGTGAGCAAT 853

Qy    363 ArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIle 382
Db    854 AGATATGGAAACCCGGAGGACCTAAAGTATCTGATAGATAAAGCACATAGCTTGGGTTTA 913

Qy    383 ValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsn 402
Db    914 CAGGTTCTGGTGGATGTAGTTCACAGTCATGCAAGCAATAATGTCACTGATGGCCTCAAT 973

Qy    403 MetPheAspCys---------ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyr 419
Db    974 GGCTTTGATATTGGCCAAGGTTCTCAAGAATCCTACTTTCATGCTGGAGAGCGAGGGTAC 1033

Qy    420 HisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeu 439
Db   1034 CATAAGTTGTGGGATAGCAGGCTGTTCAACTATGCCAATTGGGAGGTTCTTCGTTTCCTT 1093

Qy    440 LeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGly 459
Db   1094 CTTTCCAACTTGAGGTGGTGGCTAGAAGAGTATAACTTTGACGGATTTCGATTTGATGGA 1153

Qy    460 ValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGlu 479
Db   1154 ATAACTTCTATGCTGTATGTTCATCATGGAATCAATATGGGATTTACAGGAAACTATAAT 1213

Qy    480 GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAsp 499
Db   1214 GAGTATTTCAGCGAGGCTACAGATGTTGATGCTGTGGTCTATTTAATGTTGGCCAATAAT 1273

Qy    500 LeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetPro 519
Db   1274 CTGATTCACAAGATTTTCCCAGACGCAACTGTTATTGCCGAAGATGTTTCTGGTATGCCG 1333

Qy    520 ThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAla 539
Db   1334 GGCCTTAGCCGGCCTGTTTCTGAGGGAGGAATTGGTTTTGATTACCGCCTGGCAATGGCA 1393

Qy    540 IleAlaAspLysArgIleGluLeuLeuLys---LysArgAspGluAspTrpArgValGly 558
Db   1394 ATCCCAGATAAGTGGATAGATTATTTAAAGAATAAGAATGATGAAGATTGGTCCATGAAG 1453

Qy    559 AspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGlu 578
Db   1454 GAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGAAGTGTATAGCATATGCGGAG 1513

Qy    579 SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAsp 598
Db   1514 AGCCATGATCAGTCTATTGTCGGTGACAAGACCATTGCATTTCTCCTAATGAACAAAGAG 1573

Qy    599 MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla 618
Db   1574 ATGTATTCTGGCATGTCTTGCTTGACAGATGCTTCTCCTGTTGTTGATGCAGGAATTGCG 1633

Qy    619 LeuHisLysMetIleArg-LeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPh 638
Db   1634 CTTGACAAGATGATCCATTTTTTCACAATGGCCTTGGGAGGAGAGGGGTACCTCAATTT 1693

Qy    638 eMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLe 658
Db   1694 CATGGGTAACGAGTTTGGCCATCCTGAGTGGATTGACTTCCCTAGT-------------- 1739

Qy    658 uSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPh 678
Db   1740 ------------------GAGGGCAATAATTGGAGTTATGACAAATGTAGACGCCAGTG 1780

Qy    678 eAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMe 698
Db   1781 GAACCTCGCAGATAGCGAACACTTGAGATACAAGTTTATGAATGCATTTGATAGAGCTAT 1840

Qy    698 tGlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLy 718
Db   1841 GAATTCGCTCGATGAAAAGTTCTCATTCCTCGCATCAGGAAAACAGATAGTAAGCAGCAT 1900

Qy    718 sAspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPh 738
Db   1901 GGATGATGATAATAAGGTTGTTGTGTTTGAACGTGGTGACCTGGTATTTGTATTCAACTT 1960

Qy    738 eHisTrpThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLy 758
Db   1961 CCACCCAAATAACACATACGAAGGGTATAAAGTTGGATGTGACTTGCCAGGGAAGTACAG 2020

Qy    758 sValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAl 778
Db   2021 AGTTGCACTGGACAGTGATGCTTGGGAATTTGGTGGCCATGGAAGAGCTGGTCATGATGT 2080

Qy    778 aGluTyrPheThrPhe-----------------------GluGlyTrpTyrAspAspAr 790
Db   2081 TGACCATTTCACATCACCAGAAGGAATACCTGGAGTTCCAGAAACAAATTTCAATGGTCG 2140
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Qy         790 gProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAs 810
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Db        2141 TCCAAATTCCTTCAAAGTGCTGTCTCCTGCGCGAACATGTGTGGCTTATTACAGAGTTGA 2200

Qy         810 pLysGluGluGluGluGluGluGluGluGluGluVal-------------------- 823
                |:::               |||:::   :::   ::::::
Db        2201 TGAACGCATGTCATAAACTGAAGATTACCAGACAGACATTTGTAGTGAGCTACTACCAAC 2260

Qy         824 -AlaAlaValGluGlu 828
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Db        2261 AGCCAATATCGAGGAA 2276

RESULT 15
US-09-257-894-25
; Sequence 25, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-257-894-25

Alignment Scores:
Pred. No.:              4.86e-180      Length:         1809
Score:                  1699.50        Matches:        328
Percent Similarity:     66.72%         Conservative:   87
Best Local Similarity:  52.73%         Mismatches:     164
Query Match:            38.06%         Indels:         43
DB:                     4              Gaps:           8

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-25 (1-1809)

Qy          43 SerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSer 62
                ||||||   :::||||||                             :::      ||||||
Db          16 TCGCCCTCTTCCTCGCCGACTCCGCTTCCGCCGCCGCGGCGCTCTCGCTCGCATGCT--- 72

Qy          63 GlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGlu 82
                                 |||        |||                  |||
Db          73 ------------------GATCGGGCGGCACCGCCGGGGATCGCGGGTGGCGGCAATGTG 114

Qy          83 GluLeuAspPheAlaSer---------------------------------------Ser 89
                   |||       |||
Db         115 CGCCTGAGTGTGTTGTCTGTCCAGTGCAAGGCTCGCCGGTCAGGGGTGCGGAAGGTCAAG 174

Qy          90 LeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGlu 109
                 :::                     ::::::|||   |||||||:::  |||::::::
Db         175 AGCAAATTCGCCACTGCAGCTACTGTGCAAGAAGATAAAACTATGGCAACTGCCAAAGGC 234

Qy         110 ThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProProProGlyLeuGly 129
                 :::                   |||   :::
Db         235 GATGTC------------GACCATCTC---------------------------------- 249

Qy         130 GlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArg 149
                         ||||||:::::::||||||     |||        ::::::   |||     ||||||
Db         250 ---CCCATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGG 306

Qy         150 TyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAla 169
                        ::::::   :::   :::   :::|||::::::   ||||||   ||||||:::
Db         307 ATGAAAAGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCT 366

Qy         170 PheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArg 189
               ||||||:::||||||    |||   |||               :::       |||     ||||||
Db         367 TTTTCTAAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGT 426

Qy         190 GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAla 209
               |||||||||           ||||||   |||   ||||||||||||||||||:::|||:::
Db         427 GAATGGGCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGT 486

Qy         210 AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn 229
                             |||   :::::::::||||||||||||   |||   :::   ::::::
Db         487 GCAAACCATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAATT---GACCAT 543

Qy         230 ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro 249
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Db         544 GTCAAAGGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGT 603

Qy         250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
                           |||   |||||||||   |||   |||:::                    :::
Db         604 GGAGTATGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAA 663

Qy         270 Ile------ProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePhe 287
                         |||||:::|||:::|||:::|||||||||      |||||||||   |||
Db         664 TTTGGAGCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTT 723

Qy         288 GlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMet 307
               :::||||||||||||   ||||||   :::   ||||||||||||:::|||:::||||||
Db         724 AAGCATCCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATG 783

Qy         308 SerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArg 327
               |||      :::|||   :::::::::|||       |||   |||   ||||||||||||
Db         784 AGTGGTGAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGC 843

Qy         328 IleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyr 347
               |||:::          ||||||   :::|||:::||||||:::   |||||||||||||||
Db         844 ATACGAGCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTAT 903

Qy         348 AlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrPro 367
               ||||||||||||||||||||||||||||||||||||   |||||||||   |||||||||
Db         904 GCTTCTTTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCA 963

Qy         368 AspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAsp 387
               :::|||||||||   |||:::||||||||||||   ||||||:::   ||||||||||||
Db         964 GAGGACCTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGAT 1023

Qy         388 IleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp------ 405
               :::|||||||||||||||||||||||||      ||||||||||||   :::|||
Db        1024 GTTGTCCATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGA 1083
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Qy        406 ---CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
                    |||          ||||||||:::|||   |||||||||||    :::||||||
Db       1084 CAAAGCACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGAT 1143

Qy        425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArg 444
              ||||||||||||||||     |||||||||||||||||:::|||||||||||     |||
Db       1144 AGTCGGCTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGA 1203

Qy        445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
              :::|||||||||    |||     |||||||||||||||||||||||||||||||||:::
Db       1204 TATTGGTTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTG 1263

Qy        465 TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeu 484
              |||   ||||||||::::::||||||||||||||||||||||:::|||||||||    |||
Db       1264 TATCATCACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTG 1323

Qy        485 AlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeu 504
                 |||   ||||||||||||||||||:::||||||    |||    |||:::|||   |||
Db       1324 GACACAGCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTC 1383

Qy        505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
                 |||:::|||       :::    ||||||||||||||||||      |||    |||
Db       1384 TTGCCAGAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCA 1443

Qy        525 ValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
              |||   |||||||||||||||||||||||||||     |||||||||    |||:::
Db       1444 GTTGATGAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGG 1503

Qy        545 IleGluLeuLeuLysLysArgAspGlu---AspTrpArgValGlyAspIleValHisThr 563
              |||:::    ||||||    :::|||:::    :::|||    :::|||:::|||    ||||||
Db       1504 ATTGACTACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACT 1563

Qy        564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
              |||||||||||||||:::::|||||||||::::::|||||||||||||||||||||:::
Db       1564 TTGACTAACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCT 1623

Qy        584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
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Db       1624 ATTGTTGGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATG 1683

Qy        604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
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Db       1684 TCAGACTTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATT 1743

Qy        624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
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Db       1744 CACTTCATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGAAATGAGTTT 1803

Qy        644 GlyHis 645
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Job time : 269 secs

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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:         July  6, 2003, 03:05:21 ; Search time 337 Seconds
                                          (without alignments)
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Title:          US-10-056-454A-15_COPY_49_882
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Searched:       1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters:      2171862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10056454/runat_01072003_145502_8338/app_query.fasta_1.1031
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10056454_@CGN_1_1_191_@runat_01072003_145502_8338
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

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1		4320	96.8	3074	9	US-10-254-534-1	Sequence 1, Appli
2		3309.5	74.1	2418	9	US-09-938-842A-872	Sequence 872, App
3		3266	73.1	2577	9	US-09-938-842A-337	Sequence 337, App
4		3037	68.0	3039	10	US-09-792-127-3	Sequence 3, Appli
5		2997	67.1	2559	10	US-09-792-127-1	Sequence 1, Appli
6		2462	55.1	1393	9	US-10-254-534-3	Sequence 3, Appli
7		2058	46.1	2955	9	US-09-918-624B-30	Sequence 30, Appl
8		2058	46.1	2955	10	US-09-880-107-2148	Sequence 2148, Ap
9		2058	46.1	2994	9	US-10-084-817-92	Sequence 92, Appl
10	c	627	14.0	602	10	US-09-770-149-955	Sequence 955, App
11		530.5	11.9	1830121	9	US-10-329-960-1	Sequence 1, Appli
12		513.5	11.5	2193	9	US-09-738-626-1354	Sequence 1354, Ap
13	c	513.5	11.5	3309400	9	US-09-738-626-1	Sequence 1, Appli
14		484.5	10.9	1877	10	US-09-974-300-653	Sequence 653, App
15		463.5	10.4	604	10	US-09-925-300-453	Sequence 453, App
16		453	10.1	2514	9	US-10-156-761-2792	Sequence 2792, Ap
17		453	10.1	9025608	9	US-10-156-761-1	Sequence 1, Appli
18		422.5	9.5	1776	9	US-10-156-761-7377	Sequence 7377, Ap
19	c	419	9.4	601	9	US-10-025-380-304	Sequence 304, App
20	c	419	9.4	601	10	US-09-922-217-304	Sequence 304, App
21	c	419	9.4	601	10	US-09-833-263-304	Sequence 304, App
22		317	7.1	441	10	US-09-770-444-893	Sequence 893, App
23		305.5	6.8	543	10	US-09-815-343-373	Sequence 373, App
24		261.5	5.9	1680	10	US-09-908-855-14	Sequence 14, Appl
25		249.5	5.6	1743	9	US-10-156-761-2147	Sequence 2147, Ap
26	c	247	5.5	310	9	US-10-102-524-1616	Sequence 1616, Ap
27		244.5	5.5	3033	9	US-10-212-219-5	Sequence 5, Appli
28		244.5	5.5	3309400	9	US-09-738-626-1	Sequence 1, Appli
29		240.5	5.4	204	10	US-09-878-574-12567	Sequence 12567, A
30		239.5	5.4	1785	9	US-09-738-626-2326	Sequence 2326, Ap
31		226	5.1	661	10	US-09-765-272-77	Sequence 77, Appl
32		226	5.1	6142	9	US-10-014-436-1	Sequence 1, Appli
33		223	5.0	2437	9	US-10-238-091-6	Sequence 6, Appli
34		210.5	4.7	976	10	US-09-765-272-79	Sequence 79, Appl
35		209.5	4.7	576	10	US-09-815-343-924	Sequence 924, App
36		207.5	4.6	2736	10	US-09-833-435A-14	Sequence 14, Appl
37		205	4.6	2106	9	US-10-156-761-2139	Sequence 2139, Ap
38		203	4.5	5058	9	US-09-252-088-22	Sequence 22, Appl
39		202.5	4.5	2352	9	US-09-938-842A-218	Sequence 218, App
40		195	4.4	2508	9	US-09-738-626-2305	Sequence 2305, Ap
41		194	4.3	2997	9	US-10-238-091-1	Sequence 1, Appli
42		194	4.3	2997	9	US-10-238-091-2	Sequence 2, Appli
43		187.5	4.2	1965	10	US-09-815-242-9714	Sequence 9714, Ap
44		184	4.1	2247	9	US-10-156-761-2776	Sequence 2776, Ap
45		182	4.1	2151	9	US-10-127-032-72	Sequence 72, Appl

ALIGNMENTS

```
RESULT 1
US-10-254-534-1
; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/10/254,534
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: US/09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Unknown
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;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (189)..(2825)
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (189)..(332)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (333)..(2825)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (92)..(2156)
;   OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
;   OTHER INFORMATION: n wherein n = A, C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (285)..(287)
;   OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1404)..(1406)
;   OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1428)..(1430)
;   OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1896)..(1898)
;   OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2154)..(2156)
;   OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-10-254-534-1

Alignment Scores:
Pred. No.:              0              Length:        3074
Score:                  4320.00        Matches:       812
Percent Similarity:     97.96%         Conservative:  5
Best Local Similarity:  97.36%         Mismatches:    13
Query Match:            96.75%         Indels:        4
DB:                     9              Gaps:          1

US-10-056-454A-15_COPY_49_882 (1-834) x US-10-254-534-1 (1-3074)

Qy          1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        333 GAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTC 392

Qy         21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACT 452

Qy         41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC 512

Qy         61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 GCTAGGCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 572

Qy         81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 GTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 632

Qy        101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAG 692

Qy        121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 752

Qy        141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 812

Qy        161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 GACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACT 872

Qy        181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
              ||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        873 CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTC 932

Qy        201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 992

Qy        221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1052

Qy        241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATC 1112

Qy        261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
              |||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1113 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1172

Qy        281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 GAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1232

Qy        301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1292

Qy        321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1293 AGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCT 1352

Qy        341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       1353 ATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCA 1412

Qy        361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 AGCAGCCGTTTTGGAACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1472

Qy        381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGA 1532

Qy        401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db       1533 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1592

Qy        421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1593 TGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTC 1652

Qy        441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db       1653 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1712

Qy        461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
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Db       1713 ACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAA 1772

Qy        481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1773 TACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1832

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1833 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1892

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              |||   ||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db       1893 TTTTNTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1952

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1953 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2012

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2013 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2072

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       2073 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGAGAAGGATATGTAT 2132

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2133 GATTTTATGGCTCTGGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2192

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2193 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2252

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2253 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2312

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2313 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2372

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       2373 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2432

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2433 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2492

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2493 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2552

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              |||||||||||||||||||||||||||||||     ||||||||||||||||||||||||
Db       2553 ACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCC 2612

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2613 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 2672

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2673 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2732

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::|||||||||||||||||||||||||||||||||            |||||||||||||||
Db       2733 AGAACAGCAGTGGTCTATGCACTAGTAGACAAA------------GAAGAAGAAGAAGAA 2780

Qy        821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
              ||||||||||||    ||||||||||||||||||||||||||
Db       2781 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2822
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RESULT 2
US-09-938-842A-872
; Sequence 872, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 872
;   LENGTH: 2418
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

Alignment Scores:
Pred. No.:              0              Length:         2418
Score:                  3309.50        Matches:        601
Percent Similarity:     84.18%         Conservative:   80
Best Local Similarity:  74.29%         Mismatches:     73
Query Match:            74.12%         Indels:         55
DB:                     9              Gaps:           4

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-938-842A-872 (1-2418)

Qy          6 AsnSerGluPheArgProSerThr------ValAlaAlaSerGlyLysValLeuValPro 23
               ::::::||||||      |||:::       ::::::||||||    ||||||||||||||
Db        148 TCTGCGGAGTTTGATTCTTCGTCACAAGCTATCTCTGCTTCTGAGAAAGTCTTAGTACCT 207

Qy         24 GlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThrGluThrSer 43
                        |||                 :::       |||
Db        208 GATAATCTTGATGATGATCCCAGAGGTTTTTCACAGATATTT----------------- 249

Qy         44 ProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGln 63
                                         |||::::::|||      |||||||||:::
Db        250 ------------------------GATCTAGAAAGTCAAACAATGGAATATACTGAGGCA 285

Qy         64 IleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGlu 83
              ::::::||||||:::
Db        286 GTAAGAACAGAAGAC--------------------------------------------- 300

Qy         84 LeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThr 103
                                                                    :::|||
Db        301 ------------------------------------------------------CAAACA 306

Qy        104 LeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArgGlyIle 123
              :::|||      :::|||                         ::::::   |||   :::
Db        307 ATGAACGTTGTCAAGGAGAGA-----------------GGGGTGAAACCAAGAATAGTT 348

Qy        124 ProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg 143
              ||||||||||||   |||:::||||||||||||||||||||||:::|||      |||
Db        349 CCCCCACCGGGTGATGGCAAGAAAATTTATGAGATAGACCCCATGTTACGAACTTACAAC 408

Qy        144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyr 163
                 ||||||||||||||||||     ||||||||::::||||||||    ||||||||||||
Db        409 AATCATCTTGATTACCGTTATGGACAGTATAAAAGATTGCGTGAGGAAATAGACAAGTAT 468

Qy        164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
              ||||||||||||||||||||||||||||||||||||||:::||||||:::|||||||
Db        469 GAGGGTGGTCTTGAGGCATTCTCTCGTGGCTATGAAAAGTTAGGATTTTCGCGCAGTGAT 528
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Qy     184 ThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAsp 203
Db     529 GCCGGTATAACTTATAGAGAGTGGGCGCCTGGAGCTAAGGCTGCATCACTTATCGGAGAT 588

Qy     204 PheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 223
Db     589 TTCAACAACTGGAATTCTAATGCAGATATCATGACTCGGAATGAATTTGGTGTTTGGGAG 648

Qy     224 IlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLys 243
Db     649 ATCTTTTTGCCCAACAACACTGATGGTTCGCCTGCAATTCCTCATGGCTCACGTGTAAAG 708

Qy     244 IleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSer 263
Db     709 ATTCGTATGGATACTCCATCTGGCATTAAAGACTCAATTCCTGCTTGGATCAAGTTCTCG 768

Qy     264 LeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGlu 283
Db     769 GTGCAAGCTCCAGGTGAAATCCCATTCAATGGCATATACTATGATCCTCCAGAAGAGGAG 828

Qy     284 ArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSer 303
Db     829 AAGTATGTATTCAAACATCCTCAACCAAAGAGACCTAAGTCGCTAAGGATTTATGAAGCA 888

Qy     304 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu 323
Db     889 CATGTTGGCATGAGTAGCACGGAACCAATGGTCAATACGTATGCTAACTTTAGAGATGAT 948

Qy     324 ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 343
Db     949 GTTCTTCCCCGCATCAAAAAGCTTGGATATAATGCTGTTCAAATTATGGCCATACAAGAA 1008

Qy     344 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 363
Db    1009 CATTCATATTATGCCAGCTTTGGGTACCATGTCACAAACTTTTTTGCCCCAAGCAGTCGC 1068

Qy     364 PheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 383
Db    1069 TGTGGGACCCCAGAGGAACTAAAATCACTGATAGATAGAGCTCACGAGTTAGGCCTGGTA 1128

Qy     384 ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 403
Db    1129 GTTCTGATGGATATCGTTCATAGCCATGCTTCAAAAAACACATTGGATGGACTGAACATG 1188

Qy     404 PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrp 423
Db    1189 TTTGATGGAACTGATGCTCACTATTTTCACTCTGGACCTCGGGGATACCATTGGATGTGG 1248

Qy     424 AspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAla 443
Db    1249 GATTCACGACTTTTCAATTATGGGAGCTGGGAAGTATTACGATATCTCCTTTCAAATGCA 1308

Qy     444 ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet 463
Db    1309 CGGTGGTGGCTAGAAGAATACAAGTTTGATGGATTTAGATTTGATGGTGTAACCTCAATG 1368

Qy     464 MetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGly 483
Db    1369 ATGTATACTCATCATGGACTCTCGGTTGGATTTACTGGGAACTACACCGAATACTTTGGA 1428

Qy     484 LeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 503
Db    1429 TTGGAAACTGATGTGGATGCTGTGAATTATCTCATGCTGGTTAATGATATGATTCATGGG 1488

Qy     504 LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle 523
Db    1489 CTCTACCCTGAAGCGATTACCGTTGGTGAAGATGTTAGTGGTATGCCAACATTCTGTATT 1548

Qy     524 ProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys 543
Db    1549 CCTGTCCAAGATGGTGGCGTTGGATTTGACTACCGTTTACACATGGCCATAGCTGATAAG 1608

Qy     544 ArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
Db    1609 TGGATAGAAATGCTCAAGAAGAGAGATGAAGACTGGCAAATGGGCGACATCATTTACACA 1668

Qy     564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
Db    1669 CTTACCAACAGAAGGTGGTCAGAGAAGTGTATCTCTTATGCTGAAAGTCACGATCAAGCT 1728

Qy     584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db    1729 CTTGTTGGTGATAAAACAATTGCCTTCTGGTTAATGGACAAGGATATGTATGATTTCATG 1788

Qy     604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db    1789 GCAGTAGACAGACCATCAACTCCTCTTATCGATAGAGGAATAGCTTTGCACAAAATGATT 1848

Qy     624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
Db    1849 AGGCTTATAACTATGGGATTAGGCGGTGAAGGTTACTTAAATTTTATGGGAAACGAATTC 1908

Qy     644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db    1909 GGACATCCAGAATGGATTGATTTTCCCAGAGGCGAGCAGCGTCTTTCTGATGGTAGCGTG 1968

Qy     664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
Db    1969 ATTCCTGGCAACAATTTCAGTTATGACAAATGCCGCCGCAGATTTGATCTTGGGGATGCA 2028

Qy     684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
Db    2029 GATTATCTCAGATACCGCGGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAG 2088

Qy     704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db    2089 AATTACGGTTTTATGACTTCGGAGCACCAATTCATATCACGAAAAGACGAAGCAGATAGA 2148

Qy     724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db    2149 GTAATCGTATTCGAAAGAGGTGATCTCGTCTTTGTCTTTAACTTTCACTGGACCAGCAGC 2208

Qy     744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
Db    2209 TACTTTGATTACCGCATTGGTTGCTCCAAGCCTGGAAAATATAAGATCGTATTGGACTCG 2268

Qy     764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
Db    2269 GACGATCCTCTCTTTGGTGGATTCAATAGGCTCGATCGCAAGGCAGAGTACTTCACTTAT 2328

Qy     784 GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
Db    2329 GATGGCTTATACGACGAACGACCCTGCTCCTTCATGGTCTATGCACCGTGTAGAACCGCC 2388

Qy     804 ValValTyrAlaLeuValAspLysGlu 812
Db    2389 GTGGTTTATGCTTTAGCAAACCACGAT 2415
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RESULT 3
US-09-938-842A-337
; Sequence 337, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647

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;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
;   LENGTH: 2577
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

Alignment Scores:
Pred. No.:              0           Length:          2577
Score:                  3266.00     Matches:         602
Percent Similarity:     83.25%      Conservative:    89
Best Local Similarity:  72.53%      Mismatches:      113
Query Match:            73.15%      Indels:          26
DB:                     9           Gaps:            6

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-938-842A-337 (1-2577)

Qy        2 LysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeu 21
Db      160 AAGCCATCGTATGATTCTGAT------TCGTCTTCCTTAGCTACCACTGCATCTGAGAAG 213

Qy       22 ValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThrGlu 41
Db      214 CTCCGTGGCCATCAGAGTGATAGCTCTTCATCTGCCTCTGATCAAGTACAATCTCGGGAT 273

Qy       42 ThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAla 61
Db      274 ACTGTCTCTGACGATACTCAGGTGCTCGGCAATGTAGACGTTCAGAAAACTGAAGAAGCC 333

Qy       62 SerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerVal 81
Db      334 CAGGAA------ACAGAGACACTAGATCAAACTTCTGCACTCTCAACATCTGGAAGCATA 387

Qy       82 Glu---GluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
Db      388 AGTTATAAAGAAGATTTTGCA---------------------------AAGATGTCACAC 420

Qy      101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
Db      421 TCT-----------------------------GTCGACCAA------GAAGTTGGGCAG 444

Qy      121 ArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
Db      445 AGGAAGATTCCACCTCCTGGAGATGGGAAGAGAATATATGACATTGATCCTATGTTGAAC 504

Qy      141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
Db      505 AGTCATCGTAATCATCTTGATTACCGATATGGGCAGTACAGAAAACTGCGTGAAGAAATT 564

Qy      161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
Db      565 GACAAGAATGAAGGTGGTTTGGAGGCATTTTCTCGTGGTTATGAAATATTTGGCTTCACT 624

Qy      181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
Db      625 CGAAGCGCCACTGGTATCACTTACCGGGAATGGGCACCGGGAGCTAAGGCAGCATCACTG 684

Qy      201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
Db      685 ATCGGAGATTTTAATAACTGGAATGCGAAATCTGATGTTATGGCTCGGAACGACTTTGGT 744

Qy      221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
Db      745 GTGTGGGAAATATTTCTGCCAAATAATGCTGATGGCTCACCAGCAATTCCCCATGGCTCC 804

Qy      241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
Db      805 CGTGTGAAGATCCGCATGGATACCCCATCTGGTATTAAAGACTCCATTCCAGCTTGGATC 864

Qy      261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
Db      865 AAGTATTCTGTCCAGCCACCTGGCGAGATCCCATATAATGGAGTATATTATGACCCTCCT 924

Qy      281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
Db      925 GAGGAGGATAAATATGCGTTCAAACATCCTCGTCCAAAGAAACCCACATCGCTGCGTATA 984

Qy      301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
Db      985 TATGAATCACATGTTGGAATGAGTAGTACGGAACCAAAGATAAATACATATGCCAACTTT 1044

Qy      321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
Db     1045 AGAGATGATGTACTTCCCCGTATAAAAAAGCTAGGCTATAATGCTGTGCAGATAATGGCC 1104

Qy      341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
Db     1105 ATTCAAGAGCATGCCTACTATGCCAGCTTTGGGTATCATGTGACAAATTTTTTCGCACCT 1164

Qy      361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db     1165 AGCAGCCGCTTTGGAACACCTGATGACCTTAAATCTTTGATAGACAAAGCTCATGAGCTA 1224

Qy      381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db     1225 GGTCTGGTTGTTCTGATGGATATTGTGCACAGCCATGCATCAAAAAACACACTGGATGGC 1284

Qy      401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
Db     1285 CTGGACATGTTTGATGGTACTGATGGTCAATATTTCCACTCTGGATCGCGTGGTTATCAT 1344

Qy      421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
Db     1345 TGGATGTGGGATTCTCGTCTTTTCAATTACGGAAGCTGGGAAGTGCTTAGGTATCTTCTT 1404

Qy      441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db     1405 TCCAACGCGAGATGGTGGCTGGAAGAATACAAGTTTGATGGGTTCAGATTTGATGGTGTG 1464

Qy      461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db     1465 ACTTCCATGATGTACACTCATCATGGACTGCAGGTCGAATTTACTGGGAATTACAATGAG 1524

Qy      481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
Db     1525 TACTTTGGATATTCTACTGATGTTGACGCTGTGGTCTATCTAATGCTGGTGAACGATTTG 1584

Qy      501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db     1585 ATTCATGGGCTATACCCTGAGGCTATTGTTGTCGGCGAAGATGTTAGCGGGATGCCAGCT 1644

Qy      521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db     1645 TTTTGCGTTCCTGTCGAAGACGGTGGTGTGGGTTTTGACTACCGTCTACACATGGCAGTG 1704

Qy      541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db     1705 GCAGATAAATGGATTGAGCTTCTTAAGAAGAGAGACGAGGACTGGCAGGTTGGTGATATA 1764

Qy      561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db     1765 ACTTTCACGCTTACCAACAGGAGGTGGGGAGAAAAATGTGTCGTCTATGCAGAGAGTCAT 1824

Qy      581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
Db     1825 GATCAAGCCCTTGTTGGAGACAAAACGATAGCTTTCTGGCTAATGGATAAGGACATGTAT 1884

Qy      601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db     1885 GATTTCATGGCCGTTGATAGACAGGCCACTCCGCGTGTAGACCGTGGGATTGCTTTACAC 1944

Qy      621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
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Db       1945 AAAATGATCCGTCTCATTACGATGGGATTGGGTGGAGAAGGATACCTCAATTTCATGGGA 2004

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              |||||||||||||||||||||||||||||||||||||||||      :::||||||||   |||
Db       2005 AACGAATTTGGACACCCAGAATGGATCGACTTCCCAAGGACCGACCAGCACCTTCCTGAT 2064

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
               |||   ||||||   ||||||      ||||||||||||||||||||||||||||||||
Db       2065 GGCAGAGTCATCGCTGGGAATAATGGTAGTTATGATAAATGCCGACGTAGGTTTGATCTG 2124

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              |||||||||||||||||||||||||   |||||||||||||||||||||    ||||||
Db       2125 GGAGATGCAGAATATCTTAGATACCATGGACTACAAGAGTTTGATCGAGCAATGCAAAAT 2184

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||:::   |||   ||||||||||||||||||||||:::||||||||||||||||||
Db       2185 CTAGAGGAGACGTATGGTTTCATGACTTCAGAGCACCAGTACATATCCCGCAAGGATGAA 2244

Qy        721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
              |||||||||:::||||||||||||:::|||||||||:::||||||||||||||||||||
Db       2245 GGAGACAGAGTCATTGTATTCGAGAGAGGTAACTTGCTCTTCGTCTTCAACTTCCACTGG 2304

Qy        741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
              |||   ||||||||||||||||||||||   |||      ||||||||||||||||:::
Db       2305 ACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAAGTACAAAATCGTT 2364

Qy        761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
              ||||||||||||:::   |||||||||||||||   |||:::|||    :::||||||:::
Db       2365 TTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGACTCCGCGGAGTTT 2424

Qy        781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
              ||||||    :::|||   :::||||||||||||   |||    ||||||||||||||||||
Db       2425 TTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGTGTATGCACCGTGC 2484

Qy        801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
              :::||||||||||||||||||    ||||||   ::::::::::::|||
Db       2485 AGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGAACGTTCTTCTCTT 2544

Qy        821 GluGluValAlaAlaValGluGluValVal 830
                    :::       :::   |||   |||
Db       2545 GTCCCCATAGGCCTGTTACCCGAAGATGTT 2574
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RESULT 4
US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
;  APPLICANT:  Allen, Steve
;  APPLICANT:  Beckles, Diane M.
;  APPLICANT:  Butler, Karla
;  APPLICANT:  Pearlstein, Rich
;  TITLE OF INVENTION:  Starch Branching Enzyme IIb
;  FILE REFERENCE:  BB1439 US NA
;  CURRENT APPLICATION NUMBER: US/09/792,127
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER:  60/186098
;  PRIOR FILING DATE:  2000-03-01
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  Microsoft Office 97
; SEQ ID NO 3
;   LENGTH: 3039
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-792-127-3

Alignment Scores:
Pred. No.:              0               Length:         3039
Score:                  3037.00         Matches:        558
Percent Similarity:     81.52%          Conservative:   95
Best Local Similarity:  69.66%          Mismatches:     102
Query Match:            68.02%          Indels:         46
DB:                     10              Gaps:           8
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US-10-056-454A-15_COPY_49_882 (1-834) x US-09-792-127-3 (1-3039)

Qy         17 SerGlyLysValLeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGln 36
              |||||:::|||:::::|||                |||     |||     |||
Db        264 TCCGGGGAGGTGATGATCCCT------------GACGGCGGTAGTGGCGGAACA------ 305

Qy         37 PheGluPheThrGluThrSerProGluAsnSerProAlaSerThrAspValAspSerSer 56
                                                  |||   |||   |||
Db        306 ----------------------------------CCGCCTTCCATCGAC------------ 320

Qy         57 ThrMetGluHisAlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAsp 76
                                   :::::   ::::::||||||::::::
Db        321 ---------------GGTCCCGTTCAGTTCGATTCTGATGATCTGAAG------------ 353

Qy         77 LeuThrGlySerValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGly 96
                          |||      :::|||      :::|||      ||||||:::::|||||
Db        354 ------------GTTCCATTCATTGATGATGAAACAAGC------CTACAGGATGGAGGT 395

Qy         97 Lys------LeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGlu 114
              :::      :::      |||:::|||         ||||||||          ::::::
Db        396 GAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTTAGTGAAGAAATTGATGCTGAAGAC 455

Qy        115 SerAspArgIle------------------ArgGlu------ArgGlyIleProProPro 126
              :::   |||:::                  ||||||      |||   :::|||||||||
Db        456 ACGAGCAGAATGGACAAAGAATCATCTACGAGGGAGAAATTACGCATTCTGCCACCACCG 515

Qy        127 GlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeu 146
              |||   ||||||:::|||||||||||||||||||   |||   :::::::::   |||||
Db        516 GGAAATGGACAGCAAATATACGAGATTGACCCAACGCTCCGAGACTTTAAGTACCATCTT 575

Qy        147 AspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGly 166
              :::||||||||||||   |||:::::::::|||      ||||||::::::|||||||||
Db        576 GAGTATCGATATAGCCTATACAGGAGAATACGTTCAGACATTGATGAACACGAAGGAGGC 635

Qy        167 LeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIle 186
              ::::::   ||||||||||||||||||||||   ||||||   ||||||||||   ||||||
Db        636 ATGGATGTATTTTCCCGCGGTTACGAGAAGTTTGGATTTATGCGCAGCGCTGAAGGTATC 695

Qy        187 ThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsn 206
              ||||||||||||||||||   ||||||   ||||||||||||:::||||||||||||||
Db        696 ACTTACCGAGAATGGGCTCCTGGAGCAGATTCTGCAGCATTAGTTGGCGACTTCAACAAT 755

Qy        207 TrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeu 226
              ||||||      |||||||||   ||||:::::||:::   ||||||||||||||||||||
Db        756 TGGGATCCAAATGCAGACCATATGAGCAAAAATGACCTTGGTGTTTGGGAGATTTTTCTG 815

Qy        227 ProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMet 246
              |||||||||   ||||||||||||   ||||||||||||||||||||||||:::||||||
Db        816 CCAAACAATGCAGATGGTTCGCCACCAATTCCTCACGGCTCACGGGTGAAGGTGAGAATG 875

Qy        247 AspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeu 266
              |||||||||||||||:::|||||||||||||||||||||||||   ||||||:::|||
Db        876 GATACTCCATCTGGGATAAAGGATTCAATTCCTGCTTGGATCAAGTACTCCGTGCAGACT 935

Qy        267 ProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIle 286
              |||   :::||||||||||||||||||||:::|||||||||||||||||||:::|||:::
Db        936 CCAGGAGATATACCATACAATGGAATATATTATGATCCTCCCGAAGAGGAGAAGTATGTA 995

Qy        287 PheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGly 306
              |||:::|||||||||:::||||||||||||||||||||||||||||:::|||:::|||
Db        996 TTCAAGCATCCTCAACCTAAACGACCAAAATCATTGCGGATATATGAAACACATGTTGGC 1055

Qy        307 MetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuPro 326
              |||||||||||||||||||||||||||:::|||   |||||||||||||||||||||||
Db       1056 ATGAGTAGCCCGGAACCAAAGATCAACACATATGCAAACTTCAGGGATGAGGTGCTTCCA 1115

Qy        327 ArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyr 346
              |||||||||:::|||||||||||||||:::|||||||||||||||||||||||||||||
Db       1116 AGAATTAAAAGACTTGGATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATAC 1175

Qy        347 TyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThr 366
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1176 TATGGAAGCTTTGGGTACCATGTTACCAATTTCTTTGCACCAAGTAGCCGTTTTGGGTCC 1235
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Qy    367 ProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMet 386
Db   1236 CCAGAAGATTTAAAATCTTTGATTGATAGAGCTCACGAGCTTGGCTTGGTTGTCCTCATG 1295

Qy    387 AspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCys 406
Db   1296 GATGTTGTTCACAGTCACGCGTCAAATAATACCTTGGACGGGTTGAATGGTTTTGATGGC 1355

Qy    407 ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArg 426
Db   1356 ACGGATACACATTACTTCCATGGCGGTTCACGGGGCCATCACTGGATGTGGGATTCCCGT 1415

Qy    427 LeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrp 446
Db   1416 GTGTTTAACTATGGGAATAAGGAAGTTATAAGGTTTCTACTTTCCAATGCAAGATGGTGG 1475

Qy    447 LeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrIle 466
Db   1476 CTAGAGGAGTATAAGTTTGATGGTTTCCGATTCGATGGCGCGACCTCCATGATGTATACC 1535

Qy    467 HisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThr 486
Db   1536 CATCATGGATTACAAGTAACCTTTACAGGAAGCTACCATGAATATTTTGGCTTTGCCACT 1595

Qy    487 AspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhePro 506
Db   1596 GATGTAGATGCGGTCGTTTACTTGATGCTGATGAATGATCTAATTCATGGGTTTTATCCT 1655

Qy    507 AspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProValGln 526
Db   1656 GAAGCCGTAACTATCGGTGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCAA 1715

Qy    527 GluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGlu 546
Db   1716 GTTGGTGGGGTTGGTTTTGACTATCGCTTACATATGGCTGTTGCCGACAAATGGATTGAA 1775

Qy    547 LeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsn 566
Db   1776 CTTCTCAAAGGAAACGATGAAGCTTGGGAGATGGGTAATATTGTGCACACACTAACAAAC 1835

Qy    567 ArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGly 586
Db   1836 AGAAGGTGGCTGGAAAAGTGTGTTACTTATGCTGAAAGTCACGATCAAGCACTTGTTGGA 1895

Qy    587 AspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAsp 606
Db   1896 GACAAGACTATTGCATTCTGGTTGATGGACAAGGATATGTATGATTTCATGGCGCTGAAC 1955

Qy    607 ArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuVal 626
Db   1956 GGACCTTCGACGCCTAATATTGATCGTGGAATAGCACTGCATAAAATGATTAGACTTATC 2015

Qy    627 ThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisPro 646
Db   2016 ACAATGGGTCTAGGAGGAGAGGGTTATCTTAACTTTATGGGAAATGAGTTCGGGCATCCT 2075

Qy    647 GluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGly 666
Db   2076 GAATGGATAGACTTTCCAAGAGGCCCACAAGTACTTCCAAGTGGTAAGTTCATCCCAGGA 2135

Qy    667 AsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeu 686
Db   2136 AACAACAACAGTTACGACAAATGCCGTCGAAGATTTGACCTGGGTGATGCAGAATTTCTT 2195

Qy    687 ArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGlu 706
Db   2196 AGGTATCATGGTATGCAGCAGTTTGATCAGGCAATGCAGCATCTTGAGGAAAAATATGGT 2255

Qy    707 PheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleVal 726
Db   2256 TTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTG 2315

Qy    727 PheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAsp 746
Db   2316 TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAGTAGCTATTTCGAC 2375

Qy    747 TyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspPro 766
Db   2376 TACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGA 2435

Qy    767 LeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrp 786
Db   2436 CTCTTTGGTGGATTTGGTAGGATCCATCACACTGCAGAGCACGTCACTTCTGACTGCCAA 2495

Qy    787 TyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyr 806
Db   2496 CATGACAACAGGCCCCATTCATTCTCAGTGTACACTCCTAGCAGAACCTGTGTTGTCTAT 2555

Qy    807 Ala 807
Db   2556 GCT 2558
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RESULT 5
US-09-792-127-1
; Sequence 1, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIb
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-1

Alignment Scores:

Pred. No.:	0	Length:	2559
Score:	2997.00	Matches:	532
Percent Similarity:	88.13%	Conservative:	77
Best Local Similarity:	76.99%	Mismatches:	82
Query Match:	67.12%	Indels:	0
DB:	10	Gaps:	0

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-792-127-1 (1-2559)

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Qy    117 ArgIleArgGluArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAsp 136
Db      6 AGGGAGAAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGAC 65

Qy    137 ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeu 156
Db     66 CCAACGCTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTATACAGGAGAATA 125

Qy    157 ArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLys 176
Db    126 CGTTCAGACATTGATGAACACGAAGGAGGCATGGATGTATTTTCCCGCGGTTACGAGAAG 185

Qy    177 MetGlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGln 196
Db    186 TTTGGATTTATGCGCAGCGCTGAAGGTATCACTTACCGAGAATGGGCTCCTGGAGCAGAT 245

Qy    197 SerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArg 216
Db    246 TCTGCAGCATTAGTTGGCGACTTCAACAATTGGGATCCAAATGCAGACCATATGAGCAAA 305
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Qy      217 AsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIle 236
Db      306 AATGACCTTGGTGTTTGGGAGATTTTTCTGCCAAACAATGCAGATGGTTCGCCACCAATT 365

Qy      237 ProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIle 256
Db      366 CCTCACGGCTCACGGGTGAAGGTGAGAATGGATACTCCATCTGGGATAAAGGATTCAATT 425

Qy      257 ProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHis 276
Db      426 CCTGCTTGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATACAATGGAATATAT 485

Qy      277 TyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysProLys 296
Db      486 TATGATCCTCCCGAAGAGGAGAAGTATGTATTCAAGCATCCTCAACCTAAACGACCAAAA 545

Qy      297 SerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSer 316
Db      546 TCATTGCGGATATATGAAACACATGTTGGCATGAGTAGCCCGGAACCAAAGATCAACACA 605

Qy      317 TyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeu 336
Db      606 TATGCAAACTTCAGGGATGAGGTGCTTCCAAGAATTAAAAGACTTGGATACAATGCAGTG 665

Qy      337 GlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsn 356
Db      666 CAAATAATGGCAATCCAAGAGCACTCATACTATGGAAGCTTTGGGTACCATGTTACCAAT 725

Qy      357 PhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLys 376
Db      726 TTCTTTGCACCAAGTAGCCGTTTTGGGTCCCCAGAAGATTTAAAATCTTTGATTGATAGA 785

Qy      377 AlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsn 396
Db      786 GCTCACGAGCTTGGCTTGGTTGTCCTCATGGATGTTGTTCACAGTCACGCGTCAAATAAT 845

Qy      397 ThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAla 416
Db      846 ACCTTGGACGGGTTGAATGGTTTTGATGGCACGGATACACATTACTTCCATGGCGGTTCA 905

Qy      417 ArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeu 436
Db      906 CGGGGCCATCACTGGATGTGGGATTCCCGTGTGTTTAACTATGGGAATAAGGAAGTTATA 965

Qy      437 ArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArg 456
Db      966 AGGTTTCTACTTTCCAATGCAAGATGGTGGCTAGAGGAGTATAAGTTTGATGGTTTCCGA 1025

Qy      457 PheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGly 476
Db     1026 TTCGATGGCGCGACCTCCATGATGTATACCCATCATGGATTACAAGTAACCTTTACAGGA 1085

Qy      477 AsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeu 496
Db     1086 AGCTACCATGAATATTTTGGCTTTGCCACTGATGTAGATGCGGTCGTTTACTTGATGCTG 1145

Qy      497 ValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSer 516
Db     1146 ATGAATGATCTAATTCATGGGTTTTATCCTGAAGCCGTAACTATCGGTGAAGATGTTAGT 1205

Qy      517 GlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeu 536
Db     1206 GGAATGCCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGGTTGGTTTTGACTATCGCTTA 1265

Qy      537 HisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArg 556
Db     1266 CATATGGCTGTTGCCGACAAATGGATTGAACTTCTCAAAGGAAACGATGAAGCTTGGGAG 1325

Qy      557 ValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyr 576
Db     1326 ATGGGTAATATTGTGCACACACTAACAAACAGAAGGTGGCTGGAAAAGTGTGTTACTTAT 1385

Qy      577 AlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAsp 596
Db     1386 GCTGAAAGTCACGATCAAGCACTTGTTGGAGACAAGACTATTGCATTCTGGTTGATGGAC 1445

Qy      597 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGly 616
Db     1446 AAGGATATGTATGATTTCATGGCGCTGAACGGACCTTCGACGCCTAATATTGATCGTGGA 1505

Qy      617 IleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeu 636
Db     1506 ATAGCACTGCATAAAATGATTAGACTTATCACAATGGGTCTAGGAGGAGAGGGTTATCTT 1565

Qy      637 AsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGln 656
Db     1566 AACTTTATGGGAAATGAGTTCGGGCATCCTGAATGGATAGACTTTCCAAGAGGCCCACAA 1625

Qy      657 HisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArg 676
Db     1626 GTACTTCCAAGTGGTAAGTTCATCCCAGGAAACAACAACAGTTACGACAAATGCCGTCGA 1685

Qy      677 ArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArg 696
Db     1686 AGATTTGACCTGGGTGATGCAGAATTTCTTAGGTATCATGGTATGCAGCAGTTTGATCAG 1745

Qy      697 ProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSer 716
Db     1746 GCAATGCAGCATCTTGAGGAAAAATATGGTTTTATGACATCAGACCACCAGTACGTATCT 1805

Qy      717 ArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPhe 736
Db     1806 CGGAAACATGAGGAAGATAAGGTGATCGTGTTTGAAAAAGGGGACTTGGTATTTGTGTTC 1865

Qy      737 AsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLys 756
Db     1866 AACTTCCACTGGAGTAGTAGCTATTTCGACTACCGGGTCGGCTGTTTAAAGCCTGGGAAG 1925

Qy      757 TyrLysValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHis 776
Db     1926 TACAAGGTGGTCTTAGACTCGGACGCTGGACTCTTTGGTGGATTTGGTAGGATCCATCAC 1985

Qy      777 AsnAlaGluTyrPheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetVal 796
Db     1986 ACTGCAGAGCACGTCACTTCTGACTGCCAACATGACAACAGGCCCCATTCATTCTCAGTG 2045

Qy      797 TyrAlaProCysLysThrAlaValValTyrAla 807
Db     2046 TACACTCCTAGCAGAACCTGTGTTGTCTATGCT 2078
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RESULT 6
US-10-254-534-3
; Sequence 3, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393

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;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-10-254-534-3

Alignment Scores:
Pred. No.:               3.12e-274     Length:         1393
Score:                   2462.00       Matches:        454
Percent Similarity:      98.49%        Conservative:   3
Best Local Similarity:   97.84%        Mismatches:     7
Query Match:             55.14%        Indels:         0
DB:                      9             Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x US-10-254-534-3 (1-1393)

Qy        226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGT 61

Qy        246 MetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAG 121

Qy        266 LeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyr 285
              |||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db        122 CTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTAT 181

Qy        286 IlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIle 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATT 241

Qy        306 GlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeu 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTT 301

Qy        326 ProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSer 345
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        302 CCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 361

Qy        346 TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly 365
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        362 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGAA 421

Qy        366 ThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeu 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 481

Qy        386 MetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 541

Qy        406 CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSer 425
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCC 601

Qy        426 ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrp 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 661

Qy        446 TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 465
              ||||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 TGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTAT 721

Qy        466 IleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla 485
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 781

Qy        486 ThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 ACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTC 841

Qy        506 ProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 525
              |||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db        842 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTT 901

Qy        526 GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIle 545
              |||:::|||||||||||||||||||||||||||||||||||||||||||||   |||
Db        902 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 961

Qy        546 GluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThr 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1021

Qy        566 AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1081

Qy        586 GlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeu 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 1141

Qy        606 AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeu 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 GATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 1201

Qy        626 ValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHis 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 1261

Qy        646 ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIlePro 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 1321

Qy        666 GlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyr 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 1381

Qy        686 LeuArgTyrArg 689
              ||||||||||||
Db       1382 TTAAGATACCGT 1393
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RESULT 7
US-09-918-624B-30
; Sequence 30, Application US/09918624B
; Publication No. US20030113720A1
; GENERAL INFORMATION:
;  APPLICANT: Schebye, Xiao Min
;  APPLICANT:  Sornasse, Thierry
;  TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
;  FILE REFERENCE: PA-0033 US
;  CURRENT APPLICATION NUMBER: US/09/918,624B
;  CURRENT FILING DATE:  2002-12-03
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;  PRIOR APPLICATION NUMBER: 60/222,470
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PERL Program
; SEQ ID NO 30
;   LENGTH: 2955
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
US-09-918-624B-30

Alignment Scores:
Pred. No.:                5.26e-227      Length:          2955
Score:                    2058.00        Matches:         383
Percent Similarity:       71.82%         Conservative:    119
Best Local Similarity:    54.79%         Mismatches:      176
Query Match:              46.09%         Indels:          22
DB:                       9              Gaps:            7

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-918-624B-30 (1-2955)

Qy      119 ArgGluArgGlyIleProPro------------ProGlyLeuGlyGlnLysIleTyrGlu 134
Db      134 AGGCGGCGCTCAATGCCGCCCTGGCTGACGTGCCCGAA-CTGGCC---AGACTCCTGGAG 189

Qy      135 IleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLys 154
Db      190 ATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTTAGC 249

Qy      155 LysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyr 174
Db      250 CAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGCTAT 309

Qy      175 GluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyr---ArgGluTrpAlaLeu 193
Db      310 GAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTCCAAAGAATGGGCCCCG 369

Qy      194 GlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIle 213
Db      370 GGAGCAGAAGGAGTTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTACCCA 429

Qy      214 MetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySer 233
Db      430 TACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAATCT 489

Qy      234 ProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGly---Val 252
Db      490 GTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAGATC 549

Qy      253 LysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyr 272
Db      550 TTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAATTAT 609

Qy      273 AsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgPro 292
Db      610 GATTGGATACACTGGGATCCA------GAACACTCATATGAGTTTAAGCATTCCAGACCA 663

Qy      293 LysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluPro 312
Db      664 AAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAAGGA 723

Qy      313 LysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGly 332
Db      724 AAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTTGGA 783

Qy      333 TyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyr 352
Db      784 TACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTTAC 843

Qy      353 HisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSer 372
Db      844 CAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAAGAA 903

Qy      373 LeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHis 392
Db      904 CTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGCCAT 963

Qy      393 AlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe 412
Db      964 GCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTATTTT 1023

Qy      413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
Db     1024 CATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCCAGC 1083

Qy      433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPhe 452
Db     1084 TGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGCTTT 1143

Qy      453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
Db     1144 GATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGTCAA 1203

Qy      473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
Db     1204 GGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTGACT 1263

Qy      493 TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly 512
Db     1264 TACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATAGCT 1323

Qy      513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPhe 532
Db     1324 GAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGTTTT 1383

Qy      533 AspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLys---Arg 551
Db     1384 GACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTTAAA 1443

Qy      552 AspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
Db     1444 GATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTTGAA 1503

Qy      572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
Db     1504 AAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTGGCA 1563

Qy      592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
Db     1564 TTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACTCCA 1623

Qy      612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
Db     1624 GTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTTGGT 1683

Qy      632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPhe 651
Db     1684 GGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGCATCCTGAATGGTTAGACTTC 1743

Qy      652 ProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyr 671
Db     1744 CCAAGA--------------------------------AAAGGAAATAATGAGAGTTAC 1770

Qy      672 AspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeu 691
Db     1771 CATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTCCTA 1830

Qy      692 GlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGlu 711
Db     1831 AATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCTCCA 1890

Qy      712 HisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsn 731
Db     1891 CAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCAGGT 1950
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Qy        732 LeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCys 751
Db       1951 CTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGAACA 2010

Qy        752 LeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGlyGlyPhe 771
Db       2011 GCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGGCAT 2070

Qy        772 GlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrpTyrAspAspArgPro 791
Db       2071 CAGAGACTGGACCACAGCACTGACTTTTTTCTGAGGCTTTTGAACATAATGGGCGTCCC 2130

Qy        792 ArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAsp 810
Db       2131 TATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATCCTTCAGAATGTGGAT 2187
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RESULT 8
US-09-880-107-2148
; Sequence 2148, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2148
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

Alignment Scores:

Pred. No.:	5.26e-227	Length:	2955
Score:	2058.00	Matches:	383
Percent Similarity:	71.82%	Conservative:	119
Best Local Similarity:	54.79%	Mismatches:	176
Query Match:	46.09%	Indels:	22
DB:	10	Gaps:	7

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-880-107-2148 (1-2955)

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Qy        119 ArgGluArgGlyIleProPro-----------ProGlyLeuGlyGlnLysIleTyrGlu 134
Db        134 AGGCGGCGCTCAATGCCGCCCTGGCTGACGTGCCCGAA-CTGGCC---AGACTCCTGGAG 189

Qy        135 IleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLys 154
Db        190 ATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTTAGC 249

Qy        155 LysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyr 174
Db        250 CAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGCTAT 309

Qy        175 GluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyr---ArgGluTrpAlaLeu 193
Db        310 GAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTCCAAAGAATGGGCCCCG 369

Qy        194 GlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIle 213
Db        370 GGAGCAGAAGGAGTTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTACCCA 429

Qy        214 MetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySer 233
Db        430 TACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAATCT 489

Qy        234 ProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGly---Val 252
Db        490 GTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAGATC 549

Qy        253 LysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyr 272
Db        550 TTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAATTAT 609

Qy        273 AsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgPro 292
Db        610 GATTGGATACACTGGGATCCA------GAACACTCATATGAGTTTAAGCATTCCAGACCA 663

Qy        293 LysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluPro 312
Db        664 AAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAAGGA 723

Qy        313 LysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGly 332
Db        724 AAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTTGGA 783

Qy        333 TyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyr 352
Db        784 TACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTTAC 843

Qy        353 HisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSer 372
Db        844 CAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAAGAA 903

Qy        373 LeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHis 392
Db        904 CTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGCCAT 963

Qy        393 AlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe 412
Db        964 GCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTATTTT 1023

Qy        413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
Db       1024 CATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCCAGC 1083

Qy        433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPhe 452
Db       1084 TGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGCTTT 1143

Qy        453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
Db       1144 GATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGTCAA 1203

Qy        473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
Db       1204 GGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTGACT 1263

Qy        493 TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly 512
Db       1264 TACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATAGCT 1323

Qy        513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPhe 532
Db       1324 GAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGTTTT 1383

Qy        533 AspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLys---Arg 551
Db       1384 GACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTTAAA 1443

Qy        552 AspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
Db       1444 GATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTTGAA 1503
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Qy        572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
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Db       1504 AAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTGGCA 1563

Qy        592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
              ||||||||||||||     :::||||||       |||::::::       |||   |||
Db       1564 TTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACTCCA 1623

Qy        612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
              :::||||||||||||||    ||||||||||||||||||||:::|||   |||||||||
Db       1624 GTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTTGGT 1683

Qy        632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPhe 651
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1684 GGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGGCATCCTGAATGGTTAGACTTC 1743

Qy        652 ProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyr 671
              ||||||                                      ||||||    ||||||
Db       1744 CCAAGA--------------------------------AAAGGAAATAATGAGAGTTAC 1770

Qy        672 AspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeu 691
                       |||||::::|||   |||   |||    :::   ||||||||:::    |||
Db       1771 CATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTCCTA 1830

Qy        692 GlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGlu 711
                       |||||||||   |||     ||||||::::::|||   ::::::   :::
Db       1831 AATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCTCCA 1890

Qy        712 HisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsn 731
                 ::::::|||   |||   ||||||:::::::::|||    |||||||:::
Db       1891 CAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCAGGT 1950

Qy        732 LeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCys 751
              |||:::|||:::||||||||||||    :::||||||||:::|||||||||:::
Db       1951 CTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGAACA 2010

Qy        752 LeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGlyGlyPhe 771
                    ||||||||:::|||:::   ||||||||||||          :::||||||
Db       2011 GCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGGCAT 2070

Qy        772 GlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrpTyrAspAspArgPro 791
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Db       2071 CAGAGACTGGACCACAGCACTGACTTTTTTCTGAGGCTTTTGAACATAATGGGCGTCCC 2130

Qy        792 ArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAsp 810
                 |||::::::||||||   |||   :::   |||::::::          ||||||
Db       2131 TATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATCCTTCAGAATGTGGAT 2187

RESULT 9
US-10-084-817-92
; Sequence 92, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
;  APPLICANT: Susan Stuart
;  APPLICANT:  Jed G. Nuchtern
;  APPLICANT:  Sharon E. Plon
;  APPLICANT:  Jason M. Shohet
;  TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
;  FILE REFERENCE: PA-0046 US
;  CURRENT APPLICATION NUMBER: US/10/084,817
;  CURRENT FILING DATE:  2002-02-25
;  PRIOR APPLICATION NUMBER: 60/270,784
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 365
;  SOFTWARE: PERL Program
; SEQ ID NO 92
;   LENGTH: 2994
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CB1
US-10-084-817-92

  Alignment Scores:
  Pred. No.:              5.37e-227     Length:         2994
  Score:                  2058.00       Matches:        396
  Percent Similarity:     68.90%        Conservative:   129
  Best Local Similarity:  51.97%        Mismatches:     199
  Query Match:            46.09%        Indels:         39
  DB:                     9             Gaps:           10

US-10-056-454A-15_COPY_49_882 (1-834) x US-10-084-817-92 (1-2994)

Qy         56 SerThrMetGluHisAlaSerGlnIleLysThrGluAsnAspAspValGluProSerSer 75
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Db         24 TCCGCCCTAGCCGCCGCGTCCCAGCTAGAGCTCCAGCGC---CCGCTCAGGCCCCACTCG 80

Qy         76 AspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGly 95
                 |||:::|||   :::      ||||||             :::|||:::
Db         81 ACCCTCTCGGGC---CTCGGCTACTTGGACTGCGGCGGAATATGGCGGCTCCGATGACTC 137

Qy         96 GlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSer 115
                 :::|||         |||
Db        138 CCGCGGCTCGGCCCGAGGACTACG------------------------------------ 161

Qy        116 AspArgIleArgGluArgGlyIleProPro------------ProGlyLeuGlyGlnLys 131
                    |||   |||   :::||||||             |||   |||      :::
Db        162 ---------AGGCGGCGCTCAATGCCGCCCTGGCTGACGTGCCCGAA-CTGGCC---AGA 208

Qy        132 IleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSer 151
              :::   ||||||||||||   |||      |||                  ||||||
Db        209 CTCCTGGAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAG 268

Qy        152 GlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSer 171
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Db        269 CAGTTTAGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCC 328

Qy        172 ArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyr---ArgGlu 190
              ||||||||||||         |||      |||   |||   |||      |||   ::::|||
Db        329 AGAGGCTATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAA 388

Qy        191 TrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsn 210
              ||||||   ||||||:::         ||||||||||||   |||:::
Db        389 TGGCCCCGGGAGCAGAAGGAGTTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTT 448

Qy        211 AlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnVal 230
              :::               :::   ::::::|||   ||||||::::::::::|||
Db        449 TCGTACCCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAG 508

Qy        231 AspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSer 250
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Db        509 AATAAATCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGC 568

Qy        251 Gly---ValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
              |||   :::      |||   |||      |||   ::::::   |||
Db        569 GGAGAGATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAAT 628

Qy        270 IleProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePheGlnHis 289
              :::   |||:::   ||||||:::||||||      |||      |||   |||:::|||
Db        629 GTGAATTATGATTGGATACACTGGGATCCA------GAACACTCATATGAGTTTAAGCAT 682

Qy        290 ProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSer 309
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Db        683 TCCAGACCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCC 742

Qy        310 ProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLys 329
                 |||   |||:::   ||||||   :::|||         |||||||||||||||||
Db        743 CATGAAGGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAA 802

Qy        330 LysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSer 349
                 ||||||||||||   :::||||||||||||   ||||||:::||||||||||||
Db        803 GGCCTTGGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGC 862

Qy        350 PheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAspAsp 369
              |||||||||   :::|||:::|||||||||   |||||||||:::||||||||||:::::
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Db     863 TTTGGTTACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAG 922

Qy     370 LeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIleVal 389
           |||:::   |||:::|||   ||||||   :::||||||:::||||||:::|||:::|||
Db     923 CTACAAGAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTA 982

Qy     390 HisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSer 409
           |||||||||||||||   |||:::   ||||||||||||||||||||   |||||||||
Db     983 CACAGCCATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCC 1042

Qy     410 CysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsn 429
           ||||||||||||||||||   ||||||   |||   :::||||||||||||||||||
Db    1043 TGTTATTTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCC 1102

Qy     430 TyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAla 449
           |||   :::||||||||||||:::||||||||||||   |||||||||||||:::
Db    1103 TACTCCAGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAA 1162

Qy     450 PheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGly 469
           ::::::||||||||||||||||||||||||||||||:::|||   |||||||||
Db    1163 TATCGCTTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGA 1222

Qy     470 LeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAsp 489
           :::       ||||||:::|||:::|||   |||||||||||||||   |||   |||
Db    1223 GTGGGTCAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGAT 1282

Qy     490 AlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIle 509
           |||:::   ||||||||||||   |||   |||:::|||   |||   ||||||:::|||
Db    1283 GCCTTGACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATA 1342

Qy     510 ThrIleGlyGluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGly 529
           ||||||   ||||||||||||||||||||||         |||   |||:::   :::||||||
Db    1343 ACAATAGCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGG 1402

Qy     530 ValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLys 549
              ||||||||||||||||||   |||||||||   ||||||   |||:::|||||||||
Db    1403 GGTGGTTTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAA 1462

Qy     550 Lys---ArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArg 568
           :::   :::||||||||||||   :::||||||||||||:::||||||||||||||||||
Db    1463 GAGTTTAAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGC 1522

Qy     569 TrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLys 588
           :::   ||||||||:::::::||||||||||||||||||||||||||||||||||||||||
Db    1523 TACCTTGAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAG 1582

Qy     589 ThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgPro 608
           ::::::|||||||||||||||||||   :::||||||   |||::::::      |||
Db    1583 TCGCTGGCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCT 1642

Qy     609 SerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMet 628
              |||   :::|||||||||||||||   ||||||||||||||||||||||:::|||
Db    1643 TTTACTCCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCAT 1702

Qy     629 GlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrp 648
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1703 GGGCTTGGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGGCATCCTGAATGG 1762

Qy     649 IleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGln 668
           :::||||||||||||||                                 ||||||
Db    1763 TTAGACTTCCCAAGA---------------------------------AAAGGAAATAAT 1789

Qy     669 PheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyr 688
              ||||||         |||||::::|||   |||   |||   :::   |||||||||
Db    1790 GAGAGTTACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTAC 1849

Qy     689 ArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMet 708
           :::   |||      |||||||||   |||      ||||||::::::|||   ::::::
Db    1850 AAGTTCCTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTT 1909

Qy     709 ThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGlu 728
              :::            ::::::|||   |||   ||||||::::::::::|||   ||||||
Db    1910 GCAGCTCCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAA 1969

Qy     729 LysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArg 748
           :::      |||:::|||:::||||||||||||   :::||||||||||||:::|||||||||
Db    1970 AGAGCAGGTCTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGA 2029

Qy     749 IleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPhe 768
           :::               |||||||||:::|||:::   ||||||||||||            :::
Db    2030 GTTGGAACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATAT 2089

Qy     769 GlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrpTyrAsp 788
           ||||||         |||:::||||||:::   ::::::|||:::                  ::::::
Db    2090 GGAGGGCATCAGAGACTGGACCACAGCACTGACTTTTTTCTGAGGCTTTTGAACATAAT 2149

Qy     789 AspArgProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeu 808
              ||||||   |||::::::||||||   |||   :::   |||::::::
Db    2150 GGCCGTCCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATCCTTCAGAAT 2209

Qy     809 ValAsp 810
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Db    2210 GTGGAT 2215
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RESULT 10
US-09-770-149-955/c
; Sequence 955, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-955

Alignment Scores:

Pred. No.:	9.82e-63	Length:	602
Score:	627.00	Matches:	111
Percent Similarity:	88.11%	Conservative:	15
Best Local Similarity:	77.62%	Mismatches:	17
Query Match:	14.04%	Indels:	0
DB:	10	Gaps:	0

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-770-149-955 (1-602)

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Qy     670 SerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArg 689
           ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db     601 AGTTATGACAAATGCCGCCGCAGATTTGATCTTGGGGATGCAGATTATCTCAGATACCGC 542
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Qy        690 GlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThr 709
              |||||||||||||||||:::   ||||||:::||||||:::   |||   |||||||||
Db        541 GGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGACT 482

Qy        710 SerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLys 729
              ||||||||||||||||||||||||||||||||||||   ||||||:::|||||||||||||:::
Db        481 TCGGAGCACCAATTCATATCACGAAAAGACGAAGCAGATAGAGTAATCGTATTCGAAAGA 422

Qy        730 GlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIle 749
              |||:::|||||||||||||||||||||||||||||   ||||||   ||||||||||||
Db        421 GGTGATCTCGTCTTTGTCTTTAACTTTCACTGGACCAGCAGCTACTTTGATTACCGCATT 362

Qy        750 AlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGly 769
                 |||   ||||||||||||||||||:::   ||||||||||||||||||||||||||||
Db        361 GGTTGCTCCAAGCCTGGAAAATATAAGATCGTATTGGACTCGGACGATCCTCTCTTTGGT 302

Qy        770 GlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrpTyrAspAsp 789
              ||||||   |||:::|||      ||||||||||||||||:::::::|||   ||||||:::
Db        301 GGATTCAATAGGCTCGATCGCAAGGCAGAGTACTTCACTTATGATGGCTTATACGACGAA 242

Qy        790 ArgProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuVal 809
              ||||||   |||   |||||||||||||||||||:::|||||||||||||||||||
Db        241 CGACCCTGCTCCTTCATGGTCTATGCACCGTGTAGAACCGCCGTGGTTTATGCTTTAGCA 182

Qy        810 AspLysGlu 812
              :::   :::
Db        181 AACCACGAT 173
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RESULT 11
US-10-329-960-1
; Sequence 1, Application US/10329960
; Publication No. US20030099277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
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; NAME/KEY: misc_feature
; LOCATION: (9921)..(9921)
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; NAME/KEY: misc_feature
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; FEATURE:
; NAME/KEY: misc_feature

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;    LOCATION: (142750)..(142750)
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;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (145058)..(145058)
;    OTHER INFORMATION: n equals a, t, g or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (145171)..(145171)
;    OTHER INFORMATION: n equals a, t, g or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (145942)..(145942)
;    OTHER INFORMATION: n equals a, t, g or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (147197)..(147197)
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;    LOCATION: (150841)..(150841)
;    OTHER INFORMATION: n equals a, t, g or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (152500)..(152500)
;    OTHER INFORMATION: n equals a, t, g or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (152530)..(152530)

Alignment Scores:
Pred. No.:                6.62e-46      Length:          1830121
Score:                    530.50        Matches:         203
Percent Similarity:       41.65%        Conservative:    126
Best Local Similarity:    25.70%        Mismatches:      282
Query Match:              11.88%        Indels:          179
DB:                       9             Gaps:            36

US-10-056-454A-15_COPY_49_882 (1-834) x US-10-329-960-1 (1-1830121)

Qy       110 ThrIleIleAspGluSerAspArgIle------------ArgGluArgGlyIleProPro 125
             |||:::::   :::::::::|||:::             ||||||
Db   1436281 ACGTTATTGCCAGATGCCAATCGAATGGTGGTGATTGAGCGTGAAAGT------------ 1436328

Qy       126 ProGlyLeuGlyGlnLysIleTyrGluIleAsp--------------------------- 136
                       |||::::::|||   |||:::|||
Db   1436329 ---------GGTAAAGAAATAACGGAACTGGATTGTGTCGATGAGCGTGGATTTTTGTT 1436379

Qy       137 ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyr--------- 153
                :::::   |||   ||||||       |||:::          :::
Db   1436380 GGTGTTATTCCAAATTGTCGTCAATTTTTTGCTTATCAATTACAGGTTTTTGGGGTAAT 1436439

Qy       154 -----------------------LysLysLeuArgGluAlaIleAspLysTyrGluGly 165
                                                 :::      ||||||    |||
Db   1436440 GAAGCACAAATTATCGAAGATCCTTATCGTTTTCATCCAATGATTGACGATTTAGAACAA 1436499

Qy       166 GlyLeu---------GluAlaPheSerArgGlyTyrGluLysMetGlyPhe--------- 179
                |||            :::      |||   ||||||   :::|||
Db   1436500 TGGCTACTTTCTGAAGGATCTATGCTTCGCCCATATGAAGTGCTTGGTGCGCATTTTATG 1436559

Qy       180 ---ThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAla 198
                       :::|||:::   :::|||   ||||||      |||:::
Db   1436560 GAATGTGATGGTGTGAGCGGGGTGAATTTCCGCTTGTGGGCACCTAATGCAAGACGAGTT 1436619

Qy       199 AlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThr---ArgAsn 217
             ::::::::||||||||||||   ||||||                   |||      :::
Db   1436620 TCTATTGTAGGTGATTTCAACTATTGGGATGGTCGTCGCCACCCGATGCGTTTCCACTCG 1436679

Qy       218 GluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySer------------ 233
             :::   |||||||||||||:::|||||||||                  |||
Db   1436680 AAAAGTGGTGTTTGGGAGCTCTTTTACCAAAAGCCAGTTTAGGACAGCTCTATAAGTTT 1436739

Qy       234 -------------------------------ProAlaIleProHisGlySerArgVal 242
                                            |||   |||
Db   1436740 GAATTAATTGATTGCCATGGCAATCTTCGTTTGAAGGCCGATCCATTTGCCTTTAGTTCG 1436799

Qy       243 LysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyr 262
             ::::::|||   ||||||   |||   |||
Db   1436800 CAACTTCGCCCTGATACAGCTTCGCAAGTCAGT--------------------------- 1436832

Qy       263 SerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGlu 282
                      ||||||:::   :::                          :::   |||
Db   1436833 ------GCCTTGCCAAATGTAGTG--------------------GAAATGACTGAAGCA 1436865

Qy       283 GluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGlu 302
                :::         |||   :::|||               :::   |||||||||
Db   1436866 CGCAAAAAAGCAAACCAAGGCAACCAACCA---------------ATTTCTATTTATGAA 1436910

Qy       303 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe------ 320
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Db    1436911 GTGCATTTAGGATCTTGGCGTCGTAATTTAGAAAACAATTTTTGGCTAGATTACGATCAA 1436970
Qy        321 ---ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMet 339
Db    1436971 ATTGCTGATGAATTAATTCCTTATGTAAAAGAGATGGGCTTTACCCATATAGAATTTTTA 1437030
Qy        340 AlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAla 359
Db    1437031 CCGCTTTCTGAATTTCCGTTTGATGGTTCTTGGGGTTATCAACCACTTGGGCTTTATTCG 1437090
Qy        360 ProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGlu 379
Db    1437091 CCAACCAGTCGCTTTGGTTCACCTGAAGCCTTCCGCCGTTTAGTAAAACGTGCTCACGAA 1437150
Qy        380 LeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAsp 399
Db    1437151 GCAGGCATCAACGTGATTTTAGATTGGGTGCCAGGGCATTTCCCAAGTGATACG---CAT 1437207
Qy        400 GlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArg---Gly 418
Db    1437208 GGTTTAGTCGCATTTGATGGCACA---GCTTTGTATGAGCATGAAGACCCTCGCGAAGGC 1437264
Qy        419 TyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyr 438
Db    1437265 TATCATCAAGATTGGAATACCTTGATTTATAACTATGGGCGTAATGAGGTCAAAAATTTC 1437324
Qy        439 LeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAsp 458
Db    1437325 TTATCCAGTAATGCACTGTATTGGCTTGAACGTTTTGGCGTAGATGGTATTCGCGTGGAT 1437384
Qy        459 GlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyr 478
Db    1437385 GCTGTGGCTTCCATGATTTACCGTGATTATAGCCGTGCGGAGGGC--------------- 1437429
Qy        479 GluGluTyr------------PheGlyLeuAlaThrAspValAspAlaValValTyrLeu 494
Db    1437430 ---GAGTGGATTCCAAACCAATACGGCGGACGTGAAAATTTAGAAGCCATTGAGTTTTTA 1437486
Qy        495 MetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAsp 514
Db    1437487 AAACACACCAACTGGAAAATTCACAGCGAAATGGCGGGAGCAATTTCTATTGCGGAGGAA 1437546
Qy        515 ValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyr 534
Db    1437547 TCTACCTCTTTTGCAGGCGTAACCCACCCAAGCGAAAACGGCGGCTTGGGCTTCAATTTC 1437606
Qy        535 ArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAsp 554
Db    1437607 AAATGGAATATGGGCTGGATGAACGATACACTGGCTTATATG---AAGCTTGACCCCATT 1437663
Qy        555 TrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysVal 574
Db    1437664 TACCGC------CAATATCATCAC---------AACAAAATGACCTTTGGAATGGTGTAT 1437708
Qy        575 SerTyrAlaGlu------------------SerHisAspGlnAlaLeuValGlyAspLys 588
Db    1437709 CAATATAGCGAAAATTTTGTGCTACCACTTTCTCACGATGAAGTGGTTCACGGT------ 1437762
Qy        589 ThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgPro 608
Db    1437762 ------------------------------------------------------------ 1437762
Qy        609 SerThrSerLeuIleAspArg------GlyIleAlaLeuHisLysMetIleArgLeu--- 625
Db    1437763 AAATATTCACTTCTTGGCAAGATGCCAGGTGATACGTGGCAAAAATTCGCTAACTTGCGT 1437822
Qy        626 ------------ValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
Db    1437823 GCATATTACGGTTATATGTGGGGCTACCCAGGCAAAAAATTACTC---TTTATGGGGAAT 1437879
Qy        642 GluPheGlyHis---ProGluTrp---------------IleAspPheProArgAlaGlu 655
Db    1437880 GAATTTGCTCAAGGCAGAGAATGGAATTACGAAGAAAGTTTGGACTGGTTCTTGCTTGAT 1437939

Qy        656 GlnHisLeuSerAspGly------------------SerValIleProGlyAsnGlnPhe 669
Db    1437940 GAAAATATTGGCGGAGGCTGGCATAAAGGCGTATTGAAGCTGGTTAAAGACCTCAATCAA 1437999
Qy        670 SerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArg 689
Db    1438000 ATTTATCAAAAAAATCGACCGCTCTTTGAGCTCGACAACTCCCCA--------------- 1438044
Qy        690 GlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThr 709
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Qy        710 SerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLys 729
Db    1438084 TCTGTGCTCGCCTTTGAACGTCGCAGTTCAAACGGAGAACGTATTATTGTC--------- 1438134
Qy        730 GlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIle 749
Db    1438135 ---------------GTCAGTAACTTTACCCCTGTGCCTCGCCAC---AATTACCGCATC 1438176
Qy        750 AlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPhe--- 768
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Qy        769 ------------GlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGlu 784
Db    1438237 GGTTCAAACGTGGGCAATTTTGGTTGTGTC------GCAAGTGAACAAATCGAAAGCCAC 1438290
Qy        785 GlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaVal 804
Db    1438291 GGA------------CGAGRAAATTCGATTTCAGTGTCCATTCCGCCGTTAGCAACAGTT 1438338
Qy        805 ValTyrAlaLeuValAspLysGluGluGlu 814
Db    1438339 TATTTGAGATTGAAGACGAAATAATCCGAA 1438368
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RESULT 12
US-09-738-626-1354
; Sequence 1354, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1354
;   LENGTH: 2193
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-1354

Alignment Scores:

Pred. No.:	1.06e-48	Length:	2193
Score:	513.50	Matches:	198

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Percent Similarity:         41.07%     Conservative:   133
Best Local Similarity:      24.57%     Mismatches:     328
Query Match:                11.50%     Indels:         147
DB:                         9          Gaps:           35

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-738-626-1354 (1-2193)

Qy      71 ValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeu 90
           |||:::|||:::|||    :::|||    :::    |||    |||    |||
Db       7 GTTGACCCCGCGAGCCACATCACC------ATCCCTGAAGCAGATCTGGCCCGCCTGCGC 60

Qy      91 ------------------------------------------GlnLeuGlnGluGlyGly 96
                                                     :::    :::    |||
Db      61 CACTGCAACCATCACGATCCTCATGGATTTTATGGTTGGCATGAGACCGAAGCTGGTTCG 120

Qy      97 LysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAsp 116
              :::         :::          |||          :::||||||::::::
Db     121 GTTATCCGCACGCGCCAGGTCGGCGCGACGCAGGTTAATTTGCTTATCGACGACACCTCC 180

Qy     117 ArgIleArgGluArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAsp 136
              :::          :::   |||       :::|||        |||:::    ||||||
Db     181 CACGTC------------ATGACCCCT------ATCGGCGACGACATTTTCGCAATTGAC 222

Qy     137 ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyr---------------Ser 151
                        :::|||:::      |||||||||
Db     223 ---------TTAGGTCACCGCGAGCGCGCTGACTATCGCTTGGAAGTCACCTGGCCTGAT 273

Qy     152 GlnTyrLysLysLeuArgGluAlaIleAspLysTyr--------------------Glu 164
           |||      ::::::::          |||    |||                    |||
Db     274 CAAGAACCGCAGGTCAAG------GCTGATCCATACTACTTCCTCCCCACCGTAGGCGAG 327

Qy     165 GlyGlyLeuGluAlaPheSerArgGly---------------TyrGluLysMetGlyPhe 179
                 :::       ||||||   |||                :::|||    :::|||
Db     328 ATGGATATTTACCTCTTCTCTGAGGGACGCCATGAGCGTTTGTGGGAGATTCTCGGTGCC 387

Qy     180 Thr-----------------------ArgSerAlaThrGlyIleThrTyrArgGluTrp 191
                                        :::        |||       :::       |||
Db     388 AACATCAAGACCTACCAAACTGCGCTCGGAACAGTTCGTGGCACCGCATTTACTGTGTGG 447

Qy     192 AlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAla 211
           |||       |||      |||:::::::|||    ||||||    |||:::|||:::
Db     448 GCTCCAAACGCAATTGGCTGCGCAGTGGTCGGTGGCTTCAACGGTTGGAATGCATCCCAG 507

Qy     212 AspIleMet---ThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnVal 230
                 |||    :::          |||:::||||||:::|||:::|||
Db     508 CATCCGATGCGTTCTATGGGTGGTTCGGGTCTGTGGGAGCTGTTCATCCCAGGCATAGAG 567

Qy     231 AspGly-------------------------------------------SerProAla 235
           :::|||                                                   |||
Db     568 GAAGGCGAAGTGTACAAATTCGCCGTCCAAACCAGGGAAGGCCAACGTCGTGATAAGGCC 627

Qy     236 IleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSer 255
              |||       |||    ::::::          |||    |||    |||       |||
Db     628 GATCCGATGGCTCGTCGCGCAGAACTGGCGCCGGCAACCGGATCTATTGTCGCTTCCTCT 687

Qy     256 IleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIle 275
                    |||
Db     688 GAGTACCAGTGG-------------------------------------------------- 699

Qy     276 HisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysPro 295
                    |||       |||          |||                   ||||||
Db     700 ------CAGGATTCCGAGTGGCTGCGCGAGCGTTCCCAAACTGATCTCGCATCCAAGCCA 753

Qy     296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
              |||       :::||||||    |||:::|||
Db     754 ATGAGT------GTCTACGAGGTCCACCTCGGTTCTTGGCGCTGGGGT---------AAG 798

Qy     316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
           :::|||    :::          |||::::::       :::       |||||||||
Db     799 AACTATGAGGATTTGGCTACTGAGCTGGTTGATTACGTCGCAGATCTTGGCTACACCCAC 858

Qy     336 LeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
           ::::::    :::    :::    ||||||    :::       |||:::||||||    ||||||
Db     859 GTGGAATTCCTCCCTGTCGCAGAGCACCCCTTCGGTGGTTCCTGGGGTTACCAGGTCACC 918

Qy     356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAsp 375
           ::::::||||||:::||||||:::||||||||||||                ::::::|||:::|||
Db     919 GGCTACTACGCACCGACCTCTCGTTGGGGTACTCCAGATCAGTTCCGTGCGCTAGTCGAC 978

Qy     376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
                 |||       ||||||    |||:::||||||    |||       :::|||
Db     979 GCTTTCCACGCCCGCGGTATTGGCGTGATCATGGACTGGGTTCCTGCCCACTTCCCTAAG 1038

Qy     396 AsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHis---Ser 414
           :::             |||       ||||||       ::::::    |||    |||
Db    1039 GATGATTGG---GCTCTTGCCCCGCTTTGAT---GGCGAAGCCCTCTATGAACACCCTGAC 1092

Qy     415 GlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGlu 434
                 ||||||                |||    :::    :::|||::::::|||       |||
Db    1093 TGGAGGCGCGGCGAACAAAAGGATTGGGGCACCCTGGTCTTTGACTTCGGTCGCAACGAA 1152

Qy     435 ValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGly 454
           |||       :::|||::::::||||||    :::|||::::::    |||          ||||||
Db    1153 GTCCGCAACTTCCTCGTCGCTAATGCGTTGTACTGGATTGAAGAATTCCACATCGATGGT 1212

Qy     455 PheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPhe 474
              |||    |||    |||    ||||||:::|||:::    :::
Db    1213 CTGCGCGTCGACGCCGTGGCCTCCATGCTGTACCTCGATTACTCCCGTGAG--------- 1263

Qy     475 ThrGlyAsnTyrGlu---GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyr 493
              |||    :::|||          :::|||          ::::::::|||||||    :::
Db    1264 CACGGCGAATGGGAACCAAACATCTACGGTGGTCGCGAGAACCTCGAGGCAGTGCAGTTC 1323

Qy     494 LeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGlu 513
           |||       :::|||       :::          |||    |||    |||:::||||||    |||
Db    1324 CTGCAGGAAATGAACGCCACGGTGCTGCGACTGCACCCTGGTGCGCTCACCATCGCTGAG 1383

Qy     514 AspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPheAsp 533
           :::    :::    |||             |||          :::||||||:::||||||
Db    1384 GAATCAACTTCATGGCCTGGCGTGACCGCACCAACGTGGGACGGCGGCTTGGGATTCTCC 1443

Qy     534 TyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArg------ 551
              :::    :::|||                   :::|||          |||
Db    1444 CTCAAGTGGAACATGGGCTGGATGCACGACACCTTAGAGTACTTCTCCAAAAACCCTGTG 1503

Qy     552 AspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
                 :::          ::::::       :::|||                :::||||||
Db    1504 CACCGCGCATTCCACCACAGTGAGCTCACTTTCTCCTTGGTG---TACGCATTCTCTGAG 1560

Qy     572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
           :::    |||          |||||||||:::    :::    |||       ::::::
Db    1561 CGTTTTGTA---CTTCCGATCTCTCACGATGAAGTCGTCCACGGCAAGGGTTCCCTG--- 1614

Qy     592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
              |||                                                 ||||||
Db    1615 ---TGG-----------------------------------GACCGTATGCCTGGCGAT 1635

Qy     612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
              ::::::       |||       :::       :::                |||
Db    1636 ACGTGGAACAAGGCCGCTGGTCTTCGCACCTTCCTTGCGTACATGTGGTCACACCCAGGC 1695

Qy     632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGly---HisProGluTrpIleAsp 650
              :::       |||    |||||||||    |||||||||          ||||||
Db    1696 AAGAAG------CTGCTTTTCATGGGTCAGGAGTTTGGTCAGCGTGAAGAGTGG------ 1743

Qy     651 PheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSer 670
                       ||||||                         ::::::    |||    |||
Db    1744 ---------GCTGAAGGCCAGGGACTGCCATGGGATATTGTCGACGGCTGGCAAGGCGAG 1794

Qy     671 TyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGly 690
           |||    :::          |||                                |||
Db    1795 TACCACGAAGCCATCCGCACTCTGACC--------------------------CGCTCC 1827

Qy     691 LeuGlnGluPhe------AspArgProMetGlnTyrLeuGluAspLysTyrGluPheMet 708
           |||                |||    |||       :::    :::|||
Db    1828 CTCAACGGTGTCTACTCAGACTCCCCTGCGCTGCACACTCAGGAT-----------TTC 1875
```

```
Qy          709 ThrSerGluHisGlnPheIleSerArgLysAspGluGly---AspArgMetIleValPhe 727
                |||   |||           ::::::   |||:::     :::   ::::::  |||
Db         1876 ACCGGAGAAGGCTTCACATGGAATAAGGGCGACGACGCCACCAACAACATTTTGGCGTTC 1935

Qy          728 GluLys---------------GlyAsnLeuValPheValPheAsnPheHisTrpThrLys 742
                     :::                  ::::::   |||||||||        |||
Db         1936 ACTCGTTTCGGCAGCGACGGCTCCCAGATGCTGTGTGTATTCAACCTGTCTGGAACC--- 1992

Qy          743 SerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAsp 762
                |||      :::|||::::::              |||::::::|||:::  |||:::
Db         1993 TCCCAGCCTGAGTACCAGCTCGGTGTTGCAGCGGGTGGCGAATGGAAGCTCGTTCTCAAC 2052

Qy          763 SerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThr 782
                :::||||||      |||  |||            |||
Db         2053 ACTGATGATGCTGAATTCCTCGGT---GCAGAAAACGATATCGCTACTTCCGTTCAAGCA 2109

Qy          783 PheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThr 802
                               |||:::        |||:::   ::::::  |||     :::
Db         2110 GCAGCGACACCACGCGATAATTTCGCCTACTCACTCTCACTGCATGTCCCAGCGATGAGT 2169

Qy          803 AlaValValTyrAlaLeu 808
                |||      |||:::|||
Db         2170 GCTCAGTTCTACTCACTG 2187
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RESULT 13
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
;   LENGTH: 3309400
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

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Alignment Scores:
Pred. No.:              1.6e-43        Length:         3309400
Score:                  513.50         Matches:        198
Percent Similarity:     41.07%         Conservative:   133
Best Local Similarity:  24.57%         Mismatches:     328
Query Match:            11.50%         Indels:         147
DB:                     9              Gaps:           35
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US-10-056-454A-15_COPY_49_882 (1-834) x US-09-738-626-1 (1-3309400)

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Qy           71 ValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeu 90
                |||:::|||:::|||  :::|||      :::   |||  |||   |||
Db      1289467 GTTGACCCCGCGAGCCACATCACC------ATCCCTGAAGCAGATCTGGCCCGCCTGCGC 1289414

Qy           91 ----------------------------------------GlnLeuGlnGluGlyGly 96
                                                        :::   :::   |||
Db      1289413 CACTGCAACCATCACGATCCTCATGGATTTTATGGTTGGCATGAGACCGAAGCTGGTTCG 1289354

Qy           97 LysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAsp 116
                   :::      :::           |||           :::||||||::::::
Db      1289353 GTTATCCGCACGCGCCAGGTCGGCGCGACGCAGGTTAATTTGCTTATCGACGACACCTCC 1289294

Qy          117 ArgIleArgGluArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAsp 136
                                 :::   |||      :::|||     |||:::   ||||||
Db      1289293 CACGTC------------ATGACCCCT------ATCGGCGACGACATTTTCGCAATTGAC 1289252

Qy          137 ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyr---------------Ser 151
                            :::|||:::        |||||||||
Db      1289251 ---------TTAGGTCACCGCGAGCGCGCTGACTATCGCTTGGAAGTCACCTGGCCTGAT 1289201

Qy          152 GlnTyrLysLysLeuArgGluAlaIleAspLysTyr--------------------Glu 164
                |||      :::::::::        |||   |||                    |||
Db      1289200 CAAGAACCGCAGGTCAAG------GCTGATCCATACTACTTCCTCCCCACCGTAGGCGAG 1289147

Qy          165 GlyGlyLeuGluAlaPheSerArgGly--------------TyrGluLysMetGlyPhe 179
                      :::      ||||||  |||              :::|||   :::|||
Db      1289146 ATGGATATTTACCTCTTCTCTGAGGGACGCCATGAGCGTTTGTGGGAGATTCTCGGTGCC 1289087

Qy          180 Thr-----------------------ArgSerAlaThrGlyIleThrTyrArgGluTrp 191
                                             :::     |||      :::      |||
Db      1289086 AACATCAAGACCTACCAAACTGCGCTCGGAACAGTTCGTGGCACCGCATTTACTGTGTGG 1289027

Qy          192 AlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAla 211
                |||      |||        |||::::::|||   ||||||  |||:::|||:::
Db      1289026 GCTCCAAACGCAATTGGCTGCGCAGTGGTCGGTGGCTTCAACGGTTGGAATGCATCCCAG 1288967

Qy          212 AspIleMet---ThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnVal 230
                      |||   :::           |||:::||||||:::|||:::|||
Db      1288966 CATCCGATGCGTTCTATGGGTGGTTCGGGTCTGTGGGAGCTGTTCATCCCAGGCATAGAG 1288907

Qy          231 AspGly----------------------------------------------SerProAla 235
                :::|||                                                 |||
Db      1288906 GAAGGCGAAGTGTACAAATTCGCCGTCCAAACCAGGGAAGGCCAACGTCGTGATAAGGCC 1288847

Qy          236 IleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSer 255
                   |||         |||   ::::::        |||   |||  |||      |||
Db      1288846 GATCCGATGGCTCGTCGCGCAGAACTGGCGCCGGCAACCGGATCTATTGTCGCTTCCTCT 1288787

Qy          256 IleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIle 275
                         |||
Db      1288786 GAGTACCAGTGG------------------------------------------------ 1288775

Qy          276 HisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysPro 295
                               |||     |||         |||              ||||||
Db      1288774 ------CAGGATTCCGAGTGGCTGCGCGAGCGTTCCCAAACTGATCTCGCATCCAAGCCA 1288721

Qy          296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
                   |||      :::||||||  |||:::|||
Db      1288720 ATGAGT------GTCTACGAGGTCCACCTCGGTTCTTGGCGCTGGGGT---------AAG 1288676

Qy          316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
                :::|||   :::        |||::::::      :::     |||||||||
Db      1288675 AACTATGAGGATTTGGCTACTGAGCTGGTTGATTACGTCGCAGATCTTGGCTACACCCAC 1288616

Qy          336 LeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
                ::::::   :::   :::   ||||||  :::      |||:::||||||  ||||||
Db      1288615 GTGGAATTCCTCCCTGTCGCAGAGCACCCCTTCGGTGGTTCCTGGGGTTACCAGGTCACC 1288556

Qy          356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAsp 375
                   ::::::||||||:::||||||:::||||||||||||     ::::::||||:::|||
Db      1288555 GGCTACTACGCACCGACCTCTCGTTGGGGTACTCCAGATCAGTTCCGTGCGCTAGTCGAC 1288496

Qy          376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
                |||            ||||||  |||:::||||||   |||  :::|||
Db      1288495 GCTTTCCACGCCCGCGGTATTGGCGTGATCATGGACTGGGTTCCTGCCCACTTCCCTAAG 1288436

Qy          396 AsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHis---Ser 414
                :::            |||     ||||||      ::::::   |||  |||
```

```
Db   1288435 GATGATTGG---GCTCTTGCCCGCTTTGAT---GGCGAAGCCCTCTATGAACACCCTGAC 1288382

Qy       415 GlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGlu 434
                      ||||||              |||    :::   :::|||::::::|||         |||
Db   1288381 TGGAGGCGCGGCGAACAAAAGGATTGGGGCACCCTGGTCTTTGACTTCGGTCGCAACGAA 1288322

Qy       435 ValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGly 454
             |||        :::|||:::::|||||     :::|||:::::     |||          ||||||
Db   1288321 GTCCGCAACTTCCTCGTCGCTAATGCGTTGTACTGGATTGAAGAATTCCACATCGATGGT 1288262

Qy       455 PheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPhe 474
                |||    |||    |||    ||||||:::|||::     :::
Db   1288261 CTGCGCGTCGACGCCGTGGCCTCCATGCTGTACCTCGATTACTCCCGTGAG--------- 1288211

Qy       475 ThrGlyAsnTyrGlu---GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyr 493
                |||    :::|||             :::|||        ::::::::||||||     :::
Db   1288210 CACGGCGAATGGGAACCAAACATCTACGGTGGTCGCGAGAACCTCGAGGCAGTGCAGTTC 1288151

Qy       494 LeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGlu 513
             |||        :::|||        :::          |||    |||    |||:::||||||    |||
Db   1288150 CTGCAGGAAATGAACGCCACGGTGCTGCGACTGCACCCTGGTGCGCTCACCATCGCTGAG 1288091

Qy       514 AspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPheAsp 533
             :::    :::          |||                |||          :::||||||:::||||||
Db   1288090 GAATCAACTTCATGGCCTGGCGTGACCGCACCAACGTGGGACGGCGGCTTGGGATTCTCC 1288031

Qy       534 TyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArg------ 551
                :::    :::|||                   :::|||            |||
Db   1288030 CTCAAGTGGAACATGGGCTGGATGCACGACACCTTAGAGTACTTCTCCAAAAACCCTGTG 1287971

Qy       552 AspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
                   :::          ::::::        :::|||                :::||||||
Db   1287970 CACCGCGCATTCCACCACAGTGAGCTCACTTTCTCCTTGGTG---TACGCATTCTCTGAG 1287914

Qy       572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
             :::    |||                |||||||||:::    :::    |||          ::::::
Db   1287913 CGTTTTGTA---CTTCCGATCTCTCACGATGAAGTCGTCCACGGCAAGGGTTCCCTG--- 1287860

Qy       592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
                |||                                          ||||||
Db   1287859 ---TGG-----------------------------------GACCGTATGCCTGGCGAT 1287839

Qy       612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
                   ::::::          |||          :::                    |||
Db   1287838 ACGTGGAACAAGGCCGCTGGTCTTCGCACCTTCCTTGCGTACATGTGGTCACACCCAGGC 1287779

Qy       632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGly---HisProGluTrpIleAsp 650
                :::        |||    |||||||||    ||||||||||           ||||||
Db   1287778 AAGAAG------CTGCTTTTCATGGGTCAGGAGTTTGGTCAGCGTGAAGAGTGG------ 1287731

Qy       651 PheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSer 670
                         ||||||                          ::::::    |||    |||
Db   1287730 ---------GCTGAAGGCCAGGGACTGCCATGGGATATTGTCGACGGCTGGCAAGGCGAG 1287680

Qy       671 TyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGly 690
             |||    :::        |||                                       |||
Db   1287679 TACCACGAAGCCATCCGCACTCTGACC---------------------------CGCTCC 1287647

Qy       691 LeuGlnGluPhe------AspArgProMetGlnTyrLeuGluAspLysTyrGluPheMet 708
             |||                  |||    |||       :::    :::|||
Db   1287646 CTCAACGGTGTCTACTCAGACTCCCCTGCGCTGCACACTCAGGAT-----------TTC 1287599

Qy       709 ThrSerGluHisGlnPheIleSerArgLysAspGluGly---AspArgMetIleValPhe 727
             |||    |||             ::::::    |||:::          :::    ::::::    |||
Db   1287598 ACCGGAGAAGGCTTCACATGGAATAAGGGCGACGACGCCACCAACAACATTTTGGCGTTC 1287539

Qy       728 GluLys---------------GlyAsnLeuValPheValPheAsnPheHisTrpThrLys 742
                :::                       ::::::    |||||||||          |||
Db   1287538 ACTCGTTTCGGCAGCGACGGCTCCCAGATGCTGTGTGTATTCAACCTGTCTGGAACC--- 1287482

Qy       743 SerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAsp 762
             |||       :::|||::::::                 |||::::::|||:::    |||:::
Db   1287481 TCCCAGCCTGAGTACCAGCTCGGTGTTGCAGCGGGTGGCGAATGGAAGCTCGTTCTCAAC 1287422

Qy       763 SerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThr 782
             :::||||||          |||    |||             |||
Db   1287421 ACTGATGATGCTGAATTCCTCGGT---GCAGAAAACGATATCGCTACTTCCGTTCAAGCA 1287365

Qy       783 PheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThr 802
                               |||:::                |||:::    ::::::    |||          :::
Db   1287364 GCAGCGACACCACGCGATAATTTCGCCTACTCACTCTCACTGCATGTCCCAGCGATGAGT 1287305

Qy       803 AlaValValTyrAlaLeu 808
             |||       |||:::|||
Db   1287304 GCTCAGTTCTACTCACTG 1287287
```

RESULT 14
US-09-974-300-653
; Sequence 653, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 653
;   LENGTH: 1877
;   TYPE: DNA
;   ORGANISM: Bacillus licheniformis
US-09-974-300-653

Alignment Scores:

Pred. No.:	1.85e-45	Length:	1877
Score:	484.50	Matches:	166
Percent Similarity:	40.50%	Conservative:	107
Best Local Similarity:	24.63%	Mismatches:	264
Query Match:	10.85%	Indels:	137
DB:	10	Gaps:	25

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-974-300-653 (1-1877)

```
Qy       185 GlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPhe 204
             |||       :::             ||||||       |||:::          :::    |||    |||
Db       112 GGCTTCCGTTTCTGTGTTTGGCCCCGCATGCGAAGGAGGTTCGAATCGCCGGAACGTTT 171

Qy       205 AsnAsnTrpAspAlaAsnAlaAspIleMet---ThrArgAsnGluPheGlyValTrpGlu 223
             |||    |||                   |||       |||::::::    |||:::||||||
Db       172 AACGGCTGGTCCGGTGTCCTGCACCGAATGGAAAAGCGTCATCAGGAAGGCATATGGAA 231

Qy       224 IlePheLeuProAsnAsnValAspGlySer------------ProAlaIleProHisGly 239
             :::|||:::|||             :::|||                             |||
Db       232 CTGTTTATCCCCGGTATTGGAGAAGGGGAGCTGTATAAATATGAAATGATTACAGCCGCA 291

Qy       240 SerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrp 259
                :::          |||::::::    |||          :::                :::       |||
Db       292 AATGAAACGAAATTGAAGGCTGATCCTTATGCTTTTTTTTCTGAAGTGAGGCCGAAAACG 351

Qy       260 IleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspPro 279
                :::    :::    ||||||                   :::                :::
Db       352 GCATCGGTCACTTATCAATTGGCCGGA---TACCAATGGGGCGACCGGAAGTGGCAAAAG 408

Qy       280 ProGluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArg 299
                ::::::::::::    :::::::::    |||                         :::
Db       409 AAAAAGCAGCAAAAAGCCGTGTATGAAAAACCG-------------------ATTTCC 447

Qy       300 IleTyrGluSerHisIleGly------MetSerSerProGluProLysIleAsnSerTyr 317
             |||||||||    |||||||||                :::    :::       :::|||
```

```
Db      448 ATCTACGAGCTTCATATCGGTTCGTGGAAAAAGAAAGCGGATGGACGTTTTTCACATAC 507

Qy      318 ValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGln 337
                       :::   |||:::|||   :::|||:::   |||:::      ::::::
Db      508 CGGGAACTGAGCGAAACGGTCATTCCTTACGTCAAAGAACACGGATTCACACATATCGAG 567

Qy      338 IleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhe 357
            :::|||   :::     |||||    :::       |||:::|||||      |||    :::
Db      568 CTGATGCCGCTGACAGAGCACCCGTTTGACCGTTCATGGGGCTACCAGACAACAGGGTAC 627

Qy      358 PheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAla 377
            ::::::|||:::||||||:::|||    |||    ||||||          |||||||:::
Db      628 TACAGTCCGACGAGCAGATATGGCGAACCGCATGACTTGATGTATTTCATCGACCAGTGC 687

Qy      378 HisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsn--- 396
            |||:::       |||    |||:::||||||    |||       |||          :::
Db      688 CATCAGCATGAGATCGGCGTCATTATGGATTGGGTTTCCGGCCATTTTTGCAAAGATGAC 747

Qy      397 ------------ThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe 412
                              ||||||:::   :::::::::                |||
Db      748 CACGGCTTGTATTTGTTTGACGGTATGCCTCTGTATGAA---------------TATAAA 792

Qy      413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
            |||            |||       :::|||   |||    :::        |||:::    |||
Db      793 CACGAGCATGACAGG---GAAAATTGGGAATGGGGACCGCCAATTTTGACCTCGGAAAA 849

Qy      433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPhe 452
               ||||||       :::|||:::|||||||||    :::|||::::::    :::
Db      850 CGAGAAGTTCACAGTTTTTTAATCTCGAATGCGTTGTATTGGATCGAGATGTATCATATA 909

Qy      453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
            ||||||||||||    |||    |||       :::::::::|||            :::
Db      910 GATGGATTTCGAGTCGATGCGGTTGCGAACCTCCTGTATTGGCCAAACCGTCCTCAGCCT 969

Qy      473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
                         |||                                      |||:::
Db      970 GAAGCGAACGGC---------------------------------TTTGCGATCGAA 993

Qy      493 TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly 512
            :::::      :::|||:::   :::                 |||      :::    |||
Db      994 TTTATTCAAACGTTAAATGAACAGGTTTTTGCAAAAGATCCCCACTTTTTGATGATTGCA 1053

Qy      513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPhe 532
            ||||||    :::         |||             |||       |||||||||:::||||||
Db     1054 GAGGACTCCACAGACTGGCCGCTTGTGACGCATCCGACCTATGAAGGCGGTCTCGGGTTT 1113

Qy      533 AspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAsp 552
            :::|||:::
Db     1114 AATTATAAG--------------------------------------------------- 1122

Qy      553 GluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLys 572
                  |||    :::|||                                  |||
Db     1123 ------TGGAATATGGGT-----------------------------TGGATGAACGAT 1146

Qy      573 CysValSerTyrAlaGlu---SerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
               ::::::|||    |||    |||    :::|||                   ::::::
Db     1147 GTATTAACCTATATGGAAGCTTCCCCAGAACAAAGAAAACACCTGCATCATCTTGTTTCA 1206

Qy      592 PheTrpLeuMet---------------------------------------AspLysAsp 598
            |||    ||||||                                         |||:::
Db     1207 TTCTCCTTAATGTATGCCTACTCAGAAAATTACATCCTGCCGTTCTCCCACGATGAAGTG 1266

Qy      599 MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla 618
            :::|||          :::|||
Db     1267 GTGTACCGCAAAAAGTCTCTG--------------------------------------- 1287

Qy      619 LeuHisLysMet-----------------------------------------IleArg 624
            ||||||||||||                                            |||
Db     1288 CTTCATAAGATGCCCGGCGATTATTGGCAGAAATTCGCCCAGTACCGCCTGCTGATCAGT 1347

Qy      625 LeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGly 644
                     |||       |||    :::       |||    |||||||||    ||||||
Db     1348 TATTTTATGATGCACCCGGGAAAAAAG------CTTCTTTTTATGGGCGGTGAGTTTGCT 1401

Qy      645 His---ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
                   ||||||    |||                :::      |||    |||
Db     1402 CAATTTGATGAATGGAAAGACGAAGAAGAGCTCGATTGGTTTTTGGACGAT--------- 1452

Qy      664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
                             |||         :::         |||    |||
Db     1453 ---------------TTTGACATGCACCGCAAAGCCCGAATGTTTACAAAGGAGGCTCTA 1497

Qy      684 Glu---TyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGlu 702
                   |||    :::    |||    |||    |||    |||             |||    |||
Db     1498 CACCTCTACAAAAAAAGCCGTATCCTGTATGAAAATGATCATCGGCAGCAAGGATTCGAG 1557

Qy      703 AspLysTyrGluPheMetThrSerGluHisGlnPheIleSer-----------ArgLys 718
                         :::          :::|||          :::|||                |||
Db     1558 ---TGGATTGACGTTAACAATGCGGAACAGTCGATTGTATCGTTTATCCGCTATGGAAAA 1614

Qy      719 AspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPhe 738
                   |||:::    :::|||:::                                |||    ||||||
Db     1615 CAGCCCGGTGAAGCGCTGATTATC----------------------GTCTGCAATTTC 1650

Qy      739 HisTrpThrLysSer---TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyr 757
                   |||    |||    |||    :::|||||||:::                  :::|||
Db     1651 ------ACGCCTTCCGTCTATCACGAATATCGGGTCGGCGTCCCTTTTCAAACCGAATAT 1704

Qy      758 LysValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsn 777
                      |||:::||||||||||          :::||||||       :::|||:::
Db     1705 ATCGAAGTGCTTAACAGCGATGATGCAAAATACGGAGGTTCACACCAAATCAACCCAAAA 1764

Qy      778 AlaGluTyrPheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyr 797
                                 :::|||              :::|||    ||||||       :::
Db     1765 ---CGCCTTCAGGCAAGAAAAGGCGTTCTGCACGGCAAACCATACAGCATCAGCATGACA 1821

Qy      798 AlaProCysLysThrAlaValValTyrAlaLeuValAspLys 811
                |||          |||    |||:::       |||    |||
Db     1822 GTCCCTCCGCTGGGAGCTGCGGTTTTCAGAGCAGTCAAAAAG 1863
```

```
RESULT 15
US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
;   LENGTH: 604
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (12)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (517)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (540)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (567)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (593)
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```
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-453

Alignment Scores:
Pred. No.:              7.8e-44       Length:         604
Score:                  463.50        Matches:        93
Percent Similarity:     71.93%        Conservative:   30
Best Local Similarity:  54.39%        Mismatches:     40
Query Match:            10.38%        Indels:         8
DB:                     10            Gaps:           4

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-925-300-453 (1-604)

Qy        256 IleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIle 275
              |||      |||      |||   ::::::       |||    :::   |||:::   |||
Db         54 ATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAATTATGATTGGATA 113

Qy        276 HisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysPro 295
              |||:::||||||         |||         |||   |||:::|||   |||||||||||||||
Db        114 CACTGGGATCCA------GAACACTCATATGAGTTTAAGCATTCCAGACCAAAGAAGCCA 167

Qy        296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
              :::|||||||||||||||||||||||||:::|||:::||||||   |||   |||:::
Db        168 CGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAAGGAAAAGTAGCT 227

Qy        316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
              ||||||   :::|||            |||||||||||||||||   ||||||||||||
Db        228 TCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTTGGATACAACTGC 287

Qy        336 LeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
              :::|||:::|||||||||   ||||||:::|||||||||||||||||||||   :::|||
Db        288 ATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTTACCAAATCACA 347

Qy        356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAsp 375
              :::||||||||||   |||||||||:::|||||||||:::::::|||:::   |||:::|||
Db        348 AGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAAGAACTGGTAGAC 407

Qy        376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
                 ||||||   :::|||||||:::||||||:::|||:::|||   :::||||||||||
Db        408 ACAGCTCATTYCATGGGTATCATAGTCCTCTTAGATGTGGTACAAGCSCATGCTTCAAAA 467

Qy        396 AsnThr-LeuAspGlyLeuAsnMetPheAsp------CysThrAspSer---CysTyrPh 412
              |||:::   ||||||:::   ::::::            |||||||||        ||
Db        468 AATTCCAGCAGATGGGATTGGAATATGGTTTGGATGGGGACAGATTCCNGGTTAATTTT 527

Qy        412 eHisSerGlyAla------ArgGlyTyrHis 420
              |||||||           ||||||   |||
Db        528 CCATTCCTGGGANCCTAGAAGGGGACTCCAT 558

Search completed: July  6, 2003, 07:28:18
Job time : 6667 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

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Run on:         July  6, 2003, 02:17:31 ; Search time 2890 Seconds
                                          (without alignments)
                                          4673.715 Million cell updates/sec

Title:          US-10-056-454A-15_COPY_49_882
Perfect score:  4465
Sequence:       1 EKSSYNSEFRPSTVAASGKV..........EEEEEEEEVAAVEEVVVEEE 834

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10056454/runat_01072003_145500_8257/app_query.fasta_1.1031
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10056454_@CGN_1_1_2087_@runat_01072003_145500_8257 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
                1:  em_estba:*
                2:  em_esthum:*
                3:  em_estin:*
                4:  em_estmu:*
                5:  em_estov:*
                6:  em_estpl:*
                7:  em_estro:*
                8:  em_htc:*
                9:  gb_est1:*
                10:  gb_est2:*
                11:  gb_htc:*
                12:  gb_est3:*
                13:  gb_est4:*
                14:  gb_est5:*
                15:  em_estfun:*
                16:  em_estom:*
                17:  gb_gss:*
                18:  em_gss_hum:*
                19:  em_gss_inv:*
                20:  em_gss_pln:*
                21:  em_gss_vrt:*
                22:  em_gss_fun:*
                23:  em_gss_mam:*
                24:  em_gss_mus:*
                25:  em_gss_other:*
                26:  em_gss_pro:*
                27:  em_gss_rod:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2987.5	66.9	2766	11	AY109521	AY109521 Zea mays
	2	2809.5	62.9	2732	11	AY109532	AY109532 Zea mays
	3	2082	46.6	3012	11	AY105679	AY105679 Zea mays
	4	2038	45.6	2738	11	AK009815	AK009815 Mus muscu
	5	1136	25.4	728	14	BU008463	BU008463 QGH7K17.y
	6	1123	25.2	713	14	BQ986883	BQ986883 QGF10L08.
	7	1121.5	25.1	1524	10	BE636603	BE636603 rockefell
	8	1063	23.8	689	13	BI308555	BI308555 EST529965
	9	1062	23.8	801	10	BE195628	BE195628 HVSMEh008
c	10	1060	23.7	1482	17	BH770747	BH770747 LLMGtag49
	11	1044	23.4	678	10	AV939010	AV939010 AV939010
	12	1035.5	23.2	898	14	BQ716536	BQ716536 AGENCOURT
	13	1027.5	23.0	731	10	BE602527	BE602527 HVSMEh009
	14	989.5	22.2	717	14	BU005876	BU005876 QGG9F08.y
	15	976	21.9	639	10	AW065909	AW065909 687002G09
	16	973.5	21.8	621	12	BG521671	BG521671 13-3 Stev
	17	971	21.7	1088	14	BQ232004	BQ232004 AGENCOURT
	18	970	21.7	825	12	BF065047	BF065047 HV_CEb002
	19	959	21.5	646	9	AU238577	AU238577 AU238577
	20	956.5	21.4	695	14	BQ240494	BQ240494 TaE05016F
	21	951	21.3	573	13	BM526229	BM526229 sal38f02.
	22	950	21.3	651	12	BG526727	BG526727 63-11 Ste
	23	944.5	21.2	761	13	BM411030	BM411030 EST585357
c	24	937.5	21.0	918	17	CNS06W7Z	AL418101 T3 end of
	25	934.5	20.9	751	13	BI920158	BI920158 EST540093
	26	934	20.9	569	10	AV442128	AV442128 AV442128
	27	931	20.9	571	13	BI699680	BI699680 sai25g09.
	28	927	20.8	650	10	BE427534	BE427534 PSR7153 I
	29	917.5	20.5	734	9	AL043330	AL043330 DKFZp434O
	30	916	20.5	1042	13	BM456951	BM456951 AGENCOURT
	31	914	20.5	962	17	CNS06OTJ	AL408509 T7 end of
	32	907	20.3	560	14	BM885252	BM885252 sal97a08.
c	33	897.5	20.1	967	17	BH132946	BH132946 ENTPC72TF
	34	897	20.1	571	13	BI469105	BI469105 sai07e09.
	35	895	20.0	589	10	AW596011	AW596011 si96g03.y
	36	894	20.0	576	10	AW244197	AW244197 687050F06
	37	891.5	20.0	693	13	BI091718	BI091718 602859457
	38	881	19.7	575	13	BI425610	BI425610 sah69a11.
	39	878	19.7	582	13	BM309136	BM309136 sak55b02.
	40	872	19.5	801	12	BG741971	BG741971 602633412
	41	866	19.4	592	13	BJ268430	BJ268430 BJ268430
	42	863	19.3	774	9	AU139463	AU139463 AU139463
	43	861.5	19.3	671	13	BI719233	BI719233 1031042C0
	44	860.5	19.3	602	12	BG524041	BG524041 38-25 Ste
	45	860	19.3	739	9	AU004044	AU004044 AU004044

ALIGNMENTS

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RESULT 1
AY109521
LOCUS       AY109521                2766 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays CL1245_1 mRNA sequence.
ACCESSION   AY109521
VERSION     AY109521.1  GI:21213273
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 2766)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
```

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TITLE       Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 2766)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
     source          1..2766
                     /organism="Zea mays"
                     /db_xref="MaizeDB:630161"
                     /db_xref="taxon:4577"
                     /clone="CL1245_1"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      715 a    546 c    689 g    718 t     98 others
ORIGIN

Alignment Scores:
Pred. No.:              0               Length:          2766
Score:                  2987.50         Matches:         562
Percent Similarity:     79.04%          Conservative:    79
Best Local Similarity:  69.30%          Mismatches:      147
Query Match:            66.91%          Indels:          23
DB:                     11              Gaps:            6

US-10-056-454A-15_COPY_49_882 (1-834) x AY109521 (1-2766)

Qy       12 SerThrValAlaAlaSerGlyLysValLeuValProGlyThrGlnSerAspSerSerSer 31
               |||          |||   ||||||||||||||||||||         ||||||
Db       56 AGCTGCGCTGGTGCTCCTGGAAAGGTACTGGTGCCTGGAGGTGGCAGTGATGACTTGCTT 115

Qy       32 SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr 51
            ||||||     :::                   :::|||    ||||||
Db      116 TCCTCCGCAGAG------CCGGTCGTGGACACTCAACCTGAAGAA------CTACAGATA 163

Qy       52 AspValAspSerSerThrMetGluHisAlaSerGlnIleLysThrGluAsnAspAspVal 71
                              |||:::|||         |||         |||:::
Db      164 CCTGAAGCAGAACTGACTGTGGAGAAGACATCCTCCTCACCAACTCAAACA--------- 214

Qy       72 GluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeuGln 91
                              |||   :::|||   |||         :::|||   ::::::
Db      215 ------------------ACATCAGCAGTGGCTGAAGCA------AGCTCAGGAGTTGAG 250

Qy       92 LeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIle 111
               :::|||.   :::|||   |||         :::      :::         |||
Db      251 GCTGAGGAGAGGCCTGAGCTCTCAGAAGTGATTGGAGTTGGAGGTACTGGTGGAACCAAA 310

Qy      112 IleAsp------------------GluSerAspArgIleArgGlu------ArgGlyIle 123
            ||||||                  ::::::   :::   |||         |||   |||
Db      311 ATTGATGGTGCAGGCATCAAAGCCAAAGCACCACTCGTGGAGGAGAAACCACGAGTTATC 370

Qy      124 ProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg 143
            ||||||||||||   ||||||:::|||||||||||||||||||||:::|||      :::|||
Db      371 CCACCACCAGGAGATGGCCAACGAATATATGAGATTGACCCAATGTTGGAAGGGTTTCGG 430

Qy      144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyr 163
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Db      431 GGTCACCTTGACTACCGATACAGTGAATATAAGAGATTACGTGCGGCTATTGATCAACAT 490

Qy      164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
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Db      491 GAAGGTGGTTTGGATGCATTTTCACGCGGTTACGAAAAGCTTGGATTTACTCGCAGCGCT 550

Qy      184 ThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAsp 203
               ||||||||||||||||||||||||   ||||||   ||||||||||||:::||||||
Db      551 GAAGGTATCACTTACAGAGAATGGGCTCCTGGAGCATACTCTGCAGCATTAGTAGGTGAC 610

Qy      204 PheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 223
            ||||||||||||:::   |||||||||      |||      ||||||||:::||||||||||||
Db      611 TTCAACAACTGGAACCCAAATGCTGATGCTATGGCCAGAAATGAGTACGGCGTTTGGGAG 670

Qy      224 IlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLys 243
            ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db      671 ATTTTCCTGCCTAACAATGCTGATGGTTCCCCTGCTATTCCTCATGGCTCACGTGTAAAG 730

Qy      244 IleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSer 263
            ||||||||||||||||||||||||||||||||||||||||||||||||||   :::|||
Db      731 ATACGGATGGACACACCATCTGGTGTTAAGGATTCCATTCCTGCCTGGATCAAGTTTTCT 790

Qy      264 LeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGlu 283
            :::|||   |||   ||||||||||||||||||||:::||||||||||||||||||||||
Db      791 GTGCAGGCTCCAGGTGAAATACCATACAACGGTATATATTATGACCCACCTGAAGAGGAG 850

Qy      284 ArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSer 303
            :::|||:::|||:::||||||:::||||||:::||||||||||||||||||||||||||||
Db      851 AAATATGTATTCAAACACCCTCAACCTAAGCGGCCCAAGTCACTGCGGATATATGAATCA 910

Qy      304 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu 323
            |||:::||||||||||||||||||||||||:::|||   ||||||||||||||||
Db      911 CATGTTGGAATGAGTAGCCCGGAACCAAAGATAAATACATATGCTAACTTCAGAGATGAG 970

Qy      324 ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 343
            |||||||||||||||   |||||||||||||:::||||||||||||||||||||||
Db      971 GTGCTTCCAAGAATTNNNNNGCTTGGATACAATGCAGTACAGATAATGGCAATCCAGGAA 1030

Qy      344 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 363
            ||||||||||||||||||||||||||||||||||            |||||||||||||||
Db     1031 CACTCTTATTATGCAAGCTTTGGGTACCATGTTACGAANNNNNNNGCCCCAAGTAGCCGT 1090

Qy      364 PheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 383
            ||||||||||||:::||||||||||||||||||||||||||||||||||||:::::::
Db     1091 TTTGGGACTCCAGAGGACCTAAAATCTCTTATTGATAAAGCGCATGAGCTTGGCTTGCTA 1150

Qy      384 ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 403
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Db     1151 GTGCTTATGGATATTGTTCATAGTCATTCATCAAATAATACCTTGGATGGTTTGAATGGT 1210

Qy      404 PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrp 423
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Db     1211 TTCGATGGCACCGATACACATTACTTCCATGGTGGTCCACGAGGCCATCATTGGATGTGG 1270

Qy      424 AspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAla 443
            ||||||||||||||||||||||:::||||||||||||||||:::|||||||||||||||
Db     1271 GATTCTCGCCTATTCAATTATGGGAGTTGGGAAGTTTTGAGATTTCTATTGTCAAATGCG 1330

Qy      444 ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet 463
            ||||||||||||:::   :::||||||||||||||||||||||||||||||||||||||
Db     1331 AGATGGTGGCTTGAAGAATATAAATTTGATGGGTTTCGATTTGATGGGGTGACCTCCATG 1390

Qy      464 MetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGly 483
            ||||||   ||||||||||||   |||   |||||||||||||||   ||||||||||||
Db     1391 ATGTATACTCACCATGGATTACAAGTGACATTCACTGGGAACTATGGCGAGTATTTTGGA 1450

Qy      484 LeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 503
               ||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     1451 TTTGCCACTGATGTTGATGCAGTAGTTTACCTAATGCTGGTAAACGATCTTATTCGTGGG 1510

Qy      504 LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle 523
            |||:::|||:::|||::::::||||||||||||||||||||||||||||||
Db     1511 CTTTATCCAGAAGCTGTATCCATTGGCGAAGATGTCAGCGGAATGCCNNNNNNNNNNNNN 1570

Qy      524 ProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys 543

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Qy     564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
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Qy     584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db    1751 CTTGTTGGTGACAAGACAATTGCATTCTGGTTGATGGATAAGGATATGTATGATTTCATG 1810

Qy     604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db    1811 GCTCTGGACAGGCCTTCAACGCCTCGCATCGATCGTGGGATAGCATTACATAAAATGATT 1870

Qy     624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
Db    1871 AGGCTTGTCACAATGGGTTTAGGAGGTGAAGGCTATCTAAATTTCATGGGAAATGAGTTT 1930

Qy     644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db    1931 GGGCATCCTGAATGGATAGATTTTCCAAGAGGTCCTCAAAGTCTTCCAAATGGCTCCGTC 1990

Qy     664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
Db    1991 ATTCCTGGGAATAACAATAGCTTTGATAAATGCCGCCGTAGATTTGACCTTGGAGATGCA 2050

Qy     684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
Db    2051 GATTATCTTAGATATCGTGGTATGCAAGAGTTTGACCAGGCAATGCAGCACCTTGAGGGA 2110

Qy     704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db    2111 AAATATGAATTCATGACATCTGATCACTCATATGTATCACGGAAGCATGAGGAGGATAAG 2170

Qy     724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db    2171 GTGATCATCTTTGAGAGAGGAGATTTGGTCTTCGTGTTCAACTTCCACTGGAGCAATAGC 2230

Qy     744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
Db    2231 TATTTTGACTATCGCGTTGGTTGTTTCAAGCCTGGGAAGTACAAGATCGTTTTAGATTCT 2290

Qy     764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
Db    2291 GACGATGGCCTTTTCGGTGGATTTAGTCGGCTTGATCATGATGCTGAGTACTTCACTGCT 2350

Qy     784 GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
Db    2351 GACTGGCCGCATGACAACAGGCCGTGTTCTTTCTCGGTCTATGCACCCAGCAGAACAGCC 2410

Qy     804 ValValTyrAlaLeuValAspLysGluGluGlu 814
Db    2411 GTCGTATATGCACCTGCAGGTGCAGAGGACGAA 2443
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AY109532
LOCUS       AY109532              2732 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays CL1742_1 mRNA sequence.
ACCESSION   AY109532
VERSION     AY109532.1  GI:21213287
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 2732)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 2732)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
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                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      659 a    506 c    679 g    710 t    178 others
ORIGIN

Alignment Scores:
Pred. No.:                 0             Length:          2732
Score:                     2809.50       Matches:         521
Percent Similarity:        79.31%        Conservative:    73
Best Local Similarity:     69.56%        Mismatches:      134
Query Match:               62.92%        Indels:          21
DB:                        11            Gaps:            3

US-10-056-454A-15_COPY_49_882 (1-834) x AY109532 (1-2732)
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Db     299 GAGAATGATGGCCTCGCATCAAGGGCTGAC------------------------------ 328

Qy      87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db     329 ------TCGGCTCAATTCCAGTCG------------GATGAACTGGAGGTACCAGACATT 370

Qy     107 SerGluGluThr---------------IleIleAspGluSerAspArgIleArgGluArg 121
Db     371 TCTGAAGAGACAACGTGCGGTGCTGGTGTGGCTGATGCTCAAGCCTTGAACAGAGTTCGA 430

Qy     122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db     431 GTGGTNNNNNNACCAAGCGATGGACNNNNNNTATTCCAGATTGACCCCATGTTGCAAGGC 490

Qy     142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db     491 TATAAGTACCATCTTGAGTATCGGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGAT 550

Qy     162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db     551 GAACATGAAGGAGGCTTGGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATCGC 610

Qy     182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db     611 AGCGCGGAAGGTATCACATATCGAGAATGGGCTCCTGGAGCATTTTCTGCAGCATTGGTG 670

Qy     202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db     671 GGTGACTTCAACAACTGGGATCCAAATGCAGATCGTATGAGCNNNNNTGANNNNNNNNNN 730

Qy     222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db     731 NNNNNNNNNNNNCTGCCTAACAATGCAGATGGTACATCACCTATTCCTCATGGATCTCGT 790

Qy     242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db     791 GTAAAGGTGAGAATGGATACTCCATCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAG 850

Qy     262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
Db     851 TACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAA 910
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Qy        282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
              |||    :::|||:::|||:::|||    :::||||||:::|||||||||||||||||||||
Db        911 GAGGTAAAGTATGTGTTCAGGCATGCGCAACCTAAACGACCAAAATCATTGCGGATATAT 970

Qy        302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
              |||:::|||:::|||||||||||||||||||||||||||
Db        971 GAAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAAANNNNNNNNNNNNNNNNNNN 1030

Qy        322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
                                            ||||||||||||||:::||||||||||||||||
Db       1031 NNNNNNNNNNNNNNNNNGAATNNNNNNNCTTGGATACAATGCAGTGCAAATAATGGCAATC 1090

Qy        342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 361
              ||||||||||||||||||    |||||||||||||||||||            |||||||||
Db       1091 CAAGAGCACTCATATTATGGAAGCTTTGGATACCATGTAACTAANNNNNNNGCGCCAAGT 1150

Qy        362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
              ||||||||||||||||||:::|||||||||||||||||||:::|||||||||||||||||
Db       1151 AGTCGTTTTGGTACCCCAGAAGATTTGAAGTCTTTGATTGATAGAGCACATGAGCTTGGT 1210

Qy        382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
              :::::::|||||||||||:::||||||||||||||||||:::|||||||||||||||||||
Db       1211 TTGCTAGTTCTCATGGATGTGGTTCATAGTCATGCGTCAAGTAATACTCTGGATGGGTTG 1270

Qy        402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
              |||    ||||||    |||||||:::    ||||||||||||||||    ||||||:::||||||
Db       1271 AATGGTTTTGATGGTACAGATACACATTACTTTCACAGTGGTCCACGTGGCCATCACTGG 1330

Qy        422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
              |||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db       1331 ATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTTTTAAGATTTCTTCTCTCC 1390

Qy        442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
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Db       1391 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTGATGGTTTCCGTTTTGATGGTGTGACC 1450

Qy        462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
              ||||||||||||    ||||||||||||    |||    ||||||||||||:::    ||||||
Db       1451 TCCATGATGTACACTCACCACGGATTACAAGTAACATTTACGGGGAACTTCAATGAGTAT 1510

Qy        482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
              ||||||    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1511 TTTGGCTTTGCCACCGATGTAGATGCAGTGGTTTACTTGATGCTGGTAAATGATCTAATT 1570

Qy        502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
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Db       1571 CATGGACTTTATCCTGAGGCTGTAACCATTGGTGAAGATGTTAGTGGAATGCCTACATTT 1630

Qy        522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
                 :::||||||    :::|||||||||||||||||||||:::||||||||||||:::|||
Db       1631 GCCCTTCCTGTTCACGATGGTGGGGTAGGTTTTGACTATCGGATGCATATGGCTGTGGCT 1690

Qy        542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
              ||||||    |||:::|||||||||:::    ||||||    |||:::::::|||||||||||
Db       1691 GACAAATGGATTGACCTTCTCAAGCAAAGTGATGAAACTTGGAAGATGGGTGATATTGTG 1750

Qy        562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
              ||||||||||||||||||||||||    ||||||||||||:::||||||||||||||||||
Db       1751 CACACACTGACAAATAGGAGGTGGTTAGAGAAGTGTGTAACTTATGCTGAAAGTCATGAT 1810

Qy        582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1811 CAAGCATTAGTCGGCGACAAGACTATTGCGTTTTGGTTGATGGACAAGGATATGTATGAT 1870

Qy        602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
              |||||||||||||||||||||||||||||            ||||||||||||||||||||||||
Db       1871 TTCATGGCCCTCGATAGACCTTCAACTCCTACCATTGATCGTGGGATAGCATTACATAAG 1930

Qy        622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       1931 ATGATTAGACTTATCACAATGGGTTTAGGAGGAGAGGGCTATCTTAATTTCATGGGAAAT 1990

Qy        642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
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Qy        662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
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Db       2051 AAGTTTATTCCAGGGAATAACAACAGTTATGACAAATGTCGTCGAAGATTTGACCTGGGT 2110

Qy        682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
              ||||||:::||||||||||||    |||:::||||||||||||:::    ||||||:::|||
Db       2111 GATGCAGACTATCTTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCAACATCTT 2170

Qy        702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
              |||         ||||||||||||||||||:::||||||:::||||||||||||    |||
Db       2171 GAGCNNNNNTATGAATTCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAG 2230

Qy        722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
              |||:::::|||||||||||||||||:::||||||||||||||||||||||||||||
Db       2231 GATAAGGTGATTGTGTTCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAAC 2290

Qy        742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
                 ||||||    ||||||||||||    |||    |||||||||    |||||||||    |||
Db       2291 AACAGCTATTTTGACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG 2350

Qy        762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
              |||||||||         |||||||||||||||    ||||||    |||    ||||||:::|||
Db       2351 GACTCCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCACGCAGCCGAGCACTTC 2410

Qy        782 ThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLys 801
              |||    :::         :::|||:::||||||    |||         ||||||    |||      :::
Db       2411 ACCGCCGACTGTTCGCATGATAATAGGCCATATTCGTTCTCGGTTTATACACCAAGCAGA 2470

Qy        802 ThrAlaValValTyrAlaLeuValAsp 810
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Db       2471 ACATGTGTCGTCTATGCTCCAGTGGAG 2497
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RESULT 3
AY105679
LOCUS       AY105679                3012 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays PCO072723 mRNA sequence.
ACCESSION   AY105679
VERSION     AY105679.1  GI:21208757
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 3012)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 3012)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
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ORIGIN

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US-10-056-454A-15_COPY_49_882 (1-834) x AY105679 (1-3012)

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Db       227 -----------------GATCGGGCGGCACCGCCGGGGATCGCGGGTGGCGGCAATGTG 268

Qy        83 GluLeuAspPheAlaSer---------------------------------------Ser 89
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Qy        90 LeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGlu 109
Db       329 AGCAAATTCGCCACTGCAGCTACTGTGCAAGAAGATAAAACTATGGCAACTGCCAAAGGC 388

Qy       110 ThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProProProGlyLeuGly 129
Db       389 GATGTC-----------GACCATCTC------------------------------- 403

Qy       130 GlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArg 149
Db       404 ---CCCATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGG 460

Qy       150 TyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAla 169
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Qy       170 PheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArg 189
Db       521 TTTTCTAAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGT 580

Qy       190 GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAla 209
Db       581 GAATGGGCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGT 640

Qy       210 AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn 229
Db       641 GCAAACCATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAATT---GACCAT 697

Qy       230 ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro 249
Db       698 GTCAAAGGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGT 757

Qy       250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
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Qy       270 Ile------ProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePhe 287
Db       818 TTTGGAGCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTT 877

Qy       288 GlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMet 307
Db       878 AAGCATCCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATG 937

Qy       308 SerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArg 327
Db       938 AGTGGTGAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGC 997

Qy       328 IleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyr 347
Db       998 ATACGAGCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTAT 1057

Qy       348 AlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrPro 367
Db      1058 GCTTCTTTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCA 1117

Qy       368 AspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAsp 387
Db      1118 GAGGACCTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGAT 1177

Qy       388 IleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp------ 405
Db      1178 GTTGTCCATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGA 1237

Qy       406 ---CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
Db      1238 CAAAGCACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGAT 1297

Qy       425 SerArgLeu-PheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaAr 444
Db      1298 AGTCGGCTGTTTCAACTATGCTAACTGGGAGGTATTAACGTTTCTTCTTTCTAACCTGAG 1357

Qy       444 gTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMe 464
Db      1358 ATATTGGTTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCT 1417

Qy       464 tTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLe 484
Db      1418 GTATCATCACCATGGTATCAATGTGGGGCTTACTGGAAACTACCAGGAATATTTCAGTTT 1477

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Qy       504 uPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePr 524
Db      1538 CTTGCCAGAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCC 1597

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Db      1598 AGTTGATGAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATG 1657

Qy       544 gIleGluLeuLeuLysLysArgAspGlu---AspTrpArgValGlyAspIleValHisTh 563
Db      1658 GATTGACTACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATAC 1717

Qy       563 rLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAl 583
Db      1718 TTTGACTAACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTC 1777

Qy       583 aLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMe 603
Db      1778 TATTGTTGGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCAT 1837

Qy       603 tAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIl 623
Db      1838 GTCAGACTTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGAT 1897

Qy       623 eArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPh 643
Db      1898 TCACTTCATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTT 1957

Qy       643 eGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVa 663
Db      1958 TGGTCACCCAGAATGGATTGACTTTCCAAGA--------------------------- 1988

Qy       663 lIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAl 683
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Qy       683 aGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAs 703
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Db       2045 TGATCACTTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGA 2104

Qy        703 pLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspAr 723
              :::::: . |||:::::|||        |||   :::|||       ::::::   :::::
Db       2105 GAGATTTTCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAA 2164

Qy        723 gMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSe 743
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Db       2165 GGTTATTGTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAAC 2224

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LOCUS       AK009815                2738 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
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            ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME) (BRANCHER ENZYME),
            full insert sequence.
ACCESSION   AK009815
VERSION     AK009815.1  GI:12844841
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
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            clone:2310045H19.
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
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  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
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REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 2738)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
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            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
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            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0 and subtraction to
            Rot = 25.0. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
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Percent Similarity:     71.89%         Conservative:   114
Best Local Similarity:  55.20%         Mismatches:     176
Query Match:            45.64%         Indels:         16
DB:                     11             Gaps:           5

US-10-056-454A-15_COPY_49_882 (1-834) x AK009815 (1-2738)

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Qy        349 SerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAsp 368
Db        762 AGTTTTGGGTACCAAATCACGAGCTTTTTTGCAGCTTCAAGTCGTTATGGAACTCCTGAA 821

Qy        369 AspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIle 388
Db        822 GAGCTGAAAGAACTTGTTGACACAGCACATTCGATGGGCATTGTAGTCCTCCTAGATGTG 881

Qy        389 ValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAsp 408
Db        882 GTTCATAGCCATGCTTCAAAAAATTCAGAAGATGGGTTAAACATGTTTGATGGGACCGAT 941

Qy        409 SerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPhe 428
Db        942 TCCTGTTATTTTCACTCTGGACCCCGAGGGACCCATGATCTTTGGGACAGTAGATTATTT 1001

Qy        429 AsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAsp 448
Db       1002 ATCTATTCCAGCTGGGAAGTTTTAAGATTCCTTCTGTCGAACATAAGATGGTGGTTGGAG 1061

Qy        449 AlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHis 468
Db       1062 GAGTACTGCTTTGATGGCTTCCGTTTTGATGGTGTCACCTCTATGCTCTATCATCACCAC 1121

Qy        469 GlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspVal 488
Db       1122 GGAATGGGTCAAGGTTTTTCGGGTGACTATAATGAATATTTTGGACTACAAGTAGATGAA 1181

Qy        489 AspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAla 508
Db       1182 GATGCTTTGATTTATCTCATGTTGGCAAATCATTTGGCTCACACGTTGTACCCAGACTCG 1241

Qy        509 IleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProValGlnGluGly 528
Db       1242 ATAACAATAGCAGAGGATGTATCAGGGATGCCGGCTCTCTGTTCTCCAACTTCCCAGGGA 1301

Qy        529 GlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeu 548
Db       1302 GGCGGTGGTTTTGACTACAGATTAGCAATGGCTATTCCAGATAAATGGATCCAATTACTT 1361

Qy        549 LysLys---ArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArg 567
Db       1362 AAGGAATTTAAAGATGAAGACTGGAATATGGGCAATATAGTGTATACTCTCACCAATCGA 1421

Qy        568 ArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAsp 587
Db       1422 CGCTACCTTGAAAAATGTGTGGCTTATGCAGAGAGTCATGATCAGGCATTGGTTGGTGAC 1481

Qy        588 LysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArg 607
Db       1482 AAGACACTGGCGTTTTGGTTGATGGACGCTGAGATGTACACGAACATGAGCGTTCTGGCC 1541

Qy        608 ProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThr 627
Db       1542 CCTTTCACTCCAGTAATTGATCGAGGAATACAGCTTCATAAGATGATTCGTCTCATCACT 1601

Qy        628 MetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGlu 647
Db       1602 CACGGGCTCGGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAGTTTGGGCATCCTGAA 1661

Qy        648 TrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsn 667
Db       1662 TGGTTGGACTTCCCAAGG-------------------------------AAAGGAAAT 1688
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Qy        668 GlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArg 687
                    ||||||          ||||||:::|||:::|||   |||    :::   ||||||
Db       1689 AATGAGAGTTACCATTATGCCAGAAGGCAGTTTAATTTAACCGACGATGACCTTCTTCGC 1748

Qy        688 TyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPhe 707
              |||:::   |||      |||||||||   |||      ||||||::::::       :::
Db       1749 TATAAGTTCCTAAATAACTTTGACAGAGATATGAATAGACTGGAAGAAAGATGTGGTTGG 1808

Qy        708 MetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPhe 727
              :::::::::         :::::::|||   |||   |||   ::::::   |||   |||
Db       1809 CTTTCAGCTCCACAGGCCTACGTGAGTGAAAAACATGAAGCCAATAAGACAATCACCTTT 1868

Qy        728 GluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyr 747
              |||:::      |||:::|||:::||||||||||||   :::||||||||||:::||||||
Db       1869 GAGAGAGCAGGACTTCTCTTTATTTCAACTTCCACCCAAGCAAGAGCTATACGGACTAC 1928

Qy        748 ArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeu 767
              |||:::            |||||||||:::|||:::   ||||||||||||
Db       1929 CGAGTCGGGACAGCAACACCAGGGAAGTTCAAAATTGTACTAGATTCTGACGCAGCGGAG 1988

Qy        768 PheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrpTyr 787
              :::||||||       |||:::|||||||||         ||||||               :::
Db       1989 TATGGAGGTCATCAGAGACTGGACCACAACACCAACTACTTTGCTGAGGCTTTTGAACAT 2048

Qy        788 AspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAla 807
              :::   ||||||   |||::::::||||||   |||   :::   |||::::::
Db       2049 AATGGGCGCCCCTATTCTCTTCTGGTGTACATTCCAAGCCGAGTGGCTCTCATCCTTCAG 2108

Qy        808 LeuValAsp 810
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Db       2109 AATGTGGAT 2117
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RESULT 5
BU008463
LOCUS       BU008463                 728 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGH7K17.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGH7K17, mRNA sequence.
ACCESSION   BU008463
VERSION     BU008463.1  GI:22442858
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGH7  row: K  column: 17.
FEATURES             Location/Qualifiers
     source          1..728
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGH7K17"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=leaves dark grow
                     TAG_SEQ=GCTAGTCGGG"
BASE COUNT      227 a    133 c    149 g    218 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                4.27e-123      Length:          728
Score:                    1136.00        Matches:         205
Percent Similarity:       92.98%         Conservative:    20
Best Local Similarity:    84.71%         Mismatches:      17
Query Match:              25.44%         Indels:          0
DB:                       14             Gaps:            0

US-10-056-454A-15_COPY_49_882 (1-834) x BU008463 (1-728)

Qy        173 GlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAla 192
              ||||||||||||:::||||||||||||||||   ||||||||||||||||||||||||||
Db          1 GGTTATGAAAAAATTAGGTTTCACTCGAAGCAAAACAGGTATCACTTATAGAGAATGGGCA 60

Qy        193 LeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAsp 212
                 ||||||:::||||||:::|||   ||||||||||||||||||:::   |||||||||
Db         61 CCTGGGGCAAAGTCTGCTTCACTTACTGGAGATTTCAACAACTGGAATCCAAATGCTGAT 120

Qy        213 IleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGly 232
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTATGACCCGGAATGAATTTGGTGTGTGGGAGATCTTTTTGCCAAACAATGTTGATGAT 180

Qy        233 SerProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyVal 252
              |||   |||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        181 TCTTCACCTATTCCTCATGGTTCTCGAGTAAAGATTCGTATGGATACGCCATCTGGCATT 240

Qy        253 LysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyr 272
              ||||||||||||||||||||||||   :::|||:::|||   |||   ||||||||||||
Db        241 AAAGACTCGATTCCTGCTTGGATCAAGTTTTCAGTACAAGCACCTGGTGAGATTCCTTAT 300

Qy        273 AsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgPro 292
              |||||||||:::||||||||||||:::||||||:::|||:::||||||||||||||||||
Db        301 AATGGAATATACTATGATCCCCCACAAGAGGAAAAATACGTGTTTCAACATCCAAGACCA 360

Qy        293 LysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluPro 312
              |||||||||||||||||||||||||||||||:::|||:::||||||||||||   ||||||
Db        361 AAGAAGCCGAAATCTCTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCA 420

Qy        313 LysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGly 332
                 ||||||:::|||   ||||||||||||:::||||||||||||||||||||||||||||
Db        421 ATGATCAACACGTATGCTAACTTTAGAGACGATGTTCTCCCTCGCATAAAAAAACTCGGT 480

Qy        333 TyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyr 352
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TACAATGCAGTTCAAATCATGGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTAC 540

Qy        353 HisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSer 372
              |||||||||||||||||||||||||||||||:::|||:::||||||||||||   ||||||
Db        541 CATGTGACAAATTTTTTTGCACCAAGTAGTCGATGTGGAACTCCAGATGATCTTAAATCA 600

Qy        373 LeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHis 392
              :::|||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        601 ATGATTGATAAAGCACATGAATTAGGTCTTGTTGTTCTCATGGATATTGTGCATAGTCAT 660

Qy        393 AlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe 412
              :::||||||||||||||||||||||||   |||||||||   |||||||||   ||||||
Db        661 TCATCAAACAACACATTAGATGGATTANATATGTTTGATGGAACTGATAGTCAATACTTT 720

Qy        413 HisSer 414
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Db          721 CATTCT 726

RESULT 6
BQ986883
LOCUS       BQ986883                  713 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  QGF10L08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGF10L08, mRNA sequence.
ACCESSION   BQ986883
VERSION     BQ986883.1  GI:22404408
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGF10  row: L  column: 08.
FEATURES             Location/Qualifiers
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                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGF10L08"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=flowers post-fertilized
                     TAG_SEQ=TGCCATCGGG"
BASE COUNT      221 a    132 c    146 g    214 t
ORIGIN

Alignment Scores:
Pred. No.:              1.41e-121      Length:         713
Score:                  1123.00        Matches:        203
Percent Similarity:     93.67%         Conservative:   19
Best Local Similarity:  85.65%         Mismatches:     15
Query Match:            25.15%         Indels:         0
DB:                     14             Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x BQ986883 (1-713)

Qy        178 GlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSer 197
              |||||||||||||||   |||||||||||||||||||||||||||   |||||:::|||
Db          1 GGTTTCACTCGAAGCAAAACAGGTATCACTTATAGAGAATGGGCACCTGGGGCAAAGTCT 60

Qy        198 AlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsn 217
              |||:::|||||||||||||||||||||||||:::   |||||||||:::||||||||||||
Db         61 GCTTCACTTATTGGAGATTTCAACAACTGGAATCCAAATGCTGATGTTATGACCCGGAAT 120

Qy        218 GluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIlePro 237
              ||||||||||||||||||||||||||||||||||||||||||||   |||    ||||||
Db        121 GAATTTGGTGTGTGGGAGATCTTTTTGCCAAACAATGTTGATGATTCTTCACCTATTCCT 180

Qy        238 HisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIlePro 257
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        181 CATGGTTCTCGAGTAAAGATTCGTATGGATACGCCATCTGGCATTAAAGACTCGATTCCT 240

Qy        258 AlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyr 277
              |||||||||   :::|||:::|||   |||   ||||||||||||||||||||||:::|||
Db        241 GCTTGGATCAAGTTTTCAGTACAAGCACCTGGTGAGATTCCTTATAATGGAATATACTAT 300

Qy        278 AspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSer 297
              |||||||||:::|||||||:::|||:::|||||||||||||||||||||||||||||||
Db        301 GATCCCCCACAAGAGGAAAAATACGTGTTTCAACATCCAAGACCAAAGAAGCCGAAATCT 360

Qy        298 LeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyr 317
              |||||||||||||||:::|||:::||||||||||||   ||||||   ||||||:::|||
Db        361 CTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCAATGATCAACACGTAT 420

Qy        318 ValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGln 337
                 ||||||||||||:::||||||||||||||||||||||||||||||||||||:::|||
Db        421 GCTAACTTTAGAGACGATGTTCTCCCTCGCATAAAAAAACTCGGTTACAATGCAGTTCAA 480

Qy        338 IleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhe 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCATGGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTACCATGTGACAAATTTT 540

Qy        358 PheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAla 377
              |||||||||||||||||   |||||||||||||||||||||||||:::||||||||||||
Db        541 TTTGCACCAAGTAGTCGATGTGGAACTCCAGATGATCTTAAATCAATGATTGATAAAGCA 600

Qy        378 HisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThr 397
              ||||||||||||:::||||||||||||||||||||||||||||||:::||||||||||||
Db        601 CATGAATTAGGTCTTGTTGTTCTCATGGATATTGTGCATAGTCATTCATCAAACAACACA 660

Qy        398 LeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSer 414
              ||||||||||||||||||||||   |||||||||   ||||||||||||
Db        661 TTAGATGGATTAAATATGTTTGATGGAACTGATAGTCAATACTTTCATTCT 711

RESULT 7
BE636603
LOCUS       BE636603                1524 bp    mRNA    linear   EST 03-JAN-2002
DEFINITION  rockefeller.0.213 Mastigamoeba balamuthi lambda ZAP II Library
            Mastigamoeba balamuthi cDNA similar to 1,4-alpha-glucan branching
            enzyme (EC 2.4.1.1), mRNA sequence.
ACCESSION   BE636603
VERSION     BE636603.1  GI:9919714
KEYWORDS    EST.
SOURCE      Mastigamoeba balamuthi.
  ORGANISM  Mastigamoeba balamuthi
            Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
REFERENCE   1  (bases 1 to 1524)
  AUTHORS   Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
            Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
            Philippe,H.
  TITLE     The analysis of 100 genes supports the grouping of three highly
            divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
  MEDLINE   21819461
COMMENT     Contact: Muller Miklos
            Laboratory of Biochemical Parasitology
            The Rockefeller University
            1230 York Avenue, New York, NY 10021, USA
            Email: mmuller@rockvax.rockefeller.edu
            Insert Length: 1524   Std Error: 0.00
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .1524
                     /organism="Mastigamoeba balamuthi"
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                       /strain="ATCC 30984"
                       /db_xref="taxon:108607"
                       /clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
                       /note="syn: Phreatamoeba balamuthi"
BASE COUNT      277 a    525 c    461 g    261 t
ORIGIN

Alignment Scores:
Pred. No.:              7.99e-121       Length:         1524
Score:                  1121.50         Matches:        213
Percent Similarity:     69.77%          Conservative:   64
Best Local Similarity:  53.65%          Mismatches:     98
Query Match:            25.12%          Indels:         22
DB:                     10              Gaps:           5

US-10-056-454A-15_COPY_49_882 (1-834) x BE636603 (1-1524)

Qy        417 ArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeu 436
              :::|||   |||   :::||||||||||||||||||||||||||||||||||    |||
Db          8 AAGGGGCGGCACGAGCTGTGGGACAGCCGGCTGTTCAACTACGGCAACTGGGAGACGCTG 67

Qy        437 ArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArg 456
              |||:::|||||||||||||       |||::::::|||   ::::::|||||||||||||||
Db         68 CGGTTCCTGCTGAGCAACGTGGCGTGGTACATGGACGAGTACCGCTTCGACGGCTTCCGC 127

Qy        457 PheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGly 476
              ||||||||||||||||||||||:::|||:::|||||||||:::
Db        128 TTTGACGGCGTGACCTCGATGCTCTACGTGCACCACGGCATGGGCGACAAC---AACTTT 184

Qy        477 AsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeu 496
              :::|||      ::::::|||   |||   |||   ||||||:::      ||||||   |||
Db        185 GACTACCCGCACTTCTACGGCGCGGCCGTCGACAGCGACGCCCTGGCCTACCTGACGCTG 244

Qy        497 ValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSer 516
                 |||    :::||||||   :::          :::||||::::|||   ||||||||||||
Db        245 GCCAACACCGTCATCCACGAGATCAACCGCGAGGCCGTGTCCATCGCCGAGGACGTGAGC 304

Qy        517 GlyMetProThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeu 536
              |||   |||       |||   ||||||   |||||||||||||||||||||||||||||||
Db        305 GGGTTCCCGGGGCTGTGCAGGCCCGTGCCCGAGGGCGGCGTGGGGTTTGACTACAGGCTG 364

Qy        537 HisMetAlaIleAlaAsp-LysArgIleGluLeuLeuLysLys------ArgAspGluAs 554
                 ||||||      |||          :::   ::::::||||||     |||||||||||
Db        365 GCGATGGCCTGCCCCGACCTCTGGGGTCAACATCATGAAGAAGGTCCACCGCGACGAGGA 424

Qy        554 pTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysVa 574
              ||||   :::      |||      :::||||||   ||||||||||||   |||   |||::
Db        425 CTGGGACATGGACCAGATCTCCAACACCCTCGCCAACCGCCGCTGGATGGAGCCCTGCAT 484

Qy        574 lSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLe 594
              ::::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CGCCTACGCCGAGTCCCACGACCAGGCCCTCGTCGGCGACAAGACGATCGCGTTCTGGCT 544

Qy        594 uMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAs 614
              |||||||||:::|||||||||:::|||:::           |||    |||   :::|||::
Db        545 GATGGACAAGGAGATGTACGACTGGATGTCCAAGGCGCTGCCGCTGACGCCGATCATCGA 604

Qy        614 pArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGl 634
              :||||||:::|||||||||||||||||||||||||:::|||    ||||||||||||||||
Db        605 GCGGGGCATGGCGCTGCACAAGATGATCCGGCTGCTGACGTGCGGCCTCGGCGGCGAGGG 664

Qy        634 yTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAl 654
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 CTACCTGACGTTTATGGGCAACGAGTTTGGCCACCCCGAGTGGATCGACTTCCCGCGC-- 722

Qy        654 aGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCy 674
                                                   |||||||||     ||||||
Db        723 ------------------------------CCGGGCAACAACGCGAGCTACCACTACGC 751

Qy        674 sArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPh 694
                ||||||::::::   |||                |||||||||      :::   :::||
Db        752 GCGGCGGCAGTGGTCGCTGGTCAAGGACCACAACCTGCGCTACCACCAGATGGGCGACTT 811

Qy        694 eAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPh 714
              ||||      |||   :::||||||::::::        :::::::::::   :::   ::
Db        812 TGACGCGGCGATGCTGCACCTCGAGGAGCAGGTCCACTGGCTCAGCGCGGGCAACGCCTA 871

Qy        714 eIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPh 734
              ::::|||   :::         |||:::::|||||||||||||:::          |||||
Db        872 CGTCTCGCTGCGCCACGGCCTCGACAAGGTCATCGTCTTTGAGCGCGCGGGCGCCGTCTT 931

Qy        734 eValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysPr 754
              |||||||||||||||   |||   |||          ||||||:::   |||       ||
Db        932 TGTCTTCAACTTCCACCCGACGCTGAGCCTGCCGAGCTACCGCGTGCCCTGCTCGACGCC 991

Qy        754 oGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIl 774
              ||||:::|||::::::||||||   |||||||||      |||||||||   ||||||::
Db        992 CGGCAGGTACCGCCTGGCCCTCTGCTCGGACGACCTCGCGTTCGGCGGCCAGGGCCGCGT 1051

Qy        774 eAspHisAsn------------AlaGluTyrPheThrPheGluGlyTrpTyrAspAspAr 790
              :|||    :::                      |||   :::      |||   :::|||
Db       1052 CGACACGAGCGTCCCGGCCCAGACGGAGAGGTACCAGGTCTACGGCTGCTTCGAC----- 1106

Qy        790 gProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyr 806
                 |||:::|||:::|||||||||   :::|||||||:::|||:::
Db       1107 ----TACTCGCTCATGATCTACGCGCCCTCGCGCACGGCCCTCGTCTTT 1151

RESULT 8
BI308555
LOCUS       BI308555                 689 bp    mRNA    linear   EST 20-JUL-2001
DEFINITION  EST529965 GPOD Medicago truncatula cDNA clone pGPOD-7017 5' end,
            mRNA sequence.
ACCESSION   BI308555
VERSION     BI308555.1  GI:14982882
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
            ,J. and Fraser,C.M.
  TITLE     ESTs from developing reproductive tissues of Medicago truncatula
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Michael A. Grusak
            USDA/ARS Children's Nutrition Research Center
            Baylor College of Medicine
            1100 Bates Street, Houston, TX 77030-2600, USA
            Tel: 713-798-7044
            Fax: 713-798-7078
            Email: mgrusak@bcm.tmc.edu
            B395410e
             TIGR sequence name: MTOAQ93TK
             More information is available at: www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES             Location/Qualifiers
     source          1..689
                     /organism="Medicago truncatula"
                     /cultivar="A17"
                     /db_xref="taxon:3880"
                     /clone="pGPOD-7017"
                     /clone_lib="GPOD"
                     /tissue_type="immature pod walls"
                     /dev_stage="Immature pods, ranging in age from 15 to 30
                     days after pollination"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Immature pods, ranging in age from 15 to 30 days
                     after pollination,  were collected from greenhouse-grown
                     plants.  At harvest, seeds were removed from pods and
                     isolated pod walls were collected and  immediately frozen
                     in liquid nitrogen.  Pod walls were pooled for  mRNA
                     extraction. cDNA was prepared from polyA+ enriched RNA.
                     The cDNA was directionally  ligated into the Unizap XR
                     vector from Stratagene and packaged using  Gigapack III
```

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              Gold packaging extracts.  Plasmids containing cDNA inserts
              were excised from the recombinant lambda-Zap phage using
              Ex-assist helper phage and propogated in XLOLR cells."
BASE COUNT      198 a    112 c    165 g    214 t
ORIGIN

Alignment Scores:
Pred. No.:               1.64e-114     Length:          689
Score:                   1063.00       Matches:         186
Percent Similarity:      91.27%        Conservative:    23
Best Local Similarity:   81.22%        Mismatches:      20
Query Match:             23.81%        Indels:          0
DB:                      13            Gaps:            0

US-10-056-454A-15_COPY_49_882 (1-834) x BI308555 (1-689)

Qy        585 ValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAla 604
              ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db          3 GTTGGTGACAAGACACTAGCATTTTGGTTGATGGACAAGGATATGTATGACTTCATGGCT 62

Qy        605 LeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArg 624
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db         63 TTAGACAGACCATCTACTCCTCTAATCGATCGTGGTATTGCATTACACAAAATGATTAGG 122

Qy        625 LeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGly 644
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CTTATTACTATGGGCCTTGGTGGTGAAGGGTATTTAAATTTTATGGGGAATGAATTCGGC 182

Qy        645 HisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIle 664
              |||||||||||||||||||||||||||   :::|||||||||   :::|||:::|||:::
Db        183 CATCCTGAGTGGATCGATTTTCCAAGGGGTGATCAACATCTTCCTAATGGCACAGTAGTT 242

Qy        665 ProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGlu 684
              |||||||||         ||||||||||||||||||||||||||||||||||||||||||
Db        243 CCTGGGAATAACAACAGTTATGATAAATGCAGGCGTAGATTTGACTTGGGTGATGCAGAA 302

Qy        685 TyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLys 704
              |||||||||||   |||:::||||||||||||||||   |||||:::||||||:::::::
Db        303 TATCTAAGATATCATGGAATGCAAGAATTTGATCGAGCTATGCAGCACCTAGAAGAAAGA 362

Qy        705 TyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMet 724
              |||   ||||||   ||||||||||||:::||||||||||||:::||||||||||||:::
Db        363 TATGGTTTCATGATTTCTGAGCACCAATATATTTCAAGGAAAAATGAAGGTGACAGAGTT 422

Qy        725 IleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyr 744
              |||::::||||||:::   |||||||||||||||||||||||||||||||   ||||||
Db        423 ATAATCTTTGAAAGGGACAACCTGGTCTTTGTATTCAATTTTCACTGGACCAACAGTTAT 482

Qy        745 SerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAsp 764
              |||||||||::::::   ||||||||||||||||||||||||:::   ||||||||||||
Db        483 TCAGATTACAAAGTTGGCTGTTTAAAGCCAGGGAAATATAAGATTGTCTTGGATTCAGAT 542

Qy        765 AspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGlu 784
              :::   |||||||||||||||   |||::::::|||   |||||||||||||||   |||
Db        543 GAGTCCTTGTTTGGTGGCTTCAATAGGCTCAATCATACTGCTGAGTACTTCACTTCGGAA 602

Qy        785 GlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaVal 804
              |||||||||||||||||||||||||||   :::||||||||||||||||:::||||||||
Db        603 GGATGGTATGATGACCGGCCTCGTTCCTTCCTCGTTTATGCACCTTGTAGAACAGCAGTG 662

Qy        805 ValTyrAlaLeuValAspLysGluGlu 813
              ||||||||||||||||||      |||
Db        663 GTATATGCTCTTGTAGATGGAGTTGAA 689

RESULT 9
BE195628
LOCUS       BE195628                 801 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0089P20f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0089P20f,
            mRNA sequence.
ACCESSION   BE195628
VERSION     BE195628.2  GI:13188305
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 26, 2000 this sequence version replaced gi:8707823.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 408
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 611.
FEATURES             Location/Qualifiers
     source          1..801
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEh0089P20f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      220 a    146 c    198 g    236 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:               2.8e-114      Length:          801
Score:                   1062.00       Matches:         205
Percent Similarity:      85.87%        Conservative:    26
Best Local Similarity:   76.21%        Mismatches:      32
Query Match:             23.78%        Indels:          6
DB:                      10            Gaps:            0

US-10-056-454A-15_COPY_49_882 (1-834) x BE195628 (1-801)

Qy        501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
              ||||||||||||:::|||||||||||::::::||||||||||||||||||||||||||||
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```
Db          2 ATTCATGGACTTTATCCGGATGCTGTATCCATTGGTGAAGATGTCAGCGGAATGCCTACA 61

Qy        521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
              ||||||||||||||    :::||||||||||||||||||||||||||||||||||:::
Db         62 TTTTGCATCCCTGTCCCAGATGGTGGTCTTGGTTTTGACTATCGCCTGCATATGGCTGTA 121

Qy        541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
              ||||||||   |||||||||||||||:::    ||||||   |||::::::||||||||
Db        122 GCAGATAAATGGATTGAACTCCTCAAGCAAAGTGACGAATCTTGGAAAATGGGCGATATT 181

Qy        561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
              ||||||||||||||||||||||||||    ||||||||||||:::|||||||||||||||
Db        182 GTGCACACCCTAACAAATAGAAGGTGGCTTGAGAAGTGTGTCACTTATGCAGAAAGTCAT 241

Qy        581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GATCAAGCACTAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTAT 301

Qy        601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
              |||||||||||||||||||||||||||       |||||||||||||||||||||
Db        302 GATTTCATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACAT 361

Qy        621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AAAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTAATTTCATGGGA 421

Qy        641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
              ||||||||||||||||||||||||||||||||||||||||        |||
Db        422 AATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGGGGTCCGCANACTCTTCCAACC 481

Qy        661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
              |||   |||:::||||||||        ||||||||||||||||||||:::||||||||
Db        482 GGCAAAGTTCTCCCTGGCAATAACAATAGTTATGATAAATGCCGCCGTAAATTTGATCTT 541

Qy        681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
              |||||||||::::::|||||||||||||||||::::|||||||||||||:::   |||    :::
Db        542 GGAGATGCAGATTTTCTTAGATATCGTGGAATGCAAGAGTTCGATCAGGCAATGCCCCAT 601

Qy        701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
              ||||||   |||        |||||||||||||||||||||::::::||||||||   |||
Db        602 CTTGAGGGAAAAATAGGGTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACTTGAG 661

Qy        721 GlyAspArgMetIleVal-PheGluLysGlyAsnLeuValPheValPheAsnPheHisTr 740
               |||::::::    :::  ||||||:::||||||||||||||||||||||||||    ||
Db        662 GAAGATAAGGTGAACATCTTTTGAAAGAGGAAATTTGGTATTTGTTTTCAACTTTCCCTG 721

Qy        740 p-ThrLysSerTyrSerAspTyr--ArgIleAlaCysLeuLysPro-GlyLysTyr-Lys 758
              | :::    ::::::         ||||||  |||:::        |||||| ||||||||| |||
Db        722 GGAGCAATAACTTTTTTGACTACCCCGGTTGGGGGGTTCCAAGCCTTGGGAAATACCAAG 781

Qy        759 ValAlaLeuAspSer 763
              ||||||      |||
Db        782 GTGGCCTTTAAATCT 796
```

RESULT 10
BH770747/c

```
LOCUS       BH770747                1482 bp    DNA     linear   GSS 01-MAY-2002
DEFINITION  LLMGtag494 MG1363 Random Sequence Tag Library Lactococcus lactis
            subsp. cremoris genomic, DNA sequence.
ACCESSION   BH770747
VERSION     BH770747.1  GI:20373704
KEYWORDS    GSS.
SOURCE      Lactococcus lactis subsp. cremoris.
  ORGANISM  Lactococcus lactis subsp. cremoris
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Lactococcus.
REFERENCE   1  (bases 1 to 1482)
  AUTHORS   Bolotin,A., Ehrlich,S.D. and Sorokin,A.
  TITLE     Studies of genomes of dairy bacteria Lactococcus lactis
  JOURNAL   Sci. Aliments,  (2002) In press
COMMENT     Contact: Sorokin A
            Genetique Microbienne
            INRA
            CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
            Tel: 33 1 34 65 25 16
            Fax: 33 1 34 65 25 21
            Email: sorokine@jouy.inra.fr
            best homologue in strain IL1403 is glgB (88%)
            Class: shotgun
            High quality sequence start: 30
            High quality sequence stop: 1454.
FEATURES             Location/Qualifiers
     source          1..1482
                     /organism="Lactococcus lactis subsp. cremoris"
                     /strain="MG1363"
                     /db_xref="taxon:1359"
                     /clone_lib="MG1363 Random Sequence Tag Library"
                     /note="Vector: pSGMU2; Site_1: SmaI; Library of
                     chromosomal fragments of L.lactis strain MG1363 was
                     prepared by partial AluI digestion or by sonication."
BASE COUNT      455 a    304 c    257 g    465 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              1.41e-113      Length:         1482
Score:                  1060.00        Matches:        220
Percent Similarity:     65.90%         Conservative:   68
Best Local Similarity:  50.34%         Mismatches:     125
Query Match:            23.74%         Indels:         24
DB:                     17             Gaps:           9

US-10-056-454A-15_COPY_49_882 (1-834) x BH770747 (1-1482)

Qy        187 ThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsn 206
              |||:::||||||||||||||      ||||:::    |||    ||||:::|||||||||||||||
Db       1311 ACTTTCCGCGAATGGGCACCAAATGCTAAAAAAGCTTGGCTTGTTGGTGACTTTAACAAT 1252

Qy        207 TrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeu 226
              |||:::   |||    :::    :::    :::               |||    ||||||||    :::
Db       1251 TGGGAAAACAACTATGAA---CTAAAACAGGCTTATGGCGGGACTTGGGAAATTTCAGTT 1195

Qy        227 ProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMet 246
              |||                      :::|||   ||||||:::||||||||||::::::
Db       1194 CCTGGA-----------------TTATTACCTGTGGGTTCTAAAGTAAAAATAAAGTTG 1153

Qy        247 AspThrProSerGly---ValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
               |||::::|||    |||           :::|||::::::|||    |||:::
Db       1152 CTTTTGCCAACTGGAGAAGTTGTTTATCGTGTTCCTTCTTACATTATGTATGCT------ 1099

Qy        266 LeuProAspGlu---IleProTyrAsnGlyIleHisTyrAspProProGluGluGluArg 284
              ||||||:::|||               :::|||:::               |||                  :::
Db       1098 CTTCCTAATGAAAATCATGGTTTAGACGGGGTTATTACTCAGCCT-----------AAG 1051

Qy        285 TyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHis 304
              |||    :::::::::         ||||||         ::::::         ||||||||||:::|||
Db       1050 TACGAATGGAAAAATAAAAGCCCTAAACTAAGCGAAGCACCTTTGATTTATGAAGCACAT 991

Qy        305 IleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluVal 324
              ||||||:::|||:::     |||    ||||||||||||||||          |||          :::|||
Db        990 ATTGGGATTTCAACCGAAGAATACAAAATTAATTCTTACAAAGAATTCACGCGCGATGTT 931

Qy        325 LeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHis 344
              ||||||||||||||||||       |||||||||       :::|||:::|||||||||       ||||||
Db        930 TTACCCAGAATTAAAAAAGATGGTTACAATACCATTCAGCTGATGGCAATTATGGAACAC 871

Qy        345 SerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPhe 364
                       ||||||||||||||||||    |||:::||||||||||||||    ||||||||||||
Db        870 CCGCTCTATGCTAGTTTTGGTTATCAAGTTTCCAATTTTTTTGCCATCTCTAGTCGCTTT 811

Qy        365 GlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValVal 384
              |||    |||:::||||||          |||||||||||||||||||||       ||||||:::    |||
Db        810 GGTCAGCCAGAAGATTTAATGGAATTGATTGATAAAGCACATGGTTTGGGTTTGCAAGTG 751

Qy        385 LeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPhe 404
              |||:::|||:::||||||||||||||||          |||          ||||||||||||    |||
Db        750 CTTTTAGACGTGGTTCATTCACATGCTGTAAAAAATATTGAGGATGGGCTCAACTATTTT 691
```

```
Qy        405 AspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
              |||  |||:::::  ||||||||   |||   ||||||   |||     |||
Db        690 GATGGAACAGAAAATCAGTATTTTCATGAAGGCGAACGGGGAAATCATCCAGCTTGGAAG 631

Qy        425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArg 444
              :::::||||||||||||||      ||||||||   :::||||||||||||     :::
Db        630 ACGAAACTTTTAATTATGGCAAAGATGAAGTCCTTCATTTTTACTATCAAATCTAAAA 571

Qy        445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
              :::||||||||   :::   ||||||||||||||||||||||||||   ||||||:::
Db        570 TTTTGGCTAGACATTTATCATTTCGATGGCTTTCGTTTTGATGGAGTAATTTCAATGCTT 511

Qy        465 TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeu 484
              |||     ||||||||         ||||||   :::|||   :::||||||   |||
Db        510 TATCATGACCATGGTTTAGGAACTGCTTTTACA---GATTATAGTAAGTATTTTTCACTT 454

Qy        485 AlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeu 504
                |||||||||:::||||||    ||||||||||||   |||:::|||    |||
Db        453 AATACAGATGTTGAAGCCGTGACATATTTGATGCTGGCTAATGAACTAACTCATCTCTTT 394

Qy        505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
                 |||   |||   ||||||   ||||||:::|||   ||||||          :::|||
Db        393 AATCCATCAGCAACAACAATCGCCGAAGACATGTCTGCCATGCCTGGGATGGCACTACCT 334

Qy        525 ValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
              :::         ||||||:::||||||||||||||||||   |||   |||   |||
Db        333 ATCTCGGCTGGCGGAATTGGTTTTGATTATCGTTTGTCAATGGGAATTCCTGATTTTTGG 274

Qy        545 IleGluLeuLeuLys---LysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
              |||:::   ||||||   |||   |||               :::         :::
Db        273 ATTAAACAATTGAAAGAAAAAACAGATAATAGTTTAGATTTGCTAAGTTTATGGTGGGAA 214

Qy        564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
              ||||||   ||||||      ||||||   :::   |||:::||||||||||||||||||
Db        213 TTGACGACCAGACGACCTGGAGAGAAAAATATCGGTTATTCAGAAAGTCATGACCAAGCT 154

Qy        584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr--------- 600
              ||||||||||||||||||:::         ||||||   ::::::::::::|||
Db        153 TTAGTTGGTGATAAAACACTGATGATGTGGCTAGCTAATGAAGAAATCTATTGGAACATG 94

Qy        601 ------------AspPheMetAlaLeuAspArgProSerThrSerLeuIle 613
                          :::   :::|||:::|||         |||:::
Db         93 TACATCAATAGTCAATCTATCATGATTGACCAGCCAATGCTTCCCTTAGTT 43

RESULT 11
AV939010
LOCUS       AV939010               678 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV939010 K. Sato unpublished cDNA library, strain H602 adult,
            heading stage top three leaves Hordeum vulgare subsp. spontaneum
            cDNA clone bah20e24 5', mRNA sequence.
ACCESSION   AV939010
VERSION     AV939010.1  GI:18234807
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1..678
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah20e24"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT      193 a    135 c    154 g    194 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              2.81e-112     Length:         678
Score:                  1044.00       Matches:        190
Percent Similarity:     93.78%        Conservative:   21
Best Local Similarity:  84.44%        Mismatches:     13
Query Match:            23.38%        Indels:         1
DB:                     10            Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x AV939010 (1-678)

Qy        185 GlyIleThrTyrArg-GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPh 204
              ||||||||||||||     ||||||   ||||||   ||||||||||||:::||||||||
Db          5 GGTATCACTTACCGAGNAATGGGCTCCTGGNGCGCATTCTGCAGCATTAGTAGGTGACTT 64

Qy        204 eAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIl 224
               ||||||||:::   |||||||||   ||||||||::::::::||||||||||||
Db         65 CAACAATTGGAACCCAAATGCAGATACTATGACCAGAGATGATTATGGTGTTTGGGAGAT 124

Qy        224 ePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIl 244
               ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        125 TTTCCTCCCTAACAATGCTGATGGATCCCCTGCTATTCCTCATGGCTCACGTGTAAAGAT 184

Qy        244 eArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLe 264
               ||||||||||||||||||||||||||||||||||   |||||||||   :::|||:::
Db        185 ACGGATGGATACTCCATCTGGTGTGAAGGATTCAATTTCTGCTTGGATCAAGTTCTCTGT 244

Qy        264 uGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGluGluGluAr 284
               :|||   |||   |||||||||:::|||||||||:::||||||||||||||||||:::
Db        245 GCAGGCTCCAGGTGAAATACCATTCAATGGCATATATTATGATCCACCTGAAGAGGAGAA 304

Qy        284 gTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHi 304
               :|||:::|||||||||:::||||||:::|||:::||||||||||||||||||||||||
Db        305 GTATGTCTTCCAACATCCTCAACCTAAACGACCAGAGTCACTAAGGATATATGAATCACA 364

Qy        304 sIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluVa 324
               |||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        365 CATTGGAATGAGCAGCCCGGAACCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGT 424

Qy        324 lLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHi 344
               |||||||||||||||:::||||||||||||||:::||||||||||||||||||||||
Db        425 GCTGCCAAGAATTAAAAGGCTTGGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCA 484

Qy        344 sSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPh 364
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 TTCATACTATGCGAGCTTTGGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTT 544

Qy        364 eGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValVa 384
               |||||||||:::||||||||||||||||||:::|||||||||||||||::::::||
Db        545 TGGAACTCCAGAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGT 604

Qy        384 lLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPh 404
               ||||||||||||||||||||||||:::||||||||||||||||||||||||||   ||
Db        605 TCTTATGGATATTGTTCATAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTT 664

Qy        404 eAspCysThrAsp 408
               ||||   ||||||
Db        665 CGATGGCACTGAT 677

RESULT 12
BQ716536
LOCUS       BQ716536               898 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8478168 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6196860 5', mRNA sequence.
```

```
ACCESSION   BQ716536
VERSION     BQ716536.1  GI:21855433
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 898)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13605  row: p  column: 13
            High quality sequence stop: 595.
FEATURES             Location/Qualifiers
     source          1..898
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6196860"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
BASE COUNT      234 a    171 c    225 g    268 t
ORIGIN

Alignment Scores:
Pred. No.:              4.64e-111     Length:          898
Score:                  1035.50       Matches:         189
Percent Similarity:     80.14%        Conservative:    45
Best Local Similarity:  64.73%        Mismatches:      54
Query Match:            23.19%        Indels:          4
DB:                     14            Gaps:            3

US-10-056-454A-15_COPY_49_882 (1-834) x BQ716536 (1-898)

Qy        378 HisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThr 397
              |||   :::|||||:::|||||:::|||:::||||||||||||||||||     |||:::
Db          2 CATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGCCATGCTTCAAAAAATTCA 61

Qy        398 LeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArg 417
                 ||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db         62 GCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTATTTCATTCTGGACCTAGA 121

Qy        418 GlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArg 437
              |||   |||   :::||||||||||||||||||   |||   :::|||||||||||||||
Db        122 GGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCCAGCTGGGAAGTTTTAAGA 181

Qy        438 TyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPhe 457
              :::||||||||||||   ||||||||||||:::   :::::||||||||||||||||||
Db        182 TTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGCTTTGATGGATTTCGTTTT 241

Qy        458 AspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsn 477
              ||||||||||||||||||:::|||   |||||||||:::      ||||||:::|||:::
Db        242 GATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGTCAAGGTTTCTCAGGTGAT 301

Qy        478 TyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuVal 497
              |||   ||||||||||||||         |||   ||||||:::   |||||||||||
Db        302 TACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTGACTTACCTCATGTTGGCA 361

Qy        498 AsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGly 517
              |||   |||:::|||   |||   ||||||:::|||||||||   ||||||||||||||
Db        362 AATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATAGCTGAGGATGTATCAGGA 421

Qy        518 MetProThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHis 537
              ||||||         |||   |||:::   :::||||||   ||||||||||||||||||
Db        422 ATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGTTTTGACTATCGACTAGCC 481

Qy        538 MetAlaIleAlaAspLysArgIleGluLeuLeuLysLys---ArgAspGluAspTrpArg 556
              |||||||||   ||||||   |||:::||||||||||:::      :::||||||||||||
Db        482 ATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTTAAAGATGAAGACTGGAAC 541

Qy        557 ValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyr 576
              :::||||||||||||:::||||||||||||||||||:::     |||||||||:::::|||
Db        542 ATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTTGAAAAGTGCATTGCTTAT 601

Qy        577 AlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAsp 596
              ||||||||||||||||||||||||||||||||||||:::::||||||||||||||||||
Db        602 GCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTGGCATTTTGGTTGATGGAT 661

Qy        597 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGly 616
                 :::||||||      |||:::::      |||      |||      :::||||||||||
Db        662 GCCGAAATGTATACAAACATGAGTGTCCTGACTCCCTTTACTCCAGTTATTGATCGCGGA 721

Qy        617 IleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGlu---GlyTyr 635
              |||   ||||||||||||||||||||||:::|||   |||   |||   |||   ||||||
Db        722 ATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGGCTGGGTGGGAGAAAGGCTAT 781

Qy        636 LeuAsnPheMetGlyAsnGlu---PheGlyHisProGluTrpIle-AspPheProArgAl 654
              |||:::|||:::|||         :::|||   |||||||||:::  |||||||||:::
Db        782 CTCCATTTTCTGGGGAAAGGAATTTGGGGCATCCCTGAATGGGTTAGACTTTCCCCAGGA 841

Qy        654 aGluGlnHisLeuSerAspGlySerValIlePro 665
                 :::   :::   :::      :::::|||
Db        842 AAGGGAAAAAATGGGAGAGTTCCCCTTAATGCCC 875

RESULT 13
BE602527
LOCUS       BE602527                 731 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
            mRNA sequence.
ACCESSION   BE602527
VERSION     BE602527.2  GI:13190371
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Aug 21, 2000 this sequence version replaced gi:9860088.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 322
            Seq primer: AATTAACCCTCACTAAAGGG
```

```
           High quality sequence stop: 680.
FEATURES             Location/Qualifiers
     source          1..731
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEh0099J22f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoRl; Site_2: Xhol;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      194 a    132 c    186 g    216 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:              2.86e-110       Length:         731
Score:                  1027.50         Matches:        194
Percent Similarity:     86.78%          Conservative:   16
Best Local Similarity:  80.17%          Mismatches:     32
Query Match:            23.01%          Indels:         2
DB:                     10              Gaps:           0

US-10-056-454A-15_COPY_49_882 (1-834) x BE602527 (1-731)

Qy        412 PheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGly 431
              ||||||   |||:::||||||:::||||||||||||||||||||||:::||||||||||||
Db          8 TTTCATGGCGGCTCACGGGGCCATCACTGGATGTGGGATTCTCGTGTGTTCAACTACGGG 67

Qy        432 AsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLys 451
              |||    |||||||:::|||   ||||||||||||||||||||||     |||:::     :::|||
Db         68 AATAAGGAAGTTATAAGGGTTCTACTTTCCAATGCCAGATGGGGGCTTGAGGAATATAAG 127

Qy        452 PheAspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSer 471
              |||    ||||||    |||||||||    |||     |||||||||        |||||||||
Db        128 TTCCATGGGTTCCCATTCGACGGGCCCACCTTCATGATGTATACCCCCCATGGATTACAA 187

Qy        472 ValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaVal 491
              |||    |||||||||    |||    ||||||||||||    ||||||||||||||||||||
Db        188 GTACC-TTTACAGGAGC-TACCATGAATATTTTGGCTTTGCCACGGATGTAGATGCAGTT 245

Qy        492 ValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIle 511
              |||||||||||||||||||||||||||||||||||     |||:::|||:::|||:::||||||
Db        246 GTTTACTTGATGCTGGTGAATGATCTAATTCACGCGCTNTATCCTGAAGCCGTTACTATT 305

Qy        512 GlyGluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyGlyValGly 531
              ||||||||||||||||||||||||||||||     :::|||||||||    ||||||||||||
Db        306 GGTGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGGTTGGT 365

Qy        532 PheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArg 551
              ||||||||||||||||||||||||:::|||||||||    ||||||||||||||
Db        366 TTTGACTATCGCTTACATATGGCCGTTGCCGATAAATGGATTGAACTTCTCAAAGGAAGC 425

Qy        552 AspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlu 571
              ||||||    |||    :::|||:::||||||||||||||||||||||||||||||    |||
Db        426 GATGAAGGTTGGGAGATGGGTAATATTGTGCACACACTAACAAATAGAAGGTGGTTGGAA 485

Qy        572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 AAGTGTGTTACTTATGCTGAAAGTCATGATCAAGCACTTGTTGGAGACAAGACTATTGCA 545

Qy        592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
              |||||||||||||||||||||||||||||||||||||||||||:::     |||||||||
Db        546 TTCTGGTTGATGGACAAGGATATGTATGATTTCATGGCTCTGAACGGACCTTCGACACCT 605

Qy        612 LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
                 |||||||||||||||||||||||||||||||||||||||:::||||||        |||
Db        606 AATATTGATCGCGGAATAGCACTGCATAAAATGATTAGACTTATCACAATGGCTNTAGGA 665

Qy        632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPhe 651
              ||||||||||||||||||||||||||||||||||    |||||||||||||||||
Db        666 GGAGAGGGTTATCTTAACTTTATGGGAAATGAGTTCCGGCATCCTGAATGGATAGACTNT 725

Qy        652 ProArg 653
              ||||||
Db        726 CCAAGA 731

RESULT 14
BU005876
LOCUS       BU005876                 717 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGG9F08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGG9F08, mRNA sequence.
ACCESSION   BU005876
VERSION     BU005876.1  GI:22440271
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGG9  row: F  column: 08.
FEATURES             Location/Qualifiers
     source          1..717
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGG9F08"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
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                directionally cloned into a custom medium-copy vector and
                transformations made with four size classes to minimize
                size bias. Details of each source of RNA and library
                construction can be obtained at http://cgpdb.ucdavis.edu/
                TAG_LIB=QG_EFGHJ lettuce serriola
                TAG_TISSUE=germinating seeds
                TAG_SEQ=TCTGTGCGGG"
BASE COUNT      233 a    122 c    155 g    206 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              8.56e-106    Length:        717
Score:                  989.50       Matches:       183
Percent Similarity:     82.56%       Conservative:  30
Best Local Similarity:  70.93%       Mismatches:    26
Query Match:            22.16%       Indels:        20
DB:                     14           Gaps:          1

US-10-056-454A-15_COPY_49_882 (1-834) x BU005876 (1-717)

Qy        82 GluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSer 101
             ||||||:::|||        |||           :::   :::
Db         2 GAGGAAGTAGATTTAGTTTCTTTATTTGATATTGATAAA--------------------- 40

Qy       102 LysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArg 121
                                                     ||||||:::   ||||||:::
Db        41 -----------------------------------GAAAGTGAAGAAATTAGAAAATTA 64

Qy       122 GlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
                ||||||||||||||    |||:::::::||||||||||||||||||||||||:::|||
Db        65 TCGATTCCTCCTCCTGGAAAAGGGGAGAGAATATATGAAATTGATCCACTTTTAAGCAAT 124

Qy       142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
             :::|||:::||||||:::|||||||||||    |||||||||:::|||||||||||||||
Db       125 CATCGTGAACATCTTGAGTATAGATATTCACATTACAAGAAGATACGTGAAGCAATTGAC 184

Qy       162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
             ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       185 AAATATGAAGGTGGTTTGGAGGCGTTTTCACGTGGTTATGAAAAAATTAGGTTTCACTCGA 244

Qy       182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
             |||     ||||||||||||||||||||||||||||    ||||||:::||||||:::||||||
Db       245 AGCAAAACAGGTATCACTTATAGAGAATGGGCACCTGGGGCAAAGTCTGCTTCACTTATT 304

Qy       202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
             ||||||||||||||||||:::     ||||||||||:::||||||||||||||||||||||||
Db       305 GGAGATTTCAACAACTGGAATCCAAATGCTGATGTTATGACCCGGAATGAATTTGGTGTG 364

Qy       222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
             ||||||||||||||||||||||||||||||    |||         ||||||||||||||||||
Db       365 TGGGAGATCTTTTTGCCAAACAATGTTGATGATTCTTCACCTATTCCTCATGGTTCTCGA 424

Qy       242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
             ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db       425 GTAAAGATTCGTATGGATACGCCATCTGGCATTAAAGACTCGATTCCTGCTTGGATCAAG 484

Qy       262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu 281
             :::||||:::|||     |||    |||||||||||||||||||||:::|||||||||||:::
Db       485 TTTTCAGTACAAGCACCTGGTGAGATTCCTTATAATGGAATATACTATGATCCCCCACAA 544

Qy       282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
             ||||||:::|||:::||||||||||||||||||||||||||||||||||||    ||||||
Db       545 GAGGAAAAATACGTGTTTCAACATCCAAGACCAAAGAAGCCGAAATCTCTTANGATTTAT 604

Qy       302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
             |||:::|||:::|||||||||||||    ||||||       :::::::|||   |||||||||
Db       605 GAGGCACATGTGGGAATGAGTAGTACGGAACCAATGGATCACACGTATGCTAACTTTAGA 664

Qy       322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMet 339
             |||:::|||||||||||||||||||    ||||||||||||||:::|||||||||
Db       665 GACGATGTTCTCCCTCGCATAAAGAA-CTCGGTTACAATGCAGTTCAAATCATG 717

RESULT 15
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AW065909
LOCUS       AW065909                 639 bp    mRNA    linear   EST 30-MAR-2000
DEFINITION  687002G09.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
            sequence.
ACCESSION   AW065909
VERSION     AW065909.1  GI:6020981
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 687002  row: G  column: 09.
FEATURES             Location/Qualifiers
     source          1..639
                     /organism="Zea mays"
                     /cultivar="Illinois High Oil"
                     /db_xref="taxon:4577"
                     /clone_lib="687 - Early embryo from Delaware"
                     /tissue_type="embryo"
                     /dev_stage="14, 21, 28, and 35 days after pollination"
                     /lab_host="E. coli SOLR"
                     /note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
                     ; Site_2: EcoRI; Library was prepared by Statagene using
                     the Uni-ZAP XR system (Stratagene BN937328-12). Clones
                     were picked by a Q-bot after blue/white selection
                     (ampicillin resistance - use 100 micrograms/microliter).
                     Developed from a pool of equal amounts of RNA from
                     developing embryos sampled at 14, 21, 28 and 35 days after
                     pollination of the Illinois High Oil Maize Strain Cycle
                     90. This closed strain has been selected for high oil
                     concentration for 90 generations and originates from the
                     1890s era open pollinated variety Burr's White"
BASE COUNT      200 a    118 c    151 g    170 t
ORIGIN

Alignment Scores:
Pred. No.:              2.76e-104    Length:        639
Score:                  976.00       Matches:       174
Percent Similarity:     91.94%       Conservative:  20
Best Local Similarity:  82.46%       Mismatches:    17
Query Match:            21.86%       Indels:        0
DB:                     10           Gaps:          0

US-10-056-454A-15_COPY_49_882 (1-834) x AW065909 (1-639)

Qy       170 PheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArg 189
             ||||||||    |||||||||    ||||||    |||||||||    ||||||||||||||
Db         5 TTCTCCCGTAGTTATGAGAAGTTTGGATTTAATCGCAGCGCGGAAGGTATCACATATCGA 64

Qy       190 GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAla 209
             ||||||||    ||||||   ||||||||||||:::||||||||||||||||||||||
Db        65 GAATGGGCTCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACTTCAACAACTGGGATCCA 124

Qy       210 AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn 229
             ||||||||    |||::::::||||||||||||||||||||||||||||||||||||||||
Db       125 AATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAAT 184

Qy       230 ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro 249
                |||||:::         ||||||||||||||||||||||:::||||||||||||||
Db       185 GCAGATGGTACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCA 244
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Qy        250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
              |||||:::||||||||||||||||||||||||      ||||||:::|||   |||   |||
Db        245 TCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAA 304

Qy        270 IleProTyrAsnGlyIleHisTyrAspProProGluGluGluArgTyrIlePheGlnHis 289
              |||||||||:::||||||:::|||||||||||||||||      :::|||:::|||:::|||
Db        305 ATACCATATGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCAT 364

Qy        290 ProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSer 309
                 :::||||||:::||||||||||||||||||||||||||:::|||:::||||||||||||
Db        365 GCGCAACCTAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGC 424

Qy        310 ProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLys 329
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        425 CCGGAACCGAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAA 484

Qy        330 LysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSer 349
              |||||||||||||||||||:::|||||||||||||||||||||||||||||||   |||
Db        485 AAACTTGGATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGC 544

Qy        350 PheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAspAsp 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        545 TTTGGATACCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGAT 604

Qy        370 LeuLysSerLeuIleAspLysAlaHisGluLeu 380
              ||||||||||||||||||:::||||||||||||
Db        605 TTGAAGTCTTTGATTGATAGAGCACATGAGCTT 637
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Search completed: July 6, 2003, 05:35:58
Job time : 2970 secs

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:12:47 ; Search time 8049.92 Seconds
(without alignments)
11409.857 Million cell updates/sec

Title: US-10-056-454A-18_COPY_45_3200
Perfect score: 3156
Sequence: 1 AAAAACCTCCTCCACTCAGT..........TGCTGATCTAATGATGTTTT 3156

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
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16: em_fun:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3154.2	99.9	3231	6	A58168	A58168 Sequence 18
2	2955.2	93.6	3074	6	AR123355	AR123355 Sequence
3	2849.6	90.3	2982	8	STU011888	AJ011888 Solanum t
4	2847.4	90.2	3033	6	A58164	A58164 Sequence 14
5	2846.4	90.2	2992	8	STU011890	AJ011890 Solanum t
6	2838	89.9	3003	6	A58162	A58162 Sequence 12
7	2733.2	86.6	2955	8	STU011885	AJ011885 Solanum t
8	2707.6	85.8	2975	6	A58163	A58163 Sequence 13
9	2485.8	78.8	2563	6	AX256072	AX256072 Sequence
10	2474.4	78.4	2529	6	A58167	A58167 Sequence 17
11	2446.6	77.5	2523	8	STU011889	AJ011889 Solanum t
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13	2436.6	77.2	2493	8	STSBEII	AJ000004 Solanum t
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18	1442.8	45.7	3090	6	A92164	A92164 Sequence 30
19	1429.8	45.3	3360	8	AB029548	AB029548 Phaseolus
20	1390.2	44.0	3549	8	PSSBEIGEN	X80009 P.sativum m
21	1377.8	43.7	2913	6	A92162	A92162 Sequence 28
22	1372.2	43.5	1393	6	AR123356	AR123356 Sequence
23	1323	41.9	2542	8	ATU22428	U22428 Arabidopsis
24	1296	41.1	2577	6	AX412751	AX412751 Sequence
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33	1257.6	39.8	2726	8	AF338432	AF338432 Triticum
34	1257.6	39.8	2970	8	AF286319	AF286319 Triticum
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41	796.8	25.2	833	8	STU011887	AJ011887 Solanum t
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ALIGNMENTS

RESULT 1
A58168
LOCUS A58168 3231 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 18 from Patent WO9634968.
ACCESSION A58168
VERSION A58168.1 GI:3713893
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 3231)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R., Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 18 07-NOV-1996;

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COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1. .3231
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ORIGIN

  Query Match             99.9%;  Score 3154.2;  DB 6;  Length 3231;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 TTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGATTAGATTTGAAGGAGAGAAGAAGA 180
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Qy        181 AAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCT 240
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Qy        241 AATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAG 300
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Db        285 AATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAG 344

Qy        301 CACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCT 360
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Qy        481 GATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTT 540
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Qy        541 GAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAA 600
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Qy        661 ATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAG 720
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Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
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Db        765 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 824

Qy        781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
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Db        825 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 884

Qy        841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
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Db        885 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 944

Qy        901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
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Qy        961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
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Qy       1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
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Db       1185 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1244

Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
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Db       1245 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1304

Qy       1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1320
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Qy       1321 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1380
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1484

Qy       1441 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1544

Qy       1501 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1545 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1604

Qy       1561 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1664

Qy       1621 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1665 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1724

Qy       1681 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1784

Qy       1741 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1785 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1844

Qy       1801 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1845 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1904

Qy       1861 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGTGTTGGC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1905 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGTGTTGGC 1964

Qy       1921 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1965 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGG 2024

Qy       1981 GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAA 2040
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2025 GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAA 2084

Qy       2041 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCA 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2085 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCA 2144

Qy       2101 TTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCA 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2145 TTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCA 2204

Qy       2161 TTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGA 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2205 TTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGA 2264

Qy       2221 GGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2265 GGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTC 2324

Qy       2281 CCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTAT 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2325 CCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTAT 2384

Qy       2341 GATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTG 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2385 GATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTG 2444

Qy       2401 CAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAA 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2445 CAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAA 2504

Qy       2461 CACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAAC 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2505 CACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAAC 2564

Qy       2521 CTAGTTTTTGTCTTTAATTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGG 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2565 CTAGTTTTTGTCTTTAATTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGG 2624

Qy       2581 CTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTC 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2625 CTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTC 2684

Qy       2641 GGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCT 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2685 GGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCT 2744

Qy       2701 CGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAA 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2745 CGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAA 2804

Qy       2761 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACG 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2805 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACG 2864

Qy       2821 AACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAA 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2865 AACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAA 2924

Qy       2881 TATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCTTTCCACTATT 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2925 TATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCTTTCCACTATT 2984

Qy       2941 AGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAAAATCGATGAA 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2985 AGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAAAATCGATGAA 3044

Qy       3001 TTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTCTGTAAATTGT 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3045 TTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTCTGTAAATTGT 3104

Qy       3061 CATCTCTTTANATGTACAGCCCACTAGAAATCAATTATGTGAGACCTAAAAAACAATAAC 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 CATCTCTTTANATGTACAGCCCACTAGAAATCAATTATGTGAGACCTAAAAAACAATAAC 3164

Qy       3121 CATAAAATGGAAATAGTGCTGATCTAATGATGTTTT 3156
              ||||||||||||||||||||||||||||||||||||
Db       3165 CATAAAATGGAAATAGTGCTGATCTAATGATGTTTT 3200


RESULT 2
~~AR123355~~
LOCUS       AR123355                3074 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6169226.
ACCESSION   AR123355
VERSION     AR123355.1  GI:14108321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3074)
  AUTHORS   Ek,B., Khosnoodi,J., Larsson,C.-T., Larsson,H. and Rask,L.
  TITLE     Starch branching enzyme II of potato
  JOURNAL   Patent: US 6169226-A 1 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1..3074
                     /organism="unknown"
BASE COUNT      902 a    558 c    712 g    896 t      6 others
ORIGIN

  Query Match             93.6%;  Score 2955.2;  DB 6;  Length 3074;
  Best Local Similarity   98.1%;  Pred. No. 0;
  Matches 3019;  Conservative    2;  Mismatches   41;  Indels   14;  Gaps    3;

Qy          3 AAACCTCCTCCACTCAGTCTTGGGATCTCTCTCTCTCTTCACGCTTCTCTTGGGGCCTTG 62
              |||||||||||||||||||||    |  ||||||||||||||||||||||||| ||||||
Db          1 AAACCTCCTCCACTCAGTCTTTG--TTTCTCTCTCTCTTCACGCTTCTCTTGGCGCCTTG 58

Qy         63 AACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCTCTATTTTT 122
              ||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db         59 AACTCAGCAATTTGACACTCAGTTAGTTACACTNCCATCACTTATCAGATCTCTATTTTT 118

Qy        123 TCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATTTGAAGGAGAG 173
              ||||||||||||||||||||||||| |||||||           | |     ||||||||
Db        119 TCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACCCTAAGGAGAG 178

Qy        174 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 238

Qy        234 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTT 293
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        239 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTT 298

Qy        294 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATC 353
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        299 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATC 358

Qy        354 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAG 413
              |||||||||||||||||||||||||||||||||||||| ||||||| |||||||||||||
Db        359 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAG 418

Qy        414 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGC 473
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        419 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGC 478

Qy        474 ATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGA 533
              ||||||||||| |||||||||||||||||||||||||||| |||||||||||||||||||
Db        479 ATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGGCAGATTAAAACTGAGAACGA 538

Qy        534 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATC 593
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        539 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATC 598

Qy        594 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    599 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 658

Qy    654 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 718

Qy    714 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 778

Qy    774 GTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 833
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    779 GTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 838

Qy    834 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 898

Qy    894 TGAGTGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGC 953
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    899 TGAGTGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGC 958

Qy    954 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1018

Qy   1014 TGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTC 1073
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |
Db   1019 TGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCC 1078

Qy   1074 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1138

Qy   1134 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACA 1193
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   1139 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACA 1198

Qy   1194 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1258

Qy   1254 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1318

Qy   1314 AAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1373
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 AAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1378

Qy   1374 TTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGA 1433
          ||||||||||||||||||||||||||| ||||||||||||||||||||||| ||||||||
Db   1379 TTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGGAACNCCCGACGA 1438

Qy   1434 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1439 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1498

Qy   1494 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1499 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1558

Qy   1554 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1559 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1618

Qy   1614 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1619 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1678

Qy   1674 GTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1733
          || ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db   1679 GTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1738

Qy   1734 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGA 1793
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   1739 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGA 1798

Qy   1794 TGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1853
          |||||  |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1799 TGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1858

Qy   1854 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGG 1913
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   1859 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGG 1918

Qy   1914 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1919 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1978

Qy   1974 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1979 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2038

Qy   2034 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2039 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2098

Qy   2094 TATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTC 2153
          ||||||||||||||||||||| |||||||||||||||||||||||| |||||||||| ||
Db   2099 TATAGCATTCTGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTC 2158

Qy   2154 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2159 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2218

Qy   2214 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2219 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2278

Qy   2274 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2279 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2338

Qy   2334 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2339 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2398

Qy   2394 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2399 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2458

Qy   2454 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2459 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2518

Qy   2514 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2519 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2578

Qy   2574 AGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2633
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2579 AGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2638

Qy   2634 TGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGA 2693
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2639 TGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGA 2698

Qy   2694 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2699 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2758

Qy   2754 AGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2810
          |||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2759 AGACAAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2818
```

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Qy     2811 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     2819 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878

Qy     2871 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2930
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2879 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2938

Qy     2931 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAA 2990
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     2939 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGCACAAACATATGTAA 2998

Qy     2991 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3050
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2999 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3058

Qy     3051 TGTAAATTGTCATCTC 3066
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Db     3059 TGTAAATTGTCATCTC 3074
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RESULT 3
STU011888
LOCUS       STU011888               2982 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-4.
ACCESSION   AJ011888
VERSION     AJ011888.1  GI:4584508
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2982)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2982)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1. .2982
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                     /cultivar="Desiree"
                     /db_xref="taxon:4113"
                     /note="sequence SBE A-4"
     gene            140. .2776
                     /gene="SBE II"
     CDS             140. .2776
                     /gene="SBE II"
                     /EC_number="2.4.1.18"
                     /standard_name="1,4-alpha-Glucan branching enzyme"
                     /codon_start=1
                     /product="starch branching enzyme II"
                     /protein_id="CAB40746.1"
                     /db_xref="GI:4584509"
                     /translation="MVYTLSGVRFPTVPSVYKSNGFSSNGDRRNANISVFLKKHSLSR
                     KILAEKSSYNSESRPSTIAASGKVLVPGIQSDSSSSSTDQFEFAETSPENSPASTDVD
                     SSTMEHASQIKTENDDVEPSSDLTGSVEELDFASSLQLQEGGKLEESKTLNTSEETII
                     DESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
                     SRGYERMGFTRSATGITYREWAPGAQSAALIGDFNNWDANADFMTRNEFGVWEIFLPN
                     NVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIYYDPPEEERYI
                     FQHPRPKKPKSVRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYNAVQIMAIQEH
                     SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                     MFDGTDSCYFHSGARGYHWMWDFRLFNYGNWEVLRYLLSNARWWLDEFKFDGFRFDGV
                     TSMMCTHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
                     PTFCVPVQDGGVGFDYRLHMAIADKWIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEG
                     YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPRNQFSYDKCRRRFDLGDAEYLRYRGLQ
                     EFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHWTKGYSDYRIG
                     CLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYAPSRTAVVYAL
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     transit_peptide 140. .283
                     /gene="SBE II"
     mat_peptide     284. .2773
                     /gene="SBE II"
                     /product="starch branching enzyme II"
                     /EC_number="2.4.1.18"
BASE COUNT      888 a    529 c    703 g    862 t
ORIGIN

  Query Match             90.3%;  Score 2849.6;  DB 8;  Length 2982;
  Best Local Similarity   97.9%;  Pred. No. 0;
  Matches 2920;  Conservative    2;  Mismatches   46;  Indels   14;  Gaps    3;
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Qy       54 GGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATC 113
            |||||||||||||||||||||||||||||||||||||||||| | |||||| ||||||||
Db        1 GGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTGCCATCACTTATCAGATC 60

Qy      114 TCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATTT 164
            |||||||||||||||||||||||||||||||||||| |||||||          | |
Db       61 TCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACCC 120

Qy      165 GAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCC 224
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCC 180

Qy      225 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTC 284
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      181 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTC 240

Qy      285 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGA 344
            ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |
Db      241 TGTATTCTTGAAAAAACACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAA 300

Qy      345 TTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCA 404
            |||||||||||||||||||||| ||||||||||||||||||||||||| |||||||||||
Db      301 TTCCGAATCCCGACCTTCTACAATTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAATCCA 360

Qy      405 GAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAA 464
            ||||||||||||||||||||||||||| |||||||||||| |||||||| ||||||||||
Db      361 GAGTGATAGCTCCTCATCCTCAACAGATCAATTTGAGTTCGCTGAGACATCTCCAGAAAA 420

Qy      465 TTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAAC 524
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      421 TTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAAC 480

Qy      525 TGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTT 584
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      481 TGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTT 540

Qy      585 TGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATAC 644
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATAC 600

Qy      645 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 704
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 660

Qy      705 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 764
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 720

Qy      765 TGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGG 824
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      721 TGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGG 780

Qy      825 TTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 884
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      781 TTTGGAAGCTTTTTCTCGTGGTTATGAAAGAATGGGTTTCACTCGTAGTGCTACAGGTAT 840
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Qy    885 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAA 944
Db    841 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGGGATTTCAACAA 900

Qy    945 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 1004
Db    901 TTGGGACGCAAATGCTGACTTTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 960

Qy   1005 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCAT 1064
Db    961 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTAT 1020

Qy   1065 GGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1124
Db   1021 GGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1080

Qy   1125 TCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGT 1184
Db   1081 TCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATAT 1140

Qy   1185 CTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGG 1244
Db   1141 CTTCCAACACCCACGGCCAAAGAAACCAAAGTCGGTGAGAATATATGAATCTCATATTGG 1200

Qy   1245 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1304
Db   1201 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1260

Qy   1305 TCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTA 1364
Db   1261 TCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTA 1320

Qy   1365 TTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAAC 1424
Db   1321 TTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAAC 1380

Qy   1425 GCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCAT 1484
Db   1381 GCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCAT 1440

Qy   1485 GGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGG 1544
Db   1441 GGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGG 1500

Qy   1545 CACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCG 1604
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Qy   1605 CCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTG 1664
Db   1561 CCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTG 1620

Qy   1665 GTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATAC 1724
Db   1621 GTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTGTAC 1680

Qy   1725 TCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAAC 1784
Db   1681 TCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAAC 1740

Qy   1785 TGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCC 1844
Db   1741 TGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCC 1800

Qy   1845 AGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCA 1904
Db   1801 AGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTGTTCCCGTTCA 1860

Qy   1905 AGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGA 1964
Db   1861 AGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGA 1920

Qy   1965 GTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAA 2024
Db   1921 GTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAA 1980

Qy   2025 TAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG 2084
Db   1981 TAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG 2040

Qy   2085 TGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGA 2144
Db   2041 TGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGA 2100

Qy   2145 TAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGT 2204
Db   2101 TAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTACACAAGATGATTAGGCTTGT 2160

Qy   2205 AACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCC 2264
Db   2161 AACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCC 2220

Qy   2265 TGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGG 2324
Db   2221 TGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCAG 2280

Qy   2325 AAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTT 2384
Db   2281 AAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTT 2340

Qy   2385 AAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGA 2444
Db   2341 AAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGA 2400

Qy   2445 GTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGT 2504
Db   2401 GTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGT 2460

Qy   2505 ATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGA 2564
Db   2461 ATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAGGCTATTCAGA 2520

Qy   2565 CTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCC 2624
Db   2521 CTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCC 2580

Qy   2625 ACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATG 2684
Db   2581 ACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATG 2640

Qy   2685 GTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTA 2744
Db   2641 GTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTA 2700

Qy   2745 TGCACTAGTAGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGT 2801
Db   2701 TGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGT 2760

Qy   2802 AGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGC 2861
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Db   2821 TTCTTGACGTATCTGGCAATATTGCATTAGTCTTGGCGGAATTTCATGTGACAACAGGTT 2880

Qy   2922 TGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAAC--A 2979
Db   2881 TGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAA 2940

Qy   2980 AACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
Db   2941 AACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 2982
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RESULT 4
A58164
LOCUS       A58164                  3033 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 14 from Patent WO9634968.
ACCESSION   A58164
VERSION     A58164.1  GI:3713889
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3033)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 14 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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                     TSMMYIHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
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BASE COUNT      900 a     553 c     712 g     868 t
ORIGIN

  Query Match             90.2%;  Score 2847.4;  DB 6;  Length 3033;
  Best Local Similarity   97.5%;  Pred. No. 0;
  Matches 2919;  Conservative    2;  Mismatches   48;  Indels   24;  Gaps    2;

Qy         53 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGAT 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          5 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTTATCAGAT 64

Qy        113 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATT 163
              |||||||||||||||||||||||||||||||||||||||  ||| |||          | |
Db         65 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATAAAAGGATAGATTTGTAAAAACC 124

Qy        164 TGAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 223
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CTAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 184

Qy        224 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTT 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTT 244

Qy        284 CTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACG 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACA 304

Qy        344 ATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCC 403
              |||||||| ||||||||||||||||||||||||||||||||||||||| |||||| ||
Db        305 ATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCC 364

Qy        404 AGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAA 463
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        365 AGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAA 424

Qy        464 ATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 523
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Db        425 ATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 484

Qy        524 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATT 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
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Qy        584 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 604

Qy        644 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 664

Qy        704 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        764 TTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTG 823
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Qy        824 GTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTA 883
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Qy        884 TCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACA 943
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Qy       1004 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCA 1063
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Qy       1064 TGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1123
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Qy       1124 TTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATG 1183
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Qy       1184 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTG 1243
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Qy       1244 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1303
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Qy    2969 AGTGCTGAACAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
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RESULT 5
STU011890
LOCUS       STU011890              2992 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
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ACCESSION   AJ011890
VERSION     AJ011890.1  GI:4584512
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE   1  (bases 1 to 2992)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2992)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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ORIGIN

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  Matches 2918;  Conservative    2;  Mismatches   48;  Indels   24;  Gaps    2;

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Qy        2625 ACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATG 2684
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Db        2581 ACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATG 2640

Qy        2685 GTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTA 2744
               |||||||||||||||||||||||||||||||||||||||| ||| |||||||||||||||
Db        2641 GTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCTA 2700

Qy        2745 TGCACTAGTAGACA---------------AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGT 2789
               ||||||||||||||               ||||||||||||||||||||||||||| |||
Db        2701 TGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGT 2760

Qy        2790 AGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAC 2849
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2761 AGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAC 2820

Qy        2850 GCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATG 2909
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2821 GCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATG 2880

Qy        2910 TGACAAAAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAA 2969
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 TGACACAAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAA 2940

Qy        2970 GTGCTGAACAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 GTGCTGAACAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 2992
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RESULT 6
A58162
LOCUS       A58162                  3003 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 12 from Patent WO9634968.
ACCESSION   A58162
VERSION     A58162.1  GI:3713887
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3003)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 12 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1..3003
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      895 a    535 c    706 g    867 t
ORIGIN

  Query Match             89.9%;  Score 2838;  DB 6;  Length 3003;
  Best Local Similarity   97.9%;  Pred. No. 0;
  Matches 2920;  Conservative    2;  Mismatches   47;  Indels   15;  Gaps    4;

Qy          53 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGAT 112
               ||||||||||||||||||||||||||||||||||||||||||| | |||||| |||||||
Db           3 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTGCCATCACTTATCAGAT 62

Qy         113 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATT 163
               ||||||||||||||||||||||||||||||||||||| |||||||          | |  
Db          63 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACC 122

Qy         164 TGAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 223
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 CTAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 182

Qy         224 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTT 283
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         183 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATATTT 242

Qy         284 CTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACG 343
               |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||| 
Db         243 CTGTATTCTTGAAAAAACACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACA 302

Qy         344 ATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCC 403
               ||||||||||||||||||||||| ||||||||||||||||||||||||| ||||||||||
Db         303 ATTCCGAATCCCGACCTTCTACAATTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAATCC 362

Qy         404 AGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAA 463
               |||||||||||||||||||||||||||| |||||||||||| |||||||| |||||||||
Db         363 AGAGTGATAGCTCCTCATCCTCAACAGATCAATTTGAGTTCGCTGAGACATCTCCAGAAA 422

Qy         464 ATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 523
               |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db         423 ATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 482

Qy         524 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATT 583
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Db    483 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATT 542

Qy    584 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 643
Db    543 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 602

Qy    644 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 703
Db    603 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 662

Qy    704 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 763
Db    663 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 722

Qy    764 TTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTG 823
Db    723 TTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTG 782

Qy    824 GTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTA 883
Db    783 GTTTGGAAGCTTTTTCTCGTGGTTATGAAAGAATGGGTTTCACTCGTAGTGCTACAGGTA 842

Qy    884 TCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACA 943
Db    843 TCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGGGATTTCAACA 902

Qy    944 ATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTC 1003
Db    903 ATTGGGACGCAAATGCTGACTTTATGACTCGGAATGAATTTGGTGTCTGAGAGATTTTTC 962

Qy   1004 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCA 1063
Db    963 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTA 1022

Qy   1064 TGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1123
Db   1023 TGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1082

Qy   1124 TTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATG 1183
Db   1083 TTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATA 1142

Qy   1184 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTG 1243
Db   1143 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGGTGAGAATATATGAATCTCATATTG 1202

Qy   1244 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1303
Db   1203 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1262

Qy   1304 CTCGCAT-AAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 1362
Db   1263 CTCGCATAAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 1322

Qy   1363 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGA 1422
Db   1323 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGA 1382

Qy   1423 ACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 1482
Db   1383 ACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 1442

Qy   1483 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 1542
Db   1443 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 1502

Qy   1543 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCC 1602
Db   1503 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTTC 1562

Qy   1603 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 1662
Db   1563 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 1622

Qy   1663 TGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTAT 1722
Db   1623 TGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTGT 1682

Qy   1723 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 1782
Db   1683 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 1742

Qy   1783 ACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTC 1842
Db   1743 ACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTC 1802

Qy   1843 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTT 1902
Db   1803 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTGTTCCCGTT 1862

Qy   1903 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 1962
Db   1863 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 1922

Qy   1963 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 2022
Db   1923 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1982

Qy   2023 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082
Db   1983 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2042

Qy   2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142
Db   2043 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 2102

Qy   2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202
Db   2103 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTACACAAGATGATTAGGCTT 2162

Qy   2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262
Db   2163 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2222

Qy   2263 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2322
Db   2223 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2282

Qy   2323 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2382
Db   2283 AGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2342

Qy   2383 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2442
Db   2343 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2402

Qy   2443 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2502
Db   2403 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2462

Qy   2503 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2562
Db   2463 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAGGCTATTCA 2522

Qy   2563 GACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2622
Db   2523 GACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2582

Qy   2623 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGA 2682
Db   2583 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGA 2642

Qy   2683 TGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2742
Db   2643 TGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2702
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Qy        2743 TATGCACTAGTAGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTA 2799
               ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db        2703 TATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTA 2762

Qy        2800 GTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGA 2859
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Db        2763 GTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCCACATAGA 2822

Qy        2860 GCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGG 2919
               ||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Db        2823 GCTTCTTGACGTATCTGGCAATATTGCATTAGTCTTGGCGGAATTTCATGTGACAACAGG 2882

Qy        2920 TTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAAC- 2978
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db        2883 TTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACA 2942

Qy        2979 -AAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
                |||||||||||||||||||||||||||||||||||||||||||
Db        2943 AAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 2986


RESULT 7
STU011885
LOCUS       STU011885               2955 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-1.
ACCESSION   AJ011885
VERSION     AJ011885.1  GI:4584502
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2955)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2955)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1..2955
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                     /note="sequence SBE A-1"
     gene            1..2955
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                     NVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIYYDPPEEERYI
                     FQHPRPKKPKSLRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYNALRIMAIQEH
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                     MFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEFKFDGFRFDGV
                     TSMMYTHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHRLFPDAITIGEDVSGM
                     PTFCIPVQDGGVGFDYRLHMAIADKWIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEG
                     YLNFMGNEFGHPEWIDFPRAEPHLSDGSVIPGNQFSYDKCRRRFDLGDAEYLRYHGLQ
                     EFDWAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFERGNLVFVFNFHWTNSYSDYRIG
                     CLKPGKYKVVLDSDDPLFGGFGRIDHNAEYFTSEGSYDDRPCSIMVYAPSRTAVVYAL
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     transit_peptide 140..283
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     mat_peptide     284..2752
                     /gene="sbe II"
                     /product="starch branching enzyme II"
                     /EC_number="2.4.1.18"
     3'UTR           2756..2955
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BASE COUNT      865 a    542 c    689 g    859 t
ORIGIN

  Query Match             86.6%;  Score 2733.2;  DB 8;  Length 2955;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 2857;  Conservative    2;  Mismatches   85;  Indels   34;  Gaps    4;

Qy         55 GGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCT 114
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db          1 GGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTTATCAGATCT 60

Qy        115 CTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGATTAGATTTG--------- 165
              ||||||||||||||||||||||||| || |   | ||||||  ||||||||
Db         61 CTATTTTTTCTCTTAATTCCAACCAGGGGAATGAATAAAAGGATAGATTTGTAAAAACCC 120

Qy        166 -AAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCC 224
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 TAAGGAGAGAAGAAGAAAGATGGTGTATATACTCTCTGGAGTTCGTTTTCCTACTGTTCC 180

Qy        225 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTC 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTC 240

Qy        285 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGA 344
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAA 300

Qy        345 TTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCA 404
              |||||||| ||||||||||||||||||||||||||||||||||||||| ||||||| |||
Db        301 TTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCA 360

Qy        405 GAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAA 464
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Qy        465 TTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAAC 524
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
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Qy        525 TGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTT 584
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        481 TGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTT 540

Qy        585 TGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATAC 644
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Db        541 TGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATAC 600

Qy        645 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 660

Qy        705 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 720

Qy        765 TGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGG 824
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
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Db    721 TGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGG 780

Qy    825 TTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 884
Db    781 TTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 840

Qy    885 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAA 944
Db    841 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAA 900

Qy    945 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 1004
Db    901 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 960

Qy   1005 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCAT 1064
Db    961 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTAT 1020

Qy   1065 GGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1124
Db   1021 GGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1080

Qy   1125 TCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGT 1184
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Qy   2745 TGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGT 2804
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VERSION     A58163.1  GI:3713888
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SOURCE      unidentified.
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REFERENCE   1  (bases 1 to 2975)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
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Qy        115 CTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGATTAGATTTG--------- 165
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Db         66 CTATTTTTTCTCTTAATTCCAACCAGGGGAATGAATAAAAGGATAGATTTGTAAAAACCC 125

Qy        166 -AAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCC 224
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Db        126 TAAGGAGAGAAGAAGAAAGATGGTGTATATACTCTCTGGAGTTCGTTTTCCTACTGTTCC 185

Qy        225 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTC 284
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Qy        285 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGA 344
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Db        246 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAA 305

Qy        345 TTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCA 404
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              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Qy        945 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 964

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Qy       1065 GGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1124
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Qy       1245 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1304
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Qy       1305 TCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTA 1364
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Qy       1665 GTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATAC 1724
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  AUTHORS   Poulson,P. and s Rensen,I.S.
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ORIGIN

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Qy      308 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAG 367
Db       61 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAG 120

Qy      368 TTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAA 427
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Db     121 TTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAA 180

Qy     428 CAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGG 487
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||| |
Db     181 CAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAG 240

Qy     488 ATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGT 547
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Qy     548 CAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAG 607
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Qy     608 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATG 667
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Db     361 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTTTGAAGAGACAATTATTGATG 420

Qy     668 AATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATG 727
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     728 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 787
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 540

Qy     788 AGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTT 847
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Qy     848 ATGAAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG 907
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Qy     908 GTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 967
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
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Qy     968 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 1027
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 780

Qy    1028 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGG 1087
           |||||||||||||||||||||||||||||||||| ||||||||| |||||||||||||||
Db     781 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGG 840

Qy    1088 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 1147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 900

Qy    1148 GAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGA 1207
           | ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     901 GGATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGA 960

Qy    1208 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAA 1267
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
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Qy    1268 TTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACA 1327
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Qy    1328 ATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATG 1387
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Qy    1448 TTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCAT 1507
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Qy    1628 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTG 1687
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||:||
Db    1381 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATG 1440

Qy    1688 GATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGAT 1747
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Qy    1868 ATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACT 1927
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Qy    2048 TTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGC 2107
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Qy    2228 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGG 2287
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Db    1981 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCCGAGTGGATTGATTTCCCTAGGG 2040

Qy    2288 CTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAAT 2347
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Db    2041 CTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAAT 2100

Qy    2348 GCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAAT 2407
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Db    2101 GCAGACGGAGATTTGACCTGGGAGATGCAGATTATTTAAGATACCGTGGGTTGCAAGAAT 2160

Qy    2408 TTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2467
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Db    2161 TTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2220

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Db    2221 TCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTT 2280

Qy    2528 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGC 2587
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Qy      2588 CTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAA 2647
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Qy      2648 TTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAA 2707
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Qy      2708 TTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAG 2767
Db      2461 TTATGGTGTATGCACCTAGTAGGACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGCAG 2520

Qy      2768 AAGAAGAAGAAGTAGCAGTAGTAGAAGAA 2796
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RESULT 10
A58167
LOCUS       A58167                  2529 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 17 from Patent WO9634968.
ACCESSION   A58167
VERSION     A58167.1  GI:3713892
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2529)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 17 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      735 a    458 c    599 g    722 t     15 others
ORIGIN

  Query Match             78.4%;  Score 2474.4;  DB 6;  Length 2529;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 2484;  Conservative   12;  Mismatches   33;  Indels    0;  Gaps    0;

Qy       270 GAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 329
Db         1 GGATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 60

Qy       330 AAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 389
Db        61 AAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 120

Qy       390 TGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 449
Db       121 TGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 180

Qy       450 GACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGC 509
Db       181 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 240

Qy       510 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 569
Db       241 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 300

Qy       570 TGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 629
Db       301 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 360

Qy       630 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 689
Db       361 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 420

Qy       690 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 749
Db       421 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 480

Qy       750 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGA 809
Db       481 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 540

Qy       810 CAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 869
Db       541 CAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 600

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Qy       930 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 989
Db       661 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 720

Qy       990 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 1049
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Qy      1050 AGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 1109
Db       781 AGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 840

Qy      1110 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 1169
Db       841 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 900

Qy      1170 AGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 1229
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Qy      1230 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1289
Db       961 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1020

Qy      1290 AGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1349
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Qy      1350 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1409
Db      1081 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1140

Qy      1410 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1469
Db      1141 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1200

Qy      1470 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1529
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Qy      1530 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1589
Db      1261 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1320

Qy      1590 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1649
Db      1321 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1380

Qy      1650 AAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGAC 1709
Db      1381 AAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1440

Qy      1710 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1769
Db      1441 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1500

Qy      1770 CTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTAT 1829
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Db        1501 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1560

Qy        1830 TCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1889
               ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1890 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1949
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Db        1621 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1680

Qy        1950 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 2009
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Db        1681 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1740

Qy        2010 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGA 2069
               |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        1741 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCATGA 1800

Qy        2070 TCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGA 2129
               ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        1801 TCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTATGA 1860

Qy        2130 TTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 2189
               |||||||||| |||||||||||:|||||:|||||||||||||||||||||||||||||||
Db        1861 TTTTATGGCTCTGGATAGACCGYCAACAYCATTAATAGATCGTGGGATAGCATTGCACAA 1920

Qy        2190 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 2249
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Db        1921 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 1980

Qy        2250 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2309
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Qy        2310 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2369
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Db        2041 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2100

Qy        2370 AGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2429
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Qy        2670 CACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAG 2729
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Qy        2730 AACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGT 2789
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Db        2461 AACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCCGN 2520

Qy        2790 AGAAGAAGT 2798
                |||||| |
Db        2521 NGAAGAATT 2529
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RESULT 11

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STU011889
LOCUS       STU011889               2523 bp    mRNA    linear   PLN 07-APR-1999
DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
            A-5.
ACCESSION   AJ011889
VERSION     AJ011889.1  GI:4584510
KEYWORDS    SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2523)
  AUTHORS   Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
            Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
  TITLE     A minor form of starch branching enzyme in potato (Solanum
            tuberosum L.) tubers has a major effect on starch structure;
            cloning and characterisation of multiple forms of SBE II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2523)
  AUTHORS   Jobling,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
            Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES             Location/Qualifiers
     source          1..2523
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                     /cultivar="Desiree"
                     /db_xref="taxon:4113"
                     /note="sequence SBE A-5"
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                     /gene="SBE II"
     CDS             <2..2512
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                     TSPENSPASTDVDSSTMEHASQIKTENDDVEPSSDLTGSVEELDFASSLQLQEGGKLE
                     ESKTLNTSEETIIDESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLR
                     EAIDKYEGGLEAFSRGYEKMGFTRSATGITYREWAPGAQSAALIGDFNNWDANADIMT
                     RNEFGVWEIFLPNNVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYN
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                     /EC_number="2.4.1.18"
BASE COUNT      749 a    449 c    605 g    720 t
ORIGIN

  Query Match             77.5%;  Score 2446.6;  DB 8;  Length 2523;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2483;  Conservative    2;  Mismatches   26;  Indels   12;  Gaps    1;

Qy         318 GATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATC 377
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Db           1 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 60

Qy         378 GGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 437
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Db     61 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 120

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Qy    498 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 557
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Qy    678 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 737
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Qy    738 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAG 797
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Db    661 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 720

Qy   1038 TCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCC 1097
Db    721 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 780

Qy   1098 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 1157
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Qy   1278 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCA 1337
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Qy   1578 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1637
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Qy   2418 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2477
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RESULT 12
A58169
LOCUS       A58169                  2578 bp    DNA     linear   PAT 05-MAR-1998
DEFINITION  Sequence 19 from Patent WO9634968.
ACCESSION   A58169
VERSION     A58169.1  GI:3713894
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2578)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 19 07-NOV-1996;
            NAT STARCH CHEM INVEST (US)
COMMENT     Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
     source          1..2578
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BASE COUNT      770 a    462 c    616 g    730 t
ORIGIN

  Query Match             77.5%;  Score 2445;  DB 6;  Length 2578;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2482;  Conservative    2;  Mismatches   27;  Indels   12;  Gaps    1;

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Db        956 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1015

Qy       1278 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCA 1337
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Qy   1758 CTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGC 1817
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Qy   1878 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1937
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Db   1616 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1675

Qy   1938 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2118 GGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 2177
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Qy   2178 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2237
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Db   1916 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1975

Qy   2238 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2297
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Db   1976 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2035

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Db   2036 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2095

Qy   2358 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2417
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Qy   2478 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2537
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Qy   2598 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2657
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Db   2396 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2455

Qy   2718 TGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACA-----------AAGAAGA 2765
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Db   2456 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2515

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Qy   2826 GTG 2828
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RESULT 13
STSBEII
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DEFINITION  Solanum tuberosum mRNA for starch branching enzyme II.
ACCESSION   AJ000004
VERSION     AJ000004.1  GI:2764395
KEYWORDS    Sbe-II gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 2493)
  AUTHORS   Larsson,C.T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell
            Research, Genetic Center, Swedish University of Agricultural
            Sciences, Box 7055, S-750 07 Uppsala, SWEDEN
REFERENCE   2  (bases 1 to 2493)
  AUTHORS   Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H.
  TITLE     Molecular cloning and characterization of starch-branching enzyme
            II from potato
  JOURNAL   Plant Mol. Biol. 37 (3), 505-511 (1998)
  MEDLINE   98278379
   PUBMED   9617817
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BASE COUNT      742 a    445 c    595 g    711 t
ORIGIN

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Qy        448 GAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACAC 507
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Qy        508 GCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT 567
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Qy        568 GTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAG 627
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Qy        688 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 747
Db        361 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACA 420

Qy        748 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATT 807
Db        421 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATT 480

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Qy        928 ATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGT 987
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Qy        988 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 1047
Db        661 GTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCC 720

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Qy       1108 AACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCC 1167
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Qy       1168 GAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATA 1227
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Qy       1228 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTT 1287
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Qy       1648 TCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTG 1707
Db       1321 TCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTCGATGGTGTG 1380

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Qy       1768 TACTTTGGACTCGCAACTGATGTGRATGCTGCCGTGTATCTGATGCTGGCCAACGATCTT 1827
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Qy       1828 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1887
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Qy       1888 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1947
Db       1561 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1620

Qy       1948 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2007
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Qy       2008 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2067
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Qy       2068 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2127
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Qy       2488 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2547
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RESULT 14
A58166
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DEFINITION  Sequence 16 from Patent WO9634968.
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VERSION     A58166.1  GI:3713891
KEYWORDS    .
SOURCE      unidentified.
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REFERENCE   1  (bases 1 to 2576)
  AUTHORS   Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher,M. and Westcott,R.J.
  TITLE     IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
  JOURNAL   Patent: WO 9634968-A 16 07-NOV-1996;
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COMMENT     Other publication AU 5509996 961121.
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Qy    1698 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1757
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Qy      1818 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1877
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Qy      2178 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2237
Db      1914 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1973

Qy      2238 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2297
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Qy      2298 CCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2357
Db      2034 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2093

Qy      2358 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2417
Db      2094 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2153

Qy      2418 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2477
Db      2154 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2213

Qy      2478 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2537
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Qy      2538 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATA 2597
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Qy      2598 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2657
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Qy      2658 TGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2717
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Qy      2718 TGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACA------------AAGAAGA 2765
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Qy      2766 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTT 2825
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Qy      2826 GTG 2828
Db      2574 GTG 2576


RESULT 15
AB071286
LOCUS       AB071286                3123 bp    mRNA    linear   PLN 11-SEP-2001
DEFINITION  Ipomoea batatas SBE II mRNA for starch branching enzyme II,
            complete cds.
ACCESSION   AB071286
VERSION     AB071286.1  GI:15553090
KEYWORDS    .
SOURCE      Ipomoea batatas (cultivar:Kokei 14) cDNA to mRNA.
  ORGANISM  Ipomoea batatas
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
REFERENCE   1
  AUTHORS   Kimura,T. and Saito,A.
  TITLE     Ipomoea batatas mRNA for starch branching enzyme II
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3123)
  AUTHORS   Kimura,T. and Saito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2001) Takashi Kimura, National Agricultural
            Research Center for Kyushu Okinawa Region; 2421 Suya, Nishigoshi,
            Kumamoto 861-1192, Japan (E-mail:tkimura@affrc.go.jp,
            Tel:81-96-242-1150)
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                     MFDGTDSCYFHSGTRGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEYKFDGFRFDGV
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                     PTFCIPVRDGGVGFDYRLHMAIPDKWIEILKRRDEDWQMGEIVHTLTNRRWLEKCVSY
                     AESHDQALVGDKTIAFWLMDKDMYDFMALDRPATPVIDRGIALHKMIRLITMGLGGEG
                     YLNFMGNEFGHPEWIDFPRGEQRLPDGSVLPGNNFSYDKCRRRFDLGDADYLRYRGMQ
                     EFDQAMHHLEEKYGFMTAKHQYISRQDEGDRVIIFERGDLVFVFNFHWTNSYSDYRVG
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                     AKEEDEAKPVEE"
BASE COUNT      883 a    614 c    740 g    886 t
ORIGIN

  Query Match             54.4%;  Score 1717.6;  DB 8;  Length 3123;
  Best Local Similarity   78.4%;  Pred. No. 0;
  Matches 2082;  Conservative    1;  Mismatches  565;  Indels    6;  Gaps    2;

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Qy       201 TGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCTAATGGATTCAGCAGTAATGG 260
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Qy    438 TGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAAC 497
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Qy    738 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAG 797
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Qy    798 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 857
Db    726 GGAAGCAATTAACCAGTATGAGGGTGGCTTGGAAGTATTCTCTCGTGGCTATGAGAAATT 785

Qy    858 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 917
Db    786 AGGTTTCACTCGGAGTGTTACAGGTATCACCTATCGGGAGTGGGCTCCTGGAGCCACGTG 845

Qy    918 AGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 977
Db    846 GGCAACACTCATTGGAGATTTCAACAATTGGAATCCAAATGCTGATGTTATGACTCGGAA 905

Qy    978 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 1037
Db    906 TGAATTTGGTGTTTGGGAGATCTTTTTGCCAAACAATGCAGATGGCTCACCTGCAATTCC 965

Qy   1038 TCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCC 1097
Db    966 ACATGGCTCTAGAGTGAAGATACGTATGGACACTCCTTCAGGCATTAAAGACTCTATTCC 1025

Qy   1098 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 1157
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Qy   1158 TGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1217
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Qy   1218 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1277
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Qy   1458 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1517
Db   1386 CCATGAACTTGGACTGGTTGTTCTAATGGATATTGTGCACAGTCATGCGTCAAATAATAC 1445

Qy   1518 TTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG 1577
Db   1446 TTTGGATGGACTGAACATGTTTGATGGTACAGATAGTTGTTATTTCCACTCTGGAACCCG 1505

Qy   1578 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1637
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Qy   1638 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATT 1697
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Qy   1758 CTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGC 1817
Db   1686 CTACAGTGAATATTTTGGGTATGCAACCGATGTTGATGCTGTGGTGTATCTGATGCTCGT 1745

Qy   1818 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1877
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Db   1806 CATGCCAACATTTTGTATTCCCGTCAGAGATGGAGGCGTAGGTTTTGACTATCGGCTTCA 1865

Qy   1938 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1997
Db   1866 TATGGCAATTCCCGATAAATGGATTGAGATTCTCAAGAGAAGAGATGAGGATTGGCAAAT 1925

Qy   1998 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 2057
Db   1926 GGGTGAAATTGTTCACACACTTACTAACAGAAGATGGCTGGAAAAATGTGTTTCTTATGC 1985

Qy   2058 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 2117
Db   1986 TGAAAGTCACGACCAAGCTCTTGTTGGTGATAAAACTATAGCGTTCTGGTTGATGGACAA 2045

Qy   2118 GGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 2177
Db   2046 GGACATGTATGACTTCATGGCTCTGGATAGACCAGCAACGCCAGTAATAGACCGTGGAAT 2105

Qy   2178 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2237
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Qy   2238 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2297
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Qy   2538 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATA 2597
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Qy   2658 TGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2717
Db   2586 TGCAGAATTTTTCACATTCGAAGGGTATCACGATGATCGTCCTCGTTCCTTCATGGTGTA 2645

Qy   2718 TGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2777
Db   2646 CGCACCCAGTAGAACTGCAGTGGTGTACGCTCTAGCGAAGGAGGAGGACGAAGCAAAACC 2705

Qy   2778 AGTAGCAGTAGTAG 2791
Db   2706 AGTTGAGGAATGAG 2719
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Search completed: July 5, 2003, 17:59:02
Job time : 8073.92 secs

12

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 12:28:17 ; Search time 657.636 Seconds
(without alignments)
10807.357 Million cell updates/sec

Title: US-10-056-454A-18_COPY_45_3200
Perfect score: 3156
Sequence: 1 AAAAACCTCCTCCACTCAGT..........TGCTGATCTAATGATGTTTT 3156

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	3154.2	99.9	3231	17	AAT42632	Class A starch bra
	2	2958.4	93.7	3074	18	AAT69587	Potato starch bran
	3	2847.4	90.2	3033	17	AAT42630	Class A starch bra
	4	2838	89.9	3003	17	AAT42634	Class A starch bra
	5	2706	85.7	2975	17	AAT42635	Class A starch bra
	6	2485.8	78.8	2563	23	ABK50301	Potato cDNA encodi
	7	2474	78.4	2531	17	AAT17267	Class A starch bra
	8	2471.2	78.3	2529	17	AAT42637	Class A starch bra
	9	2445	77.5	2578	17	AAT42631	Class A starch bra
	10	2427.8	76.9	2576	17	AAT42636	Class A starch bra
	11	1442.8	45.7	3090	19	AAV38720	Full length cassav
	12	1377.8	43.7	2913	19	AAV38719	Full length cassav
	13	1296	41.1	2715	21	AAC45939	Arabidopsis thalia
	14	1275.6	40.4	3015	19	AAV05639	Rice type IV starc
	15	1260.4	39.9	2919	15	AAQ73750	Rice starch branch
	16	1257.6	39.8	2726	22	AAH78337	Nucleotide sequenc
	17	1203.6	38.1	2640	19	AAV70961	DNA encoding maize
	18	1200.4	38.0	2665	18	AAT69729	Plasmid pBE240 ins
	19	1200.4	38.0	2725	19	AAV29757	Zea mays starch br
	20	1185.6	37.6	3039	24	ABK15494	Wheat starch branc
	21	1182.4	37.5	2968	22	AAH78342	Nucleotide sequenc
	22	1059.8	33.6	2307	21	AAZ99938	DNA encoding part
	23	1049.8	33.3	2087	18	AAT69737	Corn starch branch
c	24	1048.2	33.2	2165	18	AAT69736	Corn starch branch
	25	963.2	30.5	1919	19	AAV38722	cDNA encoding star
	26	730	23.1	1452	21	AAC36957	Arabidopsis thalia
	27	663.8	21.0	770	23	ABK50302	Potato starch bran
	28	642.8	20.4	4563	22	AAF30910	Wheat starch branc
	29	637.4	20.2	3128	16	AAT00774	Potato starch bran
c	30	632.4	20.0	2487	18	AAT69747	Corn starch branch
	31	632.4	20.0	2565	18	AAT69752	Corn starch branch
	32	632.4	20.0	2763	19	AAV29758	Zea mays starch br
	33	632.4	20.0	2771	13	AAQ24257	Branching enzyme D
	34	632.4	20.0	2772	18	AAT69740	Plasmid pBE65 inse
	35	623.2	19.7	2909	13	AAQ27778	Potato amylose-amy
	36	618.8	19.6	2687	20	AAX34646	wSBE I-D4 cDNA seq
	37	611.8	19.4	2733	15	AAQ54674	Rice starch branch
	38	611.8	19.4	2733	15	AAQ62135	Rice starch branch
	39	598.2	19.0	3075	24	AAS94880	Human DNA sequence
	40	596.6	18.9	2899	22	AAH02926	Human shear stress
	41	596.6	18.9	2955	24	ABN95650	Gene #2148 used to
	42	593	18.8	2713	19	AAV70962	DNA encoding maize
	43	585.2	18.5	728	23	ABK50303	Potato starch bran
	44	546	17.3	1809	18	AAT69753	Corn starch branch
	45	546	17.3	1865	18	AAT69748	Corn starch branch

ALIGNMENTS

RESULT 1
AAT42632
ID AAT42632 standard; DNA; 3231 BP.
XX
AC AAT42632;
XX
DT 25-FEB-1997 (first entry)
XX
DE Class A starch branching enzyme (psbe2con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT misc_RNA 45..3200
FT /*tag= a
FT /note= "claim 34"
FT CDS 228..2855
FT /*tag= c
XX
PN WO9634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

```
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 31, 34; Page 53-55; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
CC   The same sequence is given in Figure 8, however, nucleotides
CC   1-44 omitted.
XX
SQ   Sequence 3231 BP; 960 A; 577 C; 739 G; 947 T; 8 other;

  Query Match             99.9%;  Score 3154.2;  DB 17;  Length 3231;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAACCTCCTCCACTCAGTCTTGGGATCTCTCTCTCTTCACGCTTCTCTTGGGGCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 AAAAACCTCCTCCACTCAGTCTTGGGATCTCTCTCTCTTCACGCTTCTCTTGGGGCCT 104

Qy         61 TGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCTCTATTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 TGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCTCTATTT 164

Qy        121 TTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGATTAGATTTGAAGGAGAGAAGAAGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 TTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGATTAGATTTGAAGGAGAGAAGAAGA 224

Qy        181 AAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 AAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATCT 284

Qy        241 AATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAG 344

Qy        301 CACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 CACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCT 404

Qy        361 TCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCA 464

Qy        421 TCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 TCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACT 524

Qy        481 GATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTT 584

Qy        541 GAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAA 644

Qy        601 CTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 CTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATT 704

Qy        661 ATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 ATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAG 764

Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 824

Qy        781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 884

Qy        841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 944

Qy        901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 1004

Qy        961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1064

Qy       1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1124

Qy       1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1184

Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1244

Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1304

Qy       1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1364

Qy       1321 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1424

Qy       1381 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1484

Qy       1441 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1544

Qy       1501 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1545 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1604

Qy       1561 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1664

Qy       1621 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1665 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1724

Qy       1681 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1784

Qy       1741 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1785 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1844

Qy       1801 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1845 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1904

Qy   1861 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGC 1964

Qy   1921 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGG 2024

Qy   1981 GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAA 2084

Qy   2041 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCA 2144

Qy   2101 TTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 TTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCA 2204

Qy   2161 TTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 TTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGA 2264

Qy   2221 GGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 GGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTC 2324

Qy   2281 CCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTAT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 CCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTAT 2384

Qy   2341 GATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 GATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTG 2444

Qy   2401 CAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2445 CAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAA 2504

Qy   2461 CACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAAC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2505 CACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAAC 2564

Qy   2521 CTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2565 CTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGG 2624

Qy   2581 CTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2625 CTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTC 2684

Qy   2641 GGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2685 GGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCT 2744

Qy   2701 CGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2745 CGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAA 2804

Qy   2761 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2805 GAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACG 2864

Qy   2821 AACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2865 AACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAA 2924

Qy   2881 TATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCTTTCCACTATT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2925 TATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCTTTCCACTATT 2984

Qy   2941 AGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAAAATCGATGAA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2985 AGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAAAATCGATGAA 3044

Qy   3001 TTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTCTGTAAATTGT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3045 TTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTCTGTAAATTGT 3104

Qy   3061 CATCTCTTTANATGTACAGCCCACTAGAAATCAATTATGTGAGACCTAAAAAACAATAAC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3105 CATCTCTTTANATGTACAGCCCACTAGAAATCAATTATGTGAGACCTAAAAAACAATAAC 3164

Qy   3121 CATAAAATGGAAATAGTGCTGATCTAATGATGTTTT 3156
          ||||||||||||||||||||||||||||||||||||
Db   3165 CATAAAATGGAAATAGTGCTGATCTAATGATGTTTT 3200
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RESULT 2
AAT69587
ID   AAT69587 standard; cDNA; 3074 BP.
XX
AC   AAT69587;
XX
DT   26-AUG-1997  (first entry)
XX
DE   Potato starch branching enzyme II gene (beII).
XX
KW   Starch branching enzyme II; beII gene; potato; transgenic plant;
KW   amylopectin; amylose; starch; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             189..2825
FT                   /*tag=  a
FT   sig_peptide     189..332
FT                   /*tag=  b
FT   mat_peptide     333..2822
FT                   /*tag=  c
XX
PN   WO9720040-A1.
XX
PD   05-JUN-1997.
XX
PF   28-NOV-1996;   96WO-SE01558.
XX
PR   19-APR-1996;   96SE-0001506.
PR   29-NOV-1995;   95SE-0004272.
XX
PA   (EKBB/) EK B.
PA   (KHOS/) KHOSNOODI J.
PA   (LARS/) LARSSON C.
PA   (LARS/) LARSSON H.
PA   (RASK/) RASK L.
PA   (AMYL-) AMYLOGENE HB.
XX
PI   Ek B,  Khosnoodi J,  Larsson C,  Larsson H,  Rask L;
XX
DR   WPI; 1997-310596/28.
DR   P-PSDB; AAW19113.
XX
PT   Isolated potato starch branching enzyme II - useful for altering
PT   degree of amylopectin branching and amylopectin/amylose ratio in
PT   potato starch
XX
PS   Claim 4; Page 12-15; 24pp; English.
XX
CC   A cDNA clone (AAT69587) codes for potato starch branching enzyme II
CC   (BEII) (AAW19113).  It was isolated from potato tuber cDNA by PCR
CC   amplification using primers (AAT69588-89) based on tryptic peptides
CC   of isolated BEII; the 5' and 3' ends of the sequence were detd. by
CC   RACE.  A vector comprising the whole or a functional active part of
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CC   the isolated sequence (sense or antisense), plus regulatory
CC   sequences active in potato, can be used to produce transgenic
CC   potatoes.  The starch obtd. from such plants will show a changed
CC   pattern of amylopectin branching and an altered amylopectin/amylose
CC   ratio.
XX
SQ   Sequence 3074 BP; 902 A; 560 C; 710 G; 896 T; 6 other;

  Query Match            93.7%;  Score 2958.4;  DB 18;  Length 3074;
  Best Local Similarity  98.2%;  Pred. No. 0;
  Matches 3021;  Conservative    2;  Mismatches   39;  Indels   14;  Gaps    3;

Qy          3 AAACCTCCTCCACTCAGTCTTGGGATCTCTCTCTCTTCACGCTTCTCTTGGGGCCTTG 62
Db          1 AAACCTCCTCCACTCAGTCTTTG--TTTCTCTCTCTCTTCACGCTTCTCTTGGCGCCTTG 58

Qy         63 AACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCTCTATTTTT 122
Db         59 AACTCAGCAATTTGACACTCAGTTAGTTACACTNCCATCACTTATCAGATCTCTATTTTT 118

Qy        123 TCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATTTGAAGGAGAG 173
Db        119 TCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACCCTAAGGAGAG 178

Qy        174 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 233
Db        179 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 238

Qy        234 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTT 293
Db        239 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTT 298

Qy        294 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATC 353
Db        299 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATC 358

Qy        354 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAG 413
Db        359 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAG 418

Qy        414 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGC 473
Db        419 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGC 478

Qy        474 ATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGA 533
Db        479 ATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGA 538

Qy        534 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATC 593
Db        539 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATC 598

Qy        594 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 653
Db        599 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 658

Qy        654 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 713
Db        659 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 718

Qy        714 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 773
Db        719 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 778

Qy        774 GTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 833
Db        779 GTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 838

Qy        834 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 893
Db        839 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 898

Qy        894 TGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGC 953
Db        899 TGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGC 958

Qy        954 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1013
Db        959 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1018

Qy       1014 TGTGGATGGTTCTCCTGCAATTCCTCATGGTCCAGAGTGAAGATACGCATGGACACTTC 1073
Db       1019 TGTGGATGGTTCTCCTGCAATTCCTCATGGTCCAGAGTGAAGATACGTATGGACACTCC 1078

Qy       1074 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1133
Db       1079 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1138

Qy       1134 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACA 1193
Db       1139 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACA 1198

Qy       1194 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1253
Db       1199 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1258

Qy       1254 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1313
Db       1259 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1318

Qy       1314 AAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1373
Db       1319 AAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1378

Qy       1374 TTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGA 1433
Db       1379 TTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGGAACNCCCGACGA 1438

Qy       1434 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1493
Db       1439 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1498

Qy       1494 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1553
Db       1499 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1558

Qy       1554 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1613
Db       1559 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1618

Qy       1614 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1673
Db       1619 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1678

Qy       1674 GTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1733
Db       1679 GTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1738

Qy       1734 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGA 1793
Db       1739 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGA 1798

Qy       1794 TGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1853
Db       1799 TGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1858

Qy       1854 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGG 1913
Db       1859 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGG 1918

Qy       1914 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1973
Db       1919 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1978

Qy       1974 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2033
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Db       1979 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2038

Qy       2034 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2039 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2098

Qy       2094 TATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTC 2153
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Db       2099 TATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTC 2158

Qy       2154 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2159 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2218

Qy       2214 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2219 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2278

Qy       2274 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2279 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2338

Qy       2334 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2398

Qy       2394 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2399 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2458

Qy       2454 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2459 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2518

Qy       2514 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2519 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2578

Qy       2574 AGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2633
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2579 AGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2638

Qy       2634 TGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGA 2693
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       2639 TGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGA 2698

Qy       2694 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2699 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2758

Qy       2754 AGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2810
              |||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2759 AGACAAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2818

Qy       2811 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       2819 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878

Qy       2871 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2879 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2938

Qy       2931 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAA 2990
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       2939 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGCACAAACATATGTAA 2998

Qy       2991 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2999 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3058

Qy       3051 TGTAAATTGTCATCTC 3066
              ||||||||||||||||
Db       3059 TGTAAATTGTCATCTC 3074
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RESULT 3
AAT42630
ID   AAT42630 standard; DNA; 3033 BP.
XX
AC   AAT42630;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (19con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             145..2793
FT                   /*tag=  a
FT   sig_peptide     145..288
FT                   /*tag=  b
FT   mat_peptide     289..2790
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAW06399.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 28-30; Page 42-46; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;

  Query Match             90.2%;  Score 2847.4;  DB 17;  Length 3033;
  Best Local Similarity   97.5%;  Pred. No. 0;
  Matches 2919;  Conservative    2;  Mismatches   48;  Indels   24;  Gaps    2;

Qy         53 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGAT 112
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          5 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTTATCAGAT 64

Qy        113 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATT 163
              ||||||||||||||||||||||||||||||||||||| ||| |||          | |
Db         65 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATAAAAGGATAGATTTGTAAAAACC 124

Qy        164 TGAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 223
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CTAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 184

Qy        224 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTT 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTT 244
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Qy    284 CTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACG 343
Db    245 CTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACA 304

Qy    344 ATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCC 403
Db    305 ATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCC 364

Qy    404 AGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAA 463
Db    365 AGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAA 424

Qy    464 ATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 523
Db    425 ATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 484

Qy    524 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATT 583
Db    485 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATT 544

Qy    584 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 643
Db    545 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 604

Qy    644 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 703
Db    605 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 664

Qy    704 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 763
Db    665 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 724

Qy    764 TTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTG 823
Db    725 TTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTG 784

Qy    824 GTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTA 883
Db    785 GTTTGGAAGCCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTA 844

Qy    884 TCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACA 943
Db    845 TCACTTACCGTGAGTGGGCTCTTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACA 904

Qy    944 ATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTC 1003
Db    905 ATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTC 964

Qy   1004 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCA 1063
Db    965 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTA 1024

Qy   1064 TGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1123
Db   1025 TGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1084

Qy   1124 TTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATG 1183
Db   1085 TTCCTGATGAAATTCCATATAATGGAATACATTATGATCCACCCGAAGAGGAGAGGTATA 1144

Qy   1184 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTG 1243
Db   1145 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTG 1204

Qy   1244 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1303
Db   1205 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1264

Qy   1304 CTCGCATAAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTT 1363
Db   1265 CTCGCATAAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTT 1324

Qy   1364 ATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAA 1423
Db   1325 ATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAA 1384

Qy   1424 CGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCA 1483
Db   1385 CGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCA 1444

Qy   1484 TGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACG 1543
Db   1445 TGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACT 1504

Qy   1544 GCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCC 1603
Db   1505 GCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCC 1564

Qy   1604 GCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGT 1663
Db   1565 GCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGT 1624

Qy   1664 GGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATA 1723
Db   1625 GGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATA 1684

Qy   1724 CTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAA 1783
Db   1685 TTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAA 1744

Qy   1784 CTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCC 1843
Db   1745 CTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCC 1804

Qy   1844 CAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTC 1903
Db   1805 CAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTCC 1864

Qy   1904 AAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTG 1963
Db   1865 AAGAGGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAACGGATTG 1924

Qy   1964 AGTTGCTCAAGAAACGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAA 2023
Db   1925 AGTTGCTCAAGAAACGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAA 1984

Qy   2024 ATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCG 2083
Db   1985 ATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCG 2044

Qy   2084 GTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGG 2143
Db   2045 GTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGG 2104

Qy   2144 ATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTG 2203
Db   2105 ATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTG 2164

Qy   2204 TAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACC 2263
Db   2165 TAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACC 2224

Qy   2264 CTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCG 2323
Db   2225 CTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATCCCCG 2284

Qy   2324 GAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATT 2383
Db   2285 GAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATT 2344

Qy   2384 TAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATG 2443
Db   2345 TAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAATATG 2404

Qy   2444 AGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTG 2503
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Db       2405 AGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTG 2464

Qy       2504 TATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAG 2563
Db       2465 TATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAG 2524

Qy       2564 ACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATC 2623
Db       2525 ACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATC 2584

Qy       2624 CACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGAT 2683
Db       2585 CACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGAT 2644

Qy       2684 GGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCT 2743
Db       2645 GGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTTGTAAAACAGCAGTGGTCT 2704

Qy       2744 ATGCACTAGTAGACA---------------AAGAAGAAGAAGAAGAAGAAGTAGCAGTAG 2788
Db       2705 ATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAG 2764

Qy       2789 TAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAA 2848
Db       2765 TAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAA 2824

Qy       2849 CGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCAT 2908
Db       2825 CGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCAT 2884

Qy       2909 GTGACAAAAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGA 2968
Db       2885 GTGACACAAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGA 2944

Qy       2969 AGTGCTGAACAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
Db       2945 AGTGCTGAACAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 2997
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RESULT 4
AAT42634
ID AAT42634 standard; DNA; 3003 BP.
XX
AC AAT42634;
XX
DT 03-MAR-1997 (first entry)
XX
DE Class A starch branching enzyme (10con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
PN WO9634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
DR WPI; 1996-506170/50.
XX
PT New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
PS Example 1; Page 38-39; 142pp; English.
XX
CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
SQ Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;

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  Query Match             89.9%;  Score 2838;  DB 17;  Length 3003;
  Best Local Similarity   97.9%;  Pred. No. 0;
  Matches 2920;  Conservative    2;  Mismatches   47;  Indels   15;  Gaps    4;

Qy         53 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGAT 112
Db          3 TGGGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTGCCATCACTTATCAGAT 62

Qy        113 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATT 163
Db         63 CTCTATTTTTTCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACC 122

Qy        164 TGAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 223
Db        123 CTAAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTC 182

Qy        224 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTT 283
Db        183 CATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATATTT 242

Qy        284 CTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACG 343
Db        243 CTGTATTCTTGAAAAAACACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACA 302

Qy        344 ATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCC 403
Db        303 ATTCCGAATCCCGACCTTCTACAATTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAATCC 362

Qy        404 AGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAA 463
Db        363 AGAGTGATAGCTCCTCATCCTCAACAGATCAATTTGAGTTCGCTGAGACATCTCCAGAAA 422

Qy        464 ATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 523
Db        423 ATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAA 482

Qy        524 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATT 583
Db        483 CTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATT 542

Qy        584 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 643
Db        543 TTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATA 602

Qy        644 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 703
Db        603 CTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCAC 662

Qy        704 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 763
Db        663 CTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACC 722

Qy        764 TTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTG 823
Db        723 TTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTG 782

Qy        824 GTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTA 883
Db        783 GTTTGGAAGCTTTTTCTCGTGGTTATGAAAGAATGGGTTTCACTCGTAGTGCTACAGGTA 842

Qy        884 TCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACA 943
Db        843 TCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGGGATTTCAACA 902
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Qy    944 ATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTC 1003
Db    903 ATTGGGACGCAAATGCTGACTTTATGACTCGGAATGAATTTGGTGTCTGAGAGATTTTTC 962

Qy   1004 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCA 1063
Db    963 TGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTA 1022

Qy   1064 TGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1123
Db   1023 TGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGC 1082

Qy   1124 TTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATG 1183
Db   1083 TTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATA 1142

Qy   1184 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTG 1243
Db   1143 TCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGGTGAGAATATATGAATCTCATATTG 1202

Qy   1244 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1303
Db   1203 GAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTC 1262

Qy   1304 CTCGCAT-AAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 1362
Db   1263 CTCGCATAAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCT 1322

Qy   1363 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGA 1422
Db   1323 TATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGA 1382

Qy   1423 ACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 1482
Db   1383 ACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTC 1442

Qy   1483 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 1542
Db   1443 ATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGAC 1502

Qy   1543 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCC 1602
Db   1503 GGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTTC 1562

Qy   1603 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 1662
Db   1563 CGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGG 1622

Qy   1663 TGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTAT 1722
Db   1623 TGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTGT 1682

Qy   1723 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 1782
Db   1683 ACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCA 1742

Qy   1783 ACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTC 1842
Db   1743 ACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTC 1802

Qy   1843 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTT 1902
Db   1803 CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTGTTCCCGTT 1862

Qy   1903 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 1962
Db   1863 CAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATT 1922

Qy   1963 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 2022
Db   1923 GAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 1982

Qy   2023 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082
Db   1983 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2042

Qy   2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142
Db   2043 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTG 2102

Qy   2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202
Db   2103 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTACACAAGATGATTAGGCTT 2162

Qy   2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262
Db   2163 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2222

Qy   2263 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2322
Db   2223 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2282

Qy   2323 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2382
Db   2283 AGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2342

Qy   2383 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2442
Db   2343 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2402

Qy   2443 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2502
Db   2403 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2462

Qy   2503 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTCACTGGACAAAAAGCTATTCA 2562
Db   2463 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTCACTGGACAAAAGGCTATTCA 2522

Qy   2563 GACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2622
Db   2523 GACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2582

Qy   2623 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGA 2682
Db   2583 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGA 2642

Qy   2683 TGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2742
Db   2643 TGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2702

Qy   2743 TATGCACTAGTAGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTA 2799
Db   2703 TATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTA 2762

Qy   2800 GTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGA 2859
Db   2763 GTAGTAGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCCACATAGA 2822

Qy   2860 GCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGG 2919
Db   2823 GCTTCTTGACGTATCTGGCAATATTGCATTAGTCTTGGCGGAATTTCATGTGACAACAGG 2882

Qy   2920 TTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAAC- 2978
Db   2883 TTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACA 2942

Qy   2979 -AAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
Db   2943 AAAACATATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 2986
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RESULT 5
AAT42635
ID AAT42635 standard; DNA; 2975 BP.
XX

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AC   AAT42635;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (11con.seq).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;    96WO-GB01075.
XX
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 40-41; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2975 BP; 871 A; 548 C; 693 G; 863 T; 0 other;

  Query Match             85.7%;  Score 2706;  DB 17;  Length 2975;
  Best Local Similarity   95.8%;  Pred. No. 0;
  Matches 2853;  Conservative    2;  Mismatches   87;  Indels   36;  Gaps    6;

Qy         55 GGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCT 114
Db          6 GGGCCTTGAACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTTATCAGATCT 65

Qy        115 CTATTTTTTCTCTTAATTCCAACCAAGGAATGAATTAAAAGATTAGATTTG--------- 165
Db         66 CTATTTTTTCTCTTAATTCCAACCAGGGGAATGAATAAAAGGATAGATTTGTAAAAACCC 125

Qy        166 -AAGGAGAGAAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCC 224
Db        126 TAAGGAGAGAAGAAGAAAGATGGTGTATATACTCTCTGGAGTTCGTTTTCCTACTGTTCC 185

Qy        225 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTC 284
Db        186 ATCAGTGTACAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTC 245

Qy        285 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGA 344
Db        246 TGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAA 305

Qy        345 TTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCA 404
Db        306 TTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCA 365

Qy        405 GAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAA 464
Db        366 GAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAA 425

Qy        465 TTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAAC 524
Db        426 ATCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAAC 485

Qy        525 TGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTT 584
Db        486 TGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTT 545

Qy        585 TGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATAC 644
Db        546 TGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATAC 605

Qy        645 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 704
Db        606 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 665

Qy        705 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 764
Db        666 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 725

Qy        765 TGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGG 824
Db        726 TGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGG 785

Qy        825 TTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 884
Db        786 TTTGGAAGC-TTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 844

Qy        885 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAA 944
Db        845 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAA 904

Qy        945 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 1004
Db        905 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 964

Qy       1005 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCAT 1064
Db        965 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTAT 1024

Qy       1065 GGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1124
Db       1025 GGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1084

Qy       1125 TCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGT 1184
Db       1085 TCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATAT 1144

Qy       1185 CTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGG 1244
Db       1145 CTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGG 1204

Qy       1245 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1304
Db       1205 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1264

Qy       1305 TCGCATAAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTA 1364
Db       1265 TCGCATAAAAAAGCTTGGGTACAATGCGCTGCGAATTATGGCTATTCAAGAGCATTCTTA 1324

Qy       1365 TTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAAC 1424
Db       1325 TTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAAC 1384

Qy       1425 GCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCAT 1484
Db       1385 GCCCGACGACCTTAAGTCTTCGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCAT 1444

Qy       1485 GGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGG 1544
Db       1445 GGACATCGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGG 1504

Qy       1545 CACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCG 1604
Db       1505 CACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATT-CCG 1563
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Qy   1605 CCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTG 1664
Db   1564 CCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTG 1623

Qy   1665 GTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATAC 1724
Db   1624 GTTGGATGAGTTCAAATTTGATGGATTTAGATTCGATGGTGTGACATCAATGATGTATAC 1683

Qy   1725 TCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAAC 1784
Db   1684 TCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAAC 1743

Qy   1785 TGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGCTTTTCCC 1844
Db   1744 TGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATAGGCTTTTCCC 1803

Qy   1845 AGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCA 1904
Db   1804 AGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCA 1863

Qy   1905 AGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGA 1964
Db   1864 AGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGA 1923

Qy   1965 GTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAA 2024
Db   1924 GTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAA 1983

Qy   2025 TAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG 2084
Db   1984 TAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG 2043

Qy   2085 TGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGA 2144
Db   2044 TGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCTGGA 2103

Qy   2145 TAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGT 2204
Db   2104 TAGACCGCCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGT 2163

Qy   2205 AACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCC 2264
Db   2164 AACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCC 2223

Qy   2265 TGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGG 2324
Db   2224 TGAGTGGATTGATTTCCCTAGGGCTGAGCCACACCTTTCTGATGGCTCAGTAATTCCCGG 2283

Qy   2325 AAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTT 2384
Db   2284 AAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTT 2343

Qy   2385 AAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGA 2444
Db   2344 AAGATACCATGGGTTACAAGAATTTGACTGGGCTATGCAGTATCTTGAAGATAAATATGA 2403

Qy   2445 GTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGT 2504
Db   2404 GTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGT 2463

Qy   2505 ATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGA 2564
Db   2464 ATTTGAAAGAGGAAACCTAGTTTTCGTCTTTAATTTTCACTGGACAAATAGCTATTCAGA 2523

Qy   2565 CTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCC 2624
Db   2524 CTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGTCTTGGACTCAGATGATCC 2583

Qy   2625 ACTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATG 2684
Db   2584 ACTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTCTGAAGGATC 2643

Qy   2685 GTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTA 2744
Db   2644 GTATGATGATCGTCCTTGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTA 2703

Qy   2745 TGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGT 2804
Db   2704 TGCACTAGTAGACA------------------AACTAGAAGTAGCAGTAGTAGAAGAACC 2745

Qy   2805 AGAAGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTC 2864
Db   2746 CATTGAAGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGTTACTTGGTCAT-- 2803

Qy   2865 TTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAA-AAGGTTTG 2923
Db   2804 ---CCACATAGAGCTTCTTGACATCAGTCTTGGCGGAATTGCATGTGACAACAAGGTTTG 2860

Qy   2924 CAATTCTTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACA 2983
Db   2861 CAGTTCTTTCCACTATTAGTAGTCCACCGATATACGCAGAGATGAAGTGCTGAACAAACA 2920

Qy   2984 TATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 3021
Db   2921 TATGTAAAATCGATGAATTTATGTCGAATGCTGGGACG 2958
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RESULT 6
ABK50301
ID   ABK50301 standard; cDNA; 2563 BP.
XX
AC   ABK50301;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Potato cDNA encoding starch branching enzyme, SBE II.
XX
KW   Potato; starch branching enzyme; SBE II; glucan branching enzyme;
KW   GBE; ss; gene; plant; transgenic; antisense; food industry;
KW   paper industry; chemical industry.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..2552
FT                   /*tag=  a
FT                   /product= "SBE II"
FT                   /partial
FT                   /note= "No start codon shown"
XX
PN   GB2360521-A.
XX
PD   26-SEP-2001.
XX
PF   20-MAR-2000; 2000GB-0006733.
XX
PR   20-MAR-2000; 2000GB-0006733.
XX
PA   (DANI-) DANISCO AS.
XX
PI   Poulsen P,  Sorensen IS;
XX
DR   WPI; 2001-650142/75.
DR   P-PSDB; AAU80169.
XX
PT   New transformed plants with reduced endogenous starch branching enzyme
PT   and heterologous glucan branching enzyme activities, useful for
PT   producing starch with improved properties, which is in the food, paper
PT   and chemical industries -
XX
PS   Example 1; Page 31-35; 61pp; English.
XX
CC   The invention relates to a transformed organism, preferably a transformed
CC   plant, having a reduced endogenous starch branching enzyme (SBE)
CC   activity, and having a heterologous glucan branching enzyme (GBE)
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CC   activity. The reduced SBE activity is effected via expression of a
CC   nucleotide sequence that is antisense to at least part of a SBE exon.
CC   Also included are a method of producing starch with altered
CC   characteristics comprising (a) providing a plant having reduced
CC   endogenous SBE activity, and having heterologous GBE activity
CC   (b) propagating the plant of (a) and optionally (c) obtaining starch
CC   from the plant; starch obtainable from the transformed plant; and
CC   a nucleic acid construct system capable of directing the expression
CC   of all or part of one or more antisense SBE exons and optionally one or
CC   more heterologous GBE. The transformed plants are useful for producing
CC   starch with modified and improved properties, which is an important raw
CC   material and used in the food, paper and chemical industries. The
CC   present sequence encodes Potato SBE II, used to make transgenic plants of
CC   the invention.
XX
SQ   Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;

  Query Match             78.8%;  Score 2485.8;  DB 23;  Length 2563;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2508;  Conservative    2;  Mismatches   39;  Indels    0;  Gaps    0;

Qy        248 TCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTC 307
Db          1 TCAGCAGTAATGGTGATCGGAGGAATGCTAATATTTCTGTATTCTTGAAAAAACACTCTC 60

Qy        308 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAG 367
Db         61 TTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAG 120

Qy        368 TTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAA 427
Db        121 TTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAA 180

Qy        428 CAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGG 487
Db        181 CAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAG 240

Qy        488 ATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGT 547
Db        241 ATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGT 300

Qy        548 CAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAG 607
Db        301 CAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAG 360

Qy        608 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATG 667
Db        361 AAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTTTGAAGAGACAATTATTGATG 420

Qy        668 AATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATG 727
Db        421 AATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATG 480

Qy        728 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 787
Db        481 AAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACA 540

Qy        788 AGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTT 847
Db        541 AGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTT 600

Qy        848 ATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG 907
Db        601 ATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG 660

Qy        908 GTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 967
Db        661 GTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTA 720

Qy        968 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 1027
Db        721 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTC 780

Qy       1028 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGG 1087
Db        781 CTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGG 840

Qy       1088 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 1147
Db        841 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATG 900

Qy       1148 GAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGA 1207
Db        901 GGATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGA 960

Qy       1208 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAA 1267
Db        961 AACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAACCTAAAA 1020

Qy       1268 TTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACA 1327
Db       1021 TTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACG 1080

Qy       1328 ATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATG 1387
Db       1081 ATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATG 1140

Qy       1388 TCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGA 1447
Db       1141 TCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACTCCCGACGACCTTAAGTCTTTGA 1200

Qy       1448 TTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCAT 1507
Db       1201 TTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCAT 1260

Qy       1508 CAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACT 1567
Db       1261 CAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACT 1320

Qy       1568 CTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGG 1627
Db       1321 CTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGG 1380

Qy       1628 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTG 1687
Db       1381 AGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATG 1440

Qy       1688 GATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGAT 1747
Db       1441 GATTTAGATTTGATGGTGTGACATCAATGATGTGTACTCACCACGGATTATCGGTGGGAT 1500

Qy       1748 TCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATC 1807
Db       1501 TCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATC 1560

Qy       1808 TGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAG 1867
Db       1561 TGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAG 1620

Qy       1868 ATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACT 1927
Db       1621 ATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACT 1680

Qy       1928 ATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGG 1987
Db       1681 ATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGG 1740

Qy       1988 ATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTG 2047
Db       1741 ATTGGAGAGTGAGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTG 1800

Qy       2048 TTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGC 2107
Db       1801 TTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGC 1860

Qy       2108 TGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAG 2167
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Db       1861 TGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAG 1920

Qy       2168 ATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAG 2227
Db       1921 ATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAG 1980

Qy       2228 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGG 2287
Db       1981 GGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCCGAGTGGATTGATTTCCCTAGGG 2040

Qy       2288 CTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAAT 2347
Db       2041 CTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAAT 2100

Qy       2348 GCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAAT 2407
Db       2101 GCAGACGGAGATTTGACCTGGGAGATGCAGATTATTTAAGATACCGTGGGTTGCAAGAAT 2160

Qy       2408 TTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2467
Db       2161 TTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGT 2220

Qy       2468 TCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTT 2527
Db       2221 TCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTT 2280

Qy       2528 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGC 2587
Db       2281 TTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGC 2340

Qy       2588 CTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAA 2647
Db       2341 CTGGAAAATACAAGGTTGCCTTGGACTCGGATGATCCACTTTTTGGTGGCTTTGGGAGAA 2400

Qy       2648 TTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAA 2707
Db       2401 TTGATCATAATGCCGAATACTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAA 2460

Qy       2708 TTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAG 2767
Db       2461 TTATGGTGTATGCACCTAGTAGGACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGCAG 2520

Qy       2768 AAGAAGAAGAAGTAGCAGTAGTAGAAGAA 2796
Db       2521 AAGAAGAAGTAGCAGTAGTAGAAGAAGAA 2549
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RESULT 7
AAT17267

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ID   AAT17267 standard; DNA; 2531 BP.
XX
AC   AAT17267;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (direct sequencing).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;    96WO-GB01075.
XX
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAR93804.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Fig 9; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
CC   This sequence was obtained by direct sequencing of PCR fragments
CC   amplified from first strand cDNA.  Nucleotides which could not
CC   be unambiguously assigned are indicated using standard IUPAC
CC   notation.
XX
SQ   Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;

  Query Match            78.4%;  Score 2474;  DB 17;  Length 2531;
  Best Local Similarity  98.2%;  Pred. No. 0;
  Matches 2483;  Conservative   13;  Mismatches   33;  Indels    0;  Gaps    0;

Qy        270 GAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 329
Db          1 GGATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 60

Qy        330 AAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 389
Db         61 AAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 120

Qy        390 TGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 449
Db        121 TGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 180

Qy        450 GACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGC 509
Db        181 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 240

Qy        510 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 569
Db        241 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 300

Qy        570 TGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 629
Db        301 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 360

Qy        630 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 689
Db        361 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 420

Qy        690 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 749
Db        421 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 480

Qy        750 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGA 809
Db        481 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 540

Qy        810 CAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 869
Db        541 CAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 600

Qy        870 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCAT 929
Db        601 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCAT 660

Qy        930 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 989
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Db        661 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 720

Qy        990 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 1049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 780

Qy       1050 AGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 1109
              |||||||||||:|||||||||| |||||||||||||||||||||||||||||||||||||
Db        781 AGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 840

Qy       1110 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 1169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 900

Qy       1170 AGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 1229
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 960

Qy       1230 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1020

Qy       1290 AGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1349
              |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db       1021 AGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1080

Qy       1350 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1140

Qy       1410 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1200

Qy       1470 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1260

Qy       1530 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1320

Qy       1590 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1380

Qy       1650 AAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGAC 1709
              |||||||||||||||||||||||||| ||||||||:||||||||||||||||||||||||
Db       1381 AAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1440

Qy       1710 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1500

Qy       1770 CTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTAT 1829
              |||||||||||||||||||||:|||||||  |||||||||||||||| ||||||||||||
Db       1501 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1560

Qy       1830 TCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1889
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1620

Qy       1890 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1680

Qy       1950 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 2009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1740

Qy       2010 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGA 2069
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db       1741 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCATGA 1800

Qy       2070 TCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGA 2129
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db       1801 TCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTATGA 1860

Qy       2130 TTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 2189
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 1920

Qy       2190 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 2249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 1980

Qy       2250 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2309
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db       1981 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGATGG 2040

Qy       2310 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2100

Qy       2370 AGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2429
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       2101 AGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2160

Qy       2430 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2220

Qy       2490 AGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTGTCTTTAATTTTCACTGGAC 2549
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db       2221 AGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTGTCTTTAATTTTCACTGGAC 2280

Qy       2550 AAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTT 2609
              ||| |||||||||||||||||||||||||| ||||||||||||||||||||||||| |||
Db       2281 AAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGCTT 2340

Qy       2610 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTT 2669
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       2341 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2400

Qy       2670 CACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAG 2729
              ||||| |||||||| |||||||||||||||:||::|||||||||||||||||||||||||
Db       2401 CACCTCTGAAGGATCGTATGATGATCGTCCYCGYYCAATTATGGTGTATGCACCTAGTAG 2460

Qy       2730 AACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGT 2789
              |||||||||||||||||||||||||||||||  ||||| ||||||||||| || |   | 
Db       2461 AACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAANCCGN 2520

Qy       2790 AGAAGAAGT 2798
               |||||| |
Db       2521 NGAAGAATT 2529
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RESULT 8
AAT42637
ID   AAT42637 standard; DNA; 2529 BP.
XX
AC   AAT42637;
XX
DT   03-MAR-1997  (first entry)
XX
DE   Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
```

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PF   03-MAY-1996;    96WO-GB01075.
XX
PR   10-APR-1996;    96GB-0007409.
PR   05-MAY-1995;    95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 51-53; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;

  Query Match             78.3%;  Score 2471.2;  DB 17;  Length 2529;
  Best Local Similarity   98.1%;  Pred. No. 0;
  Matches 2482;  Conservative   12;  Mismatches   35;  Indels    0;  Gaps    0;

Qy        270 GAATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 329
Db          1 GGATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGA 60

Qy        330 AAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 389
Db         61 AAAGTCTTCTTACAATTCCGAATCCCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCT 120

Qy        390 TGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 449
Db        121 TGTGCCTGGAAYCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATTTGAGTTCACTGA 180

Qy        450 GACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAACAATGGAACACGC 509
Db        181 GACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGC 240

Qy        510 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 569
Db        241 TAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGT 300

Qy        570 TGAAGAGTTCGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 629
Db        301 TGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTC 360

Qy        630 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 689
Db        361 TAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAG 420

Qy        690 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 749
Db        421 GGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAA 480

Qy        750 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGA 809
Db        481 CTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGA 540

Qy        810 CAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 869
Db        541 CAAGTATGAGGGTGGTTTTCAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCG 600

Qy        870 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCAT 929
Db        601 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCAT 660

Qy        930 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 989
Db        661 TGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGT 720

Qy        990 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 1049
Db        721 CTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAG 780

Qy       1050 AGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 1109
Db        781 AGTGAAGATACGYATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAA 840

Qy       1110 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 1169
Db        841 CTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGA 900

Qy       1170 AGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 1229
Db        901 AGAGGAGAGGTATRTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 960

Qy       1230 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1289
Db        961 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1020

Qy       1290 AGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1349
Db       1021 AGATGAAGTTCTTCCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1080

Qy       1350 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1409
Db       1081 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1140

Qy       1410 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1469
Db       1141 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1200

Qy       1470 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1529
Db       1201 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACT 1260

Qy       1530 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1589
Db       1261 GAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTG 1320

Qy       1590 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1649
Db       1321 GATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTC 1380

Qy       1650 AAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGAC 1709
Db       1381 AAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1440

Qy       1710 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1769
Db       1441 ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATA 1500

Qy       1770 CTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTAT 1829
Db       1501 CTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTAT 1560

Qy       1830 TCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1889
Db       1561 TCACGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1620

Qy       1890 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1949
Db       1621 TTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGC 1680

Qy       1950 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 2009
Db       1681 TGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGT 1740

Qy       2010 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGA 2069
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Db     1741 TCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATMCGCTGAAAGTCATGA 1800

Qy     2070 TCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGA 2129
Db     1801 TCAAGCTCTAGTCGGTGATAAAACTATAGCATYCTGGCTGATGGACAAGGATATGTATGA 1860

Qy     2130 TTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAA 2189
Db     1861 TTTTATGGCTCTGGATAGACCGYCAACAYCATTAATAGATCGTGGGATAGCATTGCACAA 1920

Qy     2190 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 2249
Db     1921 GATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAA 1980

Qy     2250 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2309
Db     1981 TGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGATGG 2040

Qy     2310 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2369
Db     2041 CTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGG 2100

Qy     2370 AGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2429
Db     2101 AGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2160

Qy     2430 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2489
Db     2161 TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGG 2220

Qy     2490 AGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTCACTGGAC 2549
Db     2221 AGATAGGATGATTGTATTTGAAARAGGAAACCTAGTTTTTGTCTTTAATTTCACTGGAC 2280

Qy     2550 AAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTT 2609
Db     2281 AAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGCTT 2340

Qy     2610 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTT 2669
Db     2341 GGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATATTT 2400

Qy     2670 CACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAG 2729
Db     2401 CACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAG 2460

Qy     2730 AACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGT 2789
Db     2461 AACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAANCCGN 2520

Qy     2790 AGAAGAAGT 2798
Db     2521 NGAAGAATT 2529
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RESULT 9
AAT42631

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ID   AAT42631 standard; DNA; 2578 BP.
XX
AC   AAT42631;
XX
DT   25-FEB-1997  (first entry)
XX
DE   Class A starch branching enzyme (psbe2con.seq - clone pSJ90).
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   CDS             24..2567
FT                   /*tag=  a
FT   sig_peptide     24..56
FT                   /*tag=  b
FT   mat_peptide     57..2564
FT                   /*tag=  c
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
DR   P-PSDB; AAW06400.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Claim 32; Page 55-56; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;

  Query Match             77.5%;  Score 2445;  DB 17;  Length 2578;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2482;  Conservative    2;  Mismatches   27;  Indels   12;  Gaps    1;

Qy      318 GATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATC 377
Db       56 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 115

Qy      378 GGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 437
Db      116 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 175

Qy      438 TGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAAC 497
Db      176 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 235

Qy      498 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 557
Db      236 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 295

Qy      558 TACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 617
Db      296 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 355

Qy      618 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 677
Db      356 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 415

Qy      678 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 737
Db      416 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 475

Qy      738 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAG 797
Db      476 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 535

Qy      798 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 857
Db      536 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 595
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Qy        858 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 655

Qy        918 AGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 977
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 715

Qy        978 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 775

Qy       1038 TCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCC 1097
              |||||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||
Db        776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 835

Qy       1098 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 1157
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        836 TGCTTGGATCAACTACTCTTCACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 895

Qy       1158 TGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1217
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        896 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 955

Qy       1218 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1015

Qy       1278 CGTGAATTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCA 1337
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1016 CGTGAATTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCA 1075

Qy       1338 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1135

Qy       1398 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1195

Qy       1458 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1255

Qy       1518 TTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG 1577
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1256 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1315

Qy       1578 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1637
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1316 TGGTTATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAG 1375

Qy       1638 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATT 1697
              |||||||||||||||||||||||||||||||||||||| ||||||||:||||||||||||
Db       1376 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATT 1435

Qy       1698 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1495

Qy       1758 CTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGC 1817
              |||||||||||||||||||||||||||||||||:|||||||  |||||||||||||||| 
Db       1496 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1555

Qy       1818 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1615

Qy       1878 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1675

Qy       1938 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1735

Qy       1998 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 2057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1795

Qy       2058 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 2117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1855

Qy       2118 GGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 2177
              |||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||
Db       1856 GGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAT 1915

Qy       2178 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1975

Qy       2238 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2035

Qy       2298 CCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2357
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2095

Qy       2358 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2155

Qy       2418 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2215

Qy       2478 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2275

Qy       2538 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATA 2597
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       2276 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATA 2335

Qy       2598 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2395

Qy       2658 TGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2717
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2455

Qy       2718 TGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACA------------AAGAAGA 2765
              ||||||| |||||||||||||||||||||||||||||||||            |||||||
Db       2456 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2515

Qy       2766 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTT 2825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTT 2575

Qy       2826 GTG 2828
              |||
Db       2576 GTG 2578
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RESULT 10
AAT42636
ID   AAT42636 standard; DNA; 2576 BP.
XX
AC   AAT42636;
XX
DT   03-MAR-1997  (first entry)
XX
```

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DE   Class A starch branching enzyme (86con.seq) cloned in QE32.
XX
KW   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW   amylose; viscosity; potato; ss.
XX
OS   Solanum tuberosum.
XX
PN   WO9634968-A2.
XX
PD   07-NOV-1996.
XX
PF   03-MAY-1996;   96WO-GB01075.
XX
PR   10-APR-1996;   96GB-0007409.
PR   05-MAY-1995;   95GB-0009229.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Cooke D,  Debet M,  Gidley MJ,  Jobling SA,  Safford R;
PI   Sidebottom CM, Westcott RJ;
XX
DR   WPI; 1996-506170/50.
XX
PT   New potato plant starch having high amylose content - also class A
PT   starch branching enzyme and corresp. DNA to alter the viscosity of
PT   starch; for use in food, biodegradable products, adhesives, etc.
XX
PS   Example 1; Page 49-51; 142pp; English.
XX
CC   Class A starch branching enzyme (SBE) has been obtained from
CC   potatoes.  In class A SBE mols., a flexible N-terminal domain,
CC   is found, which is not found in class B mols.
XX
SQ   Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;

  Query Match             76.9%;  Score 2427.8;  DB 17;  Length 2576;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 2478;  Conservative    2;  Mismatches   29;  Indels   14;  Gaps    2;

Qy        318 GATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCGACCTTCTACAGTTGCAGCATC 377
Db         56 GATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATC 115

Qy        378 GGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTCCTCATCCTCAACAGACCAATT 437
Db        116 GGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATT 175

Qy        438 TGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATCAACTGATGTGGATAGTTCAAC 497
Db        176 TGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAAC 235

Qy        498 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 557
Db        236 AATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCT 295

Qy        558 TACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 617
Db        296 TACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGGTGGTAA 355

Qy        618 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 677
Db        356 ACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAG 415

Qy        678 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 737
Db        416 GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCC 475

Qy        738 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAG 797
Db        476 CCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAG 535

Qy        798 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 857
Db        536 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAAT 595

Qy        858 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 917
Db        596 GGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTC 655

Qy        918 AGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 977
Db        656 AGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAA 715

Qy        978 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 1037
Db        716 TGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCC 775

Qy       1038 TCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCC 1097
Db        776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCC 835

Qy       1098 TGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 1157
Db        836 TGCTTGGATCAACTACTC--TACAGCTTCCTGATGAAATTCCATATAATGGAATATATTA 893

Qy       1158 TGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 1217
Db        894 TGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAAGTC 953

Qy       1218 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1277
Db        954 GCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATA 1013

Qy       1278 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCA 1337
Db       1014 CGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCA 1073

Qy       1338 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1397
Db       1074 AATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTT 1133

Qy       1398 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1457
Db       1134 TTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGC 1193

Qy       1458 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1517
Db       1194 TCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1253

Qy       1518 TTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG 1577
Db       1254 TTTAGATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCG 1313

Qy       1578 TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAG 1637
Db       1314 TGGTTATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAG 1373

Qy       1638 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATT 1697
Db       1374 GTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATATTGATT 1433

Qy       1698 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1757
Db       1434 TGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAA 1493

Qy       1758 CTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGC 1817
Db       1494 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGT 1553

Qy       1818 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1877
Db       1554 CAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGG 1613

Qy       1878 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1937
Db       1614 AATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCA 1673
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Qy       1938 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGT 1733

Qy       1998 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 2057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 GGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGC 1793

Qy       2058 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 2117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 TGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAA 1853

Qy       2118 GGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT 2177
              |||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||
Db       1854 GGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAT 1913

Qy       2178 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 2237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 AGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAA 1973

Qy       2238 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1974 TTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACA 2033

Qy       2298 CCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2357
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2034 CCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAG 2093

Qy       2358 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2094 ATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGC 2153

Qy       2418 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2154 TATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACG 2213

Qy       2478 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2214 AAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAA 2273

Qy       2538 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATA 2597
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       2274 TTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATA 2333

Qy       2598 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2334 CAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAA 2393

Qy       2658 TGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2717
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2394 TGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTA 2453

Qy       2718 TGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACA------------AAGAAGA 2765
              ||||||| |||||||||||||||||||||||||||||||||            |||||||
Db       2454 TGCACCTTGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGA 2513

Qy       2766 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTT 2825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2514 AGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAACTT 2573

Qy       2826 GTG 2828
              |||
Db       2574 GTG 2576
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RESULT 11
AAV38720
ID   AAV38720 standard; DNA; 3090 BP.
XX
AC   AAV38720;
XX
DT   21-SEP-1998  (first entry)
XX
DE   Full length cassava tuber cDNA in pSJ146.
XX
KW   Starch branching enzyme; SBE; cassava; ss.
XX
OS   Manihot esculenta.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    35..2760
FT                   /*tag=  a
FT                   /note= "these nycleotides are SBE II sequence, the
FT                          reminder are derived from the plamsid"
FT   CDS             131..2677
FT                   /*tag=  b
FT                   /product= SBE II
XX
PN   WO9820145-A2.
XX
PD   14-MAY-1998.
XX
PF   04-NOV-1997;   97WO-GB03032.
XX
PR   05-NOV-1996;   96GB-0023095.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Jobling SA,  Safford R;
XX
DR   WPI; 1998-286958/25.
DR   P-PSDB; AAW62600.
XX
PT   Starch branching gene from cassava - useful for producing altered
PT   plants giving modified starch
XX
PS   Claim 2; Fig 13; 67pp; English.
XX
CC   The present sequence encodes starch branching enzyme (SBE) II. It
CC   was isolated from cassava tubers. The products can be used for
CC   producing plants having altered starch quantities and qualities.
CC   They can also be used for producing altered plants such as cassava,
CC   banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
CC   and rice plants.
XX
SQ   Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;

  Query Match             45.7%;  Score 1442.8;  DB 19;  Length 3090;
  Best Local Similarity   73.1%;  Pred. No. 0;
  Matches 1923;  Conservative    2;  Mismatches  609;  Indels   96;  Gaps    2;

Qy        180 AAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTACAAATC 239
              || |  |    || ||  | || ||   | |||||||||  ||  || ||| | |||||||
Db        130 AATGGTATACTACACTGTATCAGGCATACGTTTTCCTTGTGCACCTTCACTCTACAAATC 189

Qy        240 TAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATG---TTTCTGTATTCTTGAA 296
              | |      ||||    |||| | ||| ||||    ||  ||     ||||  |  ||||||
Db        190 TCAGCTCACCAGCTTCCATGGCGGTCGAAGGACCTCTTCTGGCCTTTCCTTCCTCTTGAA 249

Qy        297 AAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATCCCG 356
              ||| |      || | |||||||||| |||| |||||| ||||| || || || |||
Db        250 GAAGGAGCTGTTTCCTCGGAAGATCTTTGCTGGAAAGTCCTCTTATGAATCTGACTCCTC 309

Qy        357 ACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAGCTC 416
              |  ||  || ||   | |||||  ||| |||||||| ||||     |||| |||| ||||
Db        310 AAATTTAACTGTCTCTGCATCTGAGAAGGTCCTTGTTCCTGATGATCAGATTGATGGCTC 369

Qy        417 CTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGCATC 476
                || || |||||| | ||||| ||     ||||| |||| |    ||   | ||||   |
Db        370 TTCTTCTTCAACATATCAATTAGAAACCACTGGCACAGTTTTGGAGGAATCCCAGGTTCT 429

Qy        477 AACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGA 536
                 |||||  || |||       |||||| | | ||     |  || |     ||  | |   |
Db        430 TGGTGATGCAGAGAGTCTTGTGATGGAAGATGATAAGAATGTTGAGGAGGATGAAGTAAA 489
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Qy    537 CGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATCACT 596
Db    490 AAAAGAGTCG-------------------------------------------------- 499

Qy    597 ACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGAC 656
Db    500 -------------------------------------------GTTCCATTGCATGAGAC 516

Qy    657 AATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCA 716
Db    517 AATTAGCATTGGAAAAAGTGAATCTAAACCAAGGTCCATTCCTCCACCTGGCAGTGGGCA 576

Qy    717 GAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTA 776
Db    577 GAGAATATATGACATAGATCCAAGCTTGGCAGGTTTCCGTCAGCATCTTGACTACCGATA 636

Qy    777 TTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTT 836
Db    637 TTCACAGTACAAAAGGCTGCGTGAGGAAATTGACAAGTATGAAGGTGGTTTGGATGCATT 696

Qy    837 TTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGA 896
Db    697 CTCTCGTGGATTTGAAAAGTTTGGTTTCTTACGCAGTGAAACAGGAATAACTTATAGGGA 756

Qy    897 GTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAA 956
Db    757 ATGGGCACCTGGAGCTACGTGGGCTGCACTTATTGGAGATTTCAACAATTGGAATCCTAA 816

Qy    957 TGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGT 1016
Db    817 TGCAGATGTCATGACTCGGAATGAGTTTGGTGTCTGGGAGATTTTTTTGCCAAATAACGC 876

Qy   1017 GGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATC 1076
Db    877 AGATGGTTCACCACCAATTCCTCATGGTTCTCGAGTAAAGATACGCATGGATACTCCATC 936

Qy   1077 AGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT 1136
Db    937 TGGCATCAAAGATTCAATTCCTGCTTGGATCAAGTTCTCAGTTCAGGCACCTGGTGAAAT 996

Qy   1137 TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCC 1196
Db    997 CCCATACAATGCCATATACTATGATCCACCAAAGGAGGAGAAGTATGTGTTCAAACATCC 1056

Qy   1197 ACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCC 1256
Db   1057 TCAGCCAAAGAGACCAAAATCACTTAGGATTTATGAATCTCATGTTGGGATGAGTAGTAT 1116

Qy   1257 GGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAA 1316
Db   1117 GGAGCCAATAATTAACACATATGCCAACTTTAGAGATGATATGCTTCCTCGCATCAAAAA 1176

Qy   1317 CCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTT 1376
Db   1177 GCTTGGCTACAATGCTGTTCAGATCATGGCTATTCAAGAGCATTCCTATTATGCTAGTTT 1236

Qy   1377 TGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCCGACGACCT 1436
Db   1237 TGGGTACCATGTCACAAACTTTTTTGCACCTAGCAGCCGATTTGGAACTCCTGATGATTT 1296

Qy   1437 TAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCA 1496
Db   1297 GAAGTCTTTAATAGATAAAGCTCATGAGTTAGGGCTGCTTGTTCTCATGGATATTGTTCA 1356

Qy   1497 CAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTG 1556
Db   1357 TAGCCATGCGTCAAATAATACGTTGGATGGGCTGAACATGTTTGATGGTACGGATAGTCA 1416

Qy   1557 TTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTA 1616
Db   1417 CTACTTCCACTCCGGATCACGGGGTCATCATTGGTTGTGGGACTCTCGCCTTTTCAACTA 1476

Qy   1617 TGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTG 1676
Db   1477 TGGAAGCTGGGAGGTGCTAAGATTTCTTCTTTCAAATGCAAGATGGTGGTTGGAAGAGTA 1536

Qy   1677 CAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATT 1736
Db   1537 CAGGTTTGATGGTTTAGATTTGATGGGGTGACTTCCATGATGTACACTCCCCATGGGTT 1596

Qy   1737 ATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGRGATGC 1796
Db   1597 GCAGGTAGCTTTTACTGGCAACTACAATGAGTACTTTGGATATGCAACTGATGTAGATGC 1656

Qy   1797 TGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTAC 1856
Db   1657 TGTGATTTATTTGATGCTTGTGAATGATATGATTCACGGTCTTTTCCCTGAGGCTGTTAC 1716

Qy   1857 CATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGT 1916
Db   1717 CATTGGTGAAGATGTTAGCGGAAAGCCAACATTTTGCATTCCAGTGGAAGATGGTGGTGT 1776

Qy   1917 TGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAA 1976
Db   1777 TGGATTTGATTACCGTCTCCACATGGCCATTGCCGATAAATGGATTGAGATTCTTAAGAA 1836

Qy   1977 ACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTC 2036
Db   1837 GAGAGATGAGGACTGGAAAATGGGTGACATTGTGCATACACTCACCAACAGAAGGTGGTT 1896

Qy   2037 GGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTAT 2096
Db   1897 GGAAAAAATGTGTTGCTTATGCTGAAAGTCATGACCAAGCTCTTGTTGGTGACAAAACTAT 1956

Qy   2097 AGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAAC 2156
Db   1957 TGCATTTTGGCTGATGGACAAGGACATGTACGACTTCATGGCTCGTGACAGACCATCTAC 2016

Qy   2157 ATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATT 2216
Db   2017 TCCTCTTATAGATCGTGGAATAGCATTGCACAAAATGATCAGGCTTATTACCATGGGCTT 2076

Qy   2217 AGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGA 2276
Db   2077 AGGCGGAGAAGGATATTTGAATTTTATGGGAAATGAATTTGGACATCCTGAGTGGATTGA 2136

Qy   2277 TTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAG 2336
Db   2137 TTTTCCAAGAGGGGATCGACATCTGCCCAATGGTAAAGTAATTCCAGGGAACAACCACAG 2196

Qy   2337 TTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGG 2396
Db   2197 TTATGATAAATGCCGTCGTAGATTTGATCTAGGTGATGCAGACTATCTAAGATATCATGG 2256

Qy   2397 GTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTC 2456
Db   2257 AATGCAAGAGTTTGATCAGGCAATGCAACATCTTGAAGAAGCCTATGGTTTCATGACTTC 2316

Qy   2457 AGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGG 2516
Db   2317 TGAGCACCAGTATATATCACGGAAGGATGAAGGAGATCGGATCATTGTCTTTGAGAGGGG 2376

Qy   2517 AAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGG 2576
Db   2377 AAACCTTGTTTTTGTATTCAACTTTCATTGGACTAACAGCTATTCAGATTACCGAGTTGG 2436

Qy   2577 CTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGG 2636
Db   2437 CTGCTTCAAGTCAGGAAAGTACAAGATTGTTTTGGACTCGGATGATGGCTTGTTTGGAGG 2496

Qy   2637 CTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCG 2696
Db   2497 CTTCAACAGGCTTAGTCATGATGCCGAGCACTTCACCTTTGACGGGTGGTATGATAACCG 2556

Qy   2697 TCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGA 2756
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Db       2557 GCCTCGGTCCTTCATGGTATATGCACCATCTAGGACAGCAGTGGTCTATGCTTTAGTAGA 2616

Qy       2757 CAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAG 2806

Db       2617 AGATGAAGAGAATGAAGCAGAGAATGAAGTAGAAAGTGAAGTGAAACCAG 2666


RESULT 12
AAV38719
ID   AAV38719 standard; cDNA; 2913 BP.
XX
AC   AAV38719;
XX
DT   21-SEP-1998  (first entry)
XX
DE   Full length cassava tuber cDNA in pSJ107.
XX
KW   Starch branching enzyme; SBE; cassava; ss.
XX
OS   Manihot esculenta.
XX
FH   Key             Location/Qualifiers
FT   CDS             21..2531
FT                   /*tag=  a
FT                   /product= SBE II
XX
PN   WO9820145-A2.
XX
PD   14-MAY-1998.
XX
PF   04-NOV-1997;   97WO-GB03032.
XX
PR   05-NOV-1996;   96GB-0023095.
XX
PA   (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI   Jobling SA,  Safford R;
XX
DR   WPI; 1998-286958/25.
DR   P-PSDB; AAW62599.
XX
PT   Starch branching gene from cassava - useful for producing altered
PT   plants giving modified starch
XX
PS   Claim 2; Fig 4; 67pp; English.
XX
CC   The present sequence encodes starch branching enzyme (SBE) II. It
CC   was isolated from cassava tubers. The products can be used for
CC   producing plants having altered starch quantities and qualities.
CC   They can also be used for producing altered plants such as cassava,
CC   banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
CC   and rice plants.
XX
SQ   Sequence 2913 BP; 818 A; 549 C; 680 G; 866 T; 0 other;

  Query Match             43.7%;  Score 1377.8;  DB 19;  Length 2913;
  Best Local Similarity   76.1%;  Pred. No. 0;
  Matches 1694;  Conservative    2;  Mismatches  529;  Indels    0;  Gaps    0;

Qy        612 TGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATC 671

Db        347 TGTTGAAGATGAAGTAAATAAAGAATCTGTTCCAATGCGGGAGACAGTTAGCATCAGAAA 406

Qy        672 TGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAAT 731

Db        407 AATTGGATCTAAACCAAGGTCCATTCCTCCACCCGGCAGAGGGCAAAGAATATATGACAT 466

Qy        732 AGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAA 791

Db        467 AGATCCAAGCTTGACAGGCTTTCGTCAACACCTAGATTACCGGTATTCACAGTACAAAAG 526

Qy        792 AATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGA 851

Db        527 ACTCCGAGAAGAAATTGACAAGTATGAAGGTAGTCTGGATGCATTTTCTCGTGGCTATGA 586

Qy        852 AAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGC 911

Db        587 AAAGTTTGGTTTCTCACGCAGTGAAACAGGAATAACTTATAGAGAGTGGGCACCAGGAGC 646

Qy        912 CCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGAC 971

Db        647 TACGTGGGCTGCATTGATTGGAGATTTCAATAACTGGAATCCTAATGCAGATGTCATGAC 706

Qy        972 TCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGC 1031

Db        707 TCAGAATGAGTGTGGTGTCTGGGAGATCTTTTTGCCGAATAATGCAGATGGTTCACCACC 766

Qy       1032 AATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTC 1091

Db        767 AATTCCCCATGGTTCTCGAGTAAAGATACGCATGGATACTCCATCTGGCAACAAAGATTC 826

Qy       1092 CATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAAT 1151

Db        827 TATTCCTGCTTGGATCAAGTTCTCAGTTCAAGCACCAGGTGAACTCCCATATAATGGCAT 886

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RESULT 14
AAV05639
ID   AAV05639 standard; cDNA to mRNA; 3015 BP.
XX
AC   AAV05639;
XX
DT   01-MAY-1998  (first entry)
XX
DE   Rice type IV starch branching enzyme cDNA.
XX
KW   Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     129..287
FT                   /*tag=  b
FT   mat_peptide     288..2651
FT                   /*tag=  c
FT                   /product= type_IV_starch_branching_enzyme
XX
PN   JP10004970-A.
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XX
PD   13-JAN-1998.
XX
PF   24-JUN-1996;   96JP-0162983.
XX
PR   24-JUN-1996;   96JP-0162983.
XX
PA   (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA   (MITK ) MITSUI TOATSU CHEN INC.
XX
DR   WPI; 1998-133625/13.
DR   P-PSDB; AAW41763.
XX
PT   Rice starch branching enzyme gene - synthesises amylopectin to yield
PT   high quality starch
XX
PS   Claim 4; Pages 5-8; 13pp; Japanese.
XX
CC   The present sequence encodes the rice type IV starch branching
CC   enzyme, which has the ability to synthesise amylopectin. The
CC   quality of starch is improved by the use of the protein.
XX
SQ   Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;

  Query Match            40.4%;  Score 1275.6;  DB 19;  Length 3015;
  Best Local Similarity  75.3%;  Pred. No. 0;
  Matches 1587;  Conservative    1;  Mismatches  520;  Indels    0;  Gaps    0;

Qy     663 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 722
Db     554 TGAACCAACTGTGGAGGATAAACCACGAGTTATCCCACCACCAGGAGATGGCAGAAGAT 613

Qy     723 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 782
Db     614 ATACCAAATTGACCCAATGCTGGAAGGATTTCGGAACCATCTTGACTACCGATACAGTGA 673

Qy     783 GTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCG 842
Db     674 ATACAAGAGAATGCGTGCAGCTATTGACCAACATGAAGGTGGCTTGGATGCATTTTCTCG 733

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Db     734 TGGTTACGAAAAGCTTGGATTCACCCGCAGCGCTGAAGGCATTACCTACCGAGAATGGGC 793

Qy     903 TCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 962
Db     794 ACCTGGAGCACAGTCTGCAGCATTAGTAGGTGACTTCAACAATTGGAACCCAAATGCAGA 853

Qy     963 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 1022
Db     854 TACTATGACCAGAAATGAGTATGGTGTTTGGGAGATTTCCCTGCCTAACAATGCTGATGG 913

Qy    1023 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGT 1082
Db     914 ATCCCCTGCTATTCCTCATGGCTCACGTGTAAAGATTCGGATGGATACACCATCTGGCGT 973

Qy    1083 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 1142
Db     974 AAAGGATTCAATTCCTGCCTGGATTAAGTTTGCTGTGCAGGCTCCAGGTGAAATACCGTA 1033

Qy    1143 TAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCC 1202
Db    1034 CAACGGTATATATTATGATCCACCTGAAGAAGAAAAATATGTATTCCAACATCCTCAACC 1093

Qy    1203 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
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Qy    1323 GTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTA 1382
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Qy    1383 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1442
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Qy    1443 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1502
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Qy    1503 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTT 1562
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Db    1574 TGATGGGTTTCGATTTGATGGGGTGACCTCCATGATGTATACTCATCATGGTTTACAGGT 1633

Qy    1743 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGRGATGCTGCCGT 1802
Db    1634 GGCATTTACTGGCAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCAGTAGT 1693

Qy    1803 GTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1862
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Qy    1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTT 1922
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Qy    1923 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1982
Db    1814 TGACTATCGTTTGCATATGGCTGTACCGGACAAATGGATCGAACTCCTCAAGCAAAGTGA 1873

Qy    1983 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2042
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Qy    2043 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 2102
Db    1934 GTGTGTTACTTATGCAGAAAGTCATGACCAAGCACTAGTTGGTGACAAGACTATTGCATT 1993

Qy    2103 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATT 2162
Db    1994 CTGGTTGATGGATAAGGATATGTATGATTTTATGGCTCTAGACAGACCTTCAACACCTCG 2053

Qy    2163 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2222
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Qy    2223 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2282
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Qy    2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGA 2342
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Qy    2343 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2402
Db    2234 TAAATGCCGTCGTAGATTTGACCTTGGAGATGCAGATTATCTTAGATATCATGGTATGCA 2293

Qy    2403 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2462
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Db        2594 TTCATTCTCGGTGTACACCCCAAGCAGAACCGCCGTCGTGTATGCACTTACAGAGGACTA 2653

Qy        2763 AGAAGAAG 2770

Db        2654 ATGATCAG 2661
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RESULT 15
AAQ73750

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ID   AAQ73750 standard; cDNA to mRNA; 2919 BP.
XX
AC   AAQ73750;
XX
DT   05-JUL-1995  (first entry)
XX
DE   Rice starch branching enzyme.
XX
KW   Starch branching enzyme; rice; starch content; ds.
XX
OS   Oryza sativa.
XX
FH   Key                Location/Qualifiers
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PF   22-OCT-1993;   93JP-0265171.
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PR   29-OCT-1992;   92JP-0291719.
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XX
DR   WPI; 1994-337418/42.
DR   P-PSDB; AAR60811.
XX
PT   New gene of branching enzyme of rice starch - useful for
PT   increasing starch yield of rice grains
XX
PS   Claim 1; Page 9-12; 13pp; Japanese.
XX
CC   The rice starch branching enzyme is encoded by the cDNA sequence
CC   AAQ73750. The starch content of rice grains can be increased by
CC   increasing the expression of branching enzyme in rice plants.
XX
SQ   Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 other;

  Query Match             39.9%;  Score 1260.4;  DB 15;  Length 2919;
  Best Local Similarity   74.6%;  Pred. No. 0;
  Matches 1582;  Conservative    1;  Mismatches  537;  Indels    0;  Gaps    0;

Qy         659 TTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGA 718

Db         504 TTGAAGAATTAGCTGCTGAGCAGAAACCACGAGTTGTCCCACCAACAGGAGATGGGCAAA 563

Qy         719 AGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATT 778

Db         564 AAATATTCCAGATGGACTCTATGCTTAATGGCTATAAGTACCATCTTGAATATCGATATA 623

Qy         779 CACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTT 838

Db         624 GCCTATATAGGAGACTGCGTTCAGACATTGATCAGTATGAAGGAGGACTGGAAACATTTT 683

Qy         839 CTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGT 898

Db         684 CTCGCGGTTATGAGAAGTTTGGATTTAATCACAGTGCTGAAGGTGTCACTTATCGAGAAT 743

Qy         899 GGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATG 958

Db         744 GGGCTCCCGGGGCACATTCTGCAGCATTAGTAGGTGACTTCAACAATTGGAATCCAAATG 803

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Qy        1079 GTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTC 1138

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Qy        1259 AGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACC 1318

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Qy        1319 TTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTG 1378

Db        1164 TTGGATACAATGCAGTGCAAATAATGGCAATTCAAGAGCATGCATATTATGGAAGCTTTG 1223

Qy        1379 GTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTA 1438

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Qy        1559 ACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATG 1618

Db        1404 ACTTTCATAGTGGTTCACGCGGCCATCATTGGATGTGGGATTCTCGCCTTTTCAACTATG 1463

Qy        1619 GAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCA 1678
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Db   1464 GGAATTGGGAAGTTCTAAGATTTCTACTATCCAATGCAAGATGGTGGCTCGAGGAGTATA 1523

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Db   1524 AGTTTGATGGTTTCAGATTTGACGGTGTAACCTCAATGATGTACACTCATCATGGATTAC 1583

Qy   1739 CGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTG 1798
Db   1584 AAGTAGCATTTACGGGGAACTACAGTGAATACTTTGGATTTGCCACTGATGCTGATGCAG 1643

Qy   1799 CCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCA 1858
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Qy   1859 TTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTG 1918
Db   1704 TCGGTGAAGATGTCAGTGGAATGCCTACATTTGCCCTTCCTGTTCAAGATGGTGGGGTTG 1763

Qy   1919 GCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAAC 1978
Db   1764 GTTTTGATTATCGCCTTCATATGGCTGTTCCTGACAAATGGATTGAACTCCTCAAGCAAA 1823

Qy   1979 GGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGG 2038
Db   1824 GTGATGAATCTTGGAAGATGGGTGATATTGTGCACACACTGACTAACAGAAGGTGGTCAG 1883

Qy   2039 AAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAG 2098
Db   1884 AGAAGTGTGTTACTTATGCTGAAAGTCATGATCAAGCACTAGTTGGTGACAAAACTATTG 1943

Qy   2099 CATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACAT 2158
Db   1944 CATTCTGGTTGATGGACAAGGATATGTATGATTTTATGGCTCTGGACAGACCGGCAACAC 2003

Qy   2159 CATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAG 2218
Db   2004 CTAGCATTGATCGTGGAATAGCATTGCATAAAATGATTAGACTTATCACAATGGGGTTAG 2063

Qy   2219 GAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATT 2278
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Qy   2339 ATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGT 2398
Db   2184 ATGATAAATGCCGTCGAAGATTTGACCTGGGTGATGCGGACTATCTTAGGTATCGTGGCA 2243

Qy   2399 TGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAG 2458
Db   2244 TGCTAGAGTTTGACCGCGCGATGCAGTCTCTCGAGGAAAAATATGGGTTCATGACATCAG 2303

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Db   2304 ACCACCAGTACATATCTCGAAAGCATGAAGAGGATAAGATGATTATATTTGAGAAGGGAG 2363

Qy   2519 ACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCT 2578
Db   2364 ATCTGGTATTTGTGTTCAACTTCCATTGGAGTAACAGCTATTTTGACTACCGTGTTGGTT 2423

Qy   2579 GGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCT 2638
Db   2424 GTTTAAAGCCAGGGAAATATAAGGTGGTCTTGGACTCAGATGCTGGACTCTTTGGTGGAT 2483

Qy   2639 TCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTC 2698
Db   2484 TTGGCAGGATCCATCACACTGCAGAGCACTTCACTGCCGATTGTTCACATGACAACAGGC 2543

Qy   2699 CTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACA 2758
Db   2544 CCTACTCGTTCTCAGTTTATTCTCCTAGCAGAACCTGCGTTGTCTATGCTCCAGCGGAAT 2603

Qy   2759 AAGAAGAAGAAGAAGAAGAA 2778
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	2955.2	93.6	3074	4	US-09-087-277-1	Sequence 1, Appli
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	3	1372.2	43.5	1393	4	US-09-087-277-3	Sequence 3, Appli
	4	1372.2	43.5	1393	4	US-09-658-499-3	Sequence 3, Appli
	5	1200.4	38.0	2665	4	US-09-257-894-1	Sequence 1, Appli
	6	1200.4	38.0	2725	3	US-08-941-445A-14	Sequence 14, Appl
	7	1049.8	33.3	2087	4	US-09-257-894-9	Sequence 9, Appli
c	8	1048.2	33.2	2165	4	US-09-257-894-8	Sequence 8, Appli
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	11	632.4	20.0	2565	4	US-09-257-894-24	Sequence 24, Appl
	12	632.4	20.0	2763	3	US-08-941-445A-16	Sequence 16, Appl
	13	632.4	20.0	2772	4	US-09-257-894-12	Sequence 12, Appl
	14	623.2	19.7	2909	4	US-08-104-158-1	Sequence 1, Appli
	~~15~~	~~546~~	~~17.3~~	~~1809~~	~~4~~	~~US-09-257-894-25~~	~~Sequence 25, Appl~~
	16	546	17.3	1865	4	US-09-257-894-20	Sequence 20, Appl
	17	371.6	11.8	11478	3	US-08-981-803-29	Sequence 29, Appl
	18	371.6	11.8	11478	4	US-08-983-440-29	Sequence 29, Appl
	19	358.2	11.3	5402	4	US-09-221-017B-194	Sequence 194, App
c	20	107	3.4	414	4	US-09-257-894-2	Sequence 2, Appli
	21	70.6	2.2	2426	4	US-08-528-026C-3	Sequence 3, Appli
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c	23	63.2	2.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c	24	56.8	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
c	25	54.6	1.7	571	4	US-09-257-894-16	Sequence 16, Appl
c	26	53.8	1.7	16442	3	US-08-781-891-208	Sequence 208, App
	27	51.4	1.6	5394	3	US-08-688-376-1	Sequence 1, Appli
c	28	49.4	1.6	188	1	US-08-115-497-21	Sequence 21, Appl
c	29	49.4	1.6	188	1	US-08-466-670-21	Sequence 21, Appl
c	30	49.4	1.6	188	2	US-08-291-011-1	Sequence 1, Appli
c	31	49.4	1.6	188	4	US-09-266-065-1	Sequence 1, Appli
c	32	49.4	1.6	405	2	US-08-299-074A-1	Sequence 1, Appli
c	33	49.4	1.6	405	4	US-09-399-773-1	Sequence 1, Appli
c	34	46.8	1.5	252	2	US-08-623-906A-1	Sequence 1, Appli
	35	46.6	1.5	661	3	US-08-961-083-77	Sequence 77, Appl
c	36	46.6	1.5	11384	4	US-08-961-527-45	Sequence 45, Appl
c	37	46.4	1.5	6701	4	US-09-004-838-107	Sequence 107, App
	38	46.4	1.5	43795	3	US-08-742-185-101	Sequence 101, App
	39	45.8	1.5	2100	1	US-07-927-316A-1	Sequence 1, Appli
	40	45.2	1.4	3211	2	US-08-574-959A-8	Sequence 8, Appli
	41	45.2	1.4	3211	4	US-09-357-014-8	Sequence 8, Appli
	42	45.2	1.4	3901	2	US-08-574-959A-6	Sequence 6, Appli
	43	45.2	1.4	3901	4	US-09-357-014-6	Sequence 6, Appli
	44	45	1.4	2691	4	US-09-298-924-5	Sequence 5, Appli
	45	43.2	1.4	3337	1	US-08-072-610-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-087-277-1
; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beII gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; FEATURE:

see search 3, ver)
✓ 1ne date
TO
Lt

```
;     NAME/KEY: misc_feature
;     LOCATION: (1404)..(1406)
;     OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;     FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: (1428)..(1430)
;     OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;     FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: (1896)..(1898)
;     OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;     OTHER INFORMATION: or Phe.
;     FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: (2154)..(2156)
;     OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

  Query Match            93.6%;  Score 2955.2;  DB 4;  Length 3074;
  Best Local Similarity  98.1%;  Pred. No. 0;
  Matches 3019;  Conservative    2;  Mismatches   41;  Indels   14;  Gaps    3;

Qy          3 AAACCTCCTCCACTCAGTCTTGGGATCTCTCTCTCTTCACGCTTCTCTTGGGGCCTTG 62
Db          1 AAACCTCCTCCACTCAGTCTTTG--TTTCTCTCTCTCTTCACGCTTCTCTTGGCGCCTTG 58

Qy         63 AACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCTCTATTTTT 122
Db         59 AACTCAGCAATTTGACACTCAGTTAGTTACACTNCCATCACTTATCAGATCTCTATTTTT 118

Qy        123 TCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATTTGAAGGAGAG 173
Db        119 TCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACCCTAAGGAGAG 178

Qy        174 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 233
Db        179 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 238

Qy        234 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTT 293
Db        239 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTT 298

Qy        294 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATC 353
Db        299 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATC 358

Qy        354 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAG 413
Db        359 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAG 418

Qy        414 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGC 473
Db        419 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGC 478

Qy        474 ATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGA 533
Db        479 ATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGGCAGATTAAAACTGAGAACGA 538

Qy        534 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATC 593
Db        539 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATC 598

Qy        594 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 653
Db        599 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 658

Qy        654 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 713
Db        659 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 718

Qy        714 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 773
Db        719 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 778

Qy        774 GTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 833
Db        779 GTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 838

Qy        834 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 893
Db        839 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 898

Qy        894 TGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGC 953
Db        899 TGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGC 958

Qy        954 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1013
Db        959 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1018

Qy       1014 TGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTC 1073
Db       1019 TGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCC 1078

Qy       1074 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1133
Db       1079 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1138

Qy       1134 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACA 1193
Db       1139 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACA 1198

Qy       1194 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1253
Db       1199 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1258

Qy       1254 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1313
Db       1259 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1318

Qy       1314 AAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1373
Db       1319 AAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1378

Qy       1374 TTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGA 1433
Db       1379 TTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGGAACNCCCGACGA 1438

Qy       1434 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1493
Db       1439 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1498

Qy       1494 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1553
Db       1499 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1558

Qy       1554 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1613
Db       1559 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1618

Qy       1614 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1673
Db       1619 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1678

Qy       1674 GTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1733
Db       1679 GTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1738

Qy       1734 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGA 1793
Db       1739 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGA 1798

Qy       1794 TGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1853
Db       1799 TGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1858
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Qy       1854 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGG 1913
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1859 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGG 1918

Qy       1914 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1919 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1978

Qy       1974 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2033
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2039 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2098

Qy       2094 TATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTC 2153
              ||||||||||||||||||||| |||||||||||||||||||||||| |||||||||| ||
Db       2099 TATAGCATTCTGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTC 2158

Qy       2154 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2159 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2218

Qy       2214 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2219 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2278

Qy       2274 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2279 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2338

Qy       2334 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2398

Qy       2394 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2399 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2458

Qy       2454 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2459 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2518

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2519 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2578

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              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2639 TGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGA 2698

Qy       2694 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2699 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2758

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Qy       2811 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
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Db       2819 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878

Qy       2871 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2930
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Db       2879 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2938

Qy       2931 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAA 2990
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Qy       2991 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3050
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Db       2999 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3058

Qy       3051 TGTAAATTGTCATCTC 3066
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Db       3059 TGTAAATTGTCATCTC 3074
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RESULT 2
US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/09/658,499
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER: 09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   NAME/KEY: CDS
;   LOCATION: (189)..(2825)
;   NAME/KEY: sig_peptide
;   LOCATION: (189)..(332)
;   NAME/KEY: mat_peptide
;   LOCATION: (333)..(2825)
;   NAME/KEY: misc_feature
;   LOCATION: (92)..(2156)
;   OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
;   OTHER INFORMATION: n wherein n = A, C, G or T.
;   NAME/KEY: misc_feature
;   LOCATION: (285)..(287)
;   OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1404)..(1406)
;   OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1428)..(1430)
;   OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;   NAME/KEY: misc_feature
;   LOCATION: (1896)..(1898)
;   OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (2154)..(2156)
;   OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1
```

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Query Match             93.6%;  Score 2955.2;  DB 4;  Length 3074;
Best Local Similarity   98.1%;  Pred. No. 0;
Matches 3019;  Conservative    2;  Mismatches   41;  Indels   14;  Gaps    3;

Qy          3 AAACCTCCTCCACTCAGTCTTGGGATCTCTCTCTCTTCACGCTTCTCTTGGGGCCTTG 62
Db          1 AAACCTCCTCCACTCAGTCTTTG--TTTCTCTCTCTCTTCACGCTTCTCTTGGCGCCTTG 58

Qy         63 AACTCAGCAATTTGACACTCAGTTAGTTACACTCCTATCACTCATCAGATCTCTATTTTT 122
Db         59 AACTCAGCAATTTGACACTCAGTTAGTTACACTNCCATCACTTATCAGATCTCTATTTTT 118

Qy        123 TCTCTTAATTCCAACCAAGGAATGAATTAAAAGAT---------TAGATTTGAAGGAGAG 173
Db        119 TCTCTTAATTCCAACCAAGGAATGAATAAAAAGATAGATTTGTAAAAACCCTAAGGAGAG 178

Qy        174 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 233
Db        179 AAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGTA 238

Qy        234 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTT 293
Db        239 CAAATCTAATGGATTCAGCAGTAATGGTGATCGGAGGAATGCTAATNTTTCTGTATTCTT 298

Qy        294 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACGATTCCGAATC 353
Db        299 GAAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCGAATC 358

Qy        354 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTACCTGGAATCCAGAGTGATAG 413
Db        359 CCGACCTTCTACAGTTGCAGCATCGGGGAAAGTCCTTGTGCCTGGAACCCAGAGTGATAG 418

Qy        414 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACAGCTCCAGAAAATTCCCCAGC 473
Db        419 CTCCTCATCCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAATTCCCCAGC 478

Qy        474 ATCAACTGATGTGGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGA 533
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Qy        534 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGTTGGATTTTGCTTCATC 593
Db        539 TGACGTTGAGCCGTCAAGTGATCTTACAGGAAGTGTTGAAGAGCTGGATTTTGCTTCATC 598

Qy        594 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 653
Db        599 ACTACAACTACAAGAAGGTGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGA 658

Qy        654 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 713
Db        659 GACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGG 718

Qy        714 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 773
Db        719 TCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAG 778

Qy        774 GTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 833
Db        779 GTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGC 838

Qy        834 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 893
Db        839 TTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCG 898

Qy        894 TGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGC 953
Db        899 TGAGTGGGCTCCTGGTGCCCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGC 958

Qy        954 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1013
Db        959 AAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAA 1018

Qy       1014 TGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTC 1073
Db       1019 TGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCC 1078

Qy       1074 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1133
Db       1079 ATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGA 1138

Qy       1134 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACA 1193
Db       1139 AATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACA 1198

Qy       1194 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1253
Db       1199 CCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAG 1258

Qy       1254 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1313
Db       1259 TCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAA 1318

Qy       1314 AAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1373
Db       1319 AAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAG 1378

Qy       1374 TTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGA 1433
Db       1379 TTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGGAACNCCCGACGA 1438

Qy       1434 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1493
Db       1439 CCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGT 1498

Qy       1494 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1553
Db       1499 TCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAG 1558

Qy       1554 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1613
Db       1559 TTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAA 1618

Qy       1614 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1673
Db       1619 CTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGA 1678

Qy       1674 GTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1733
Db       1679 GTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGG 1738

Qy       1734 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGA 1793
Db       1739 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGA 1798

Qy       1794 TGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1853
Db       1799 TGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1858

Qy       1854 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGG 1913
Db       1859 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGG 1918

Qy       1914 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1973
Db       1919 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1978

Qy       1974 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2033
Db       1979 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2038

Qy       2034 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2093
Db       2039 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2098

Qy       2094 TATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTC 2153
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Db        2099 TATAGCATTCTGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTC 2158

Qy        2154 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2159 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2218

Qy        2214 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2219 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2278

Qy        2274 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2279 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2338

Qy        2334 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2339 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2398

Qy        2394 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2399 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2458

Qy        2454 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2513
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2459 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2518

Qy        2514 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2573
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2519 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2578

Qy        2574 AGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2633
               |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2579 AGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2638

Qy        2634 TGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGA 2693
               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        2639 TGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGA 2698

Qy        2694 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2699 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2758

Qy        2754 AGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2810
               |||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2759 AGACAAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2818

Qy        2811 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        2819 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878

Qy        2871 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2930
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2879 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2938

Qy        2931 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAA 2990
               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        2939 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGCACAAACATATGTAA 2998

Qy        2991 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3050
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2999 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3058

Qy        3051 TGTAAATTGTCATCTC 3066
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Db        3059 TGTAAATTGTCATCTC 3074
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RESULT 3
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-087-277-3

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  Query Match             43.5%;  Score 1372.2;  DB 4;  Length 1393;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1377;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        1002 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 1061
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

Qy        1062 CATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 1121
                ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 120

Qy        1122 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 1181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 180

Qy        1182 TGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 1241
               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 240

Qy        1242 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 1301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 300

Qy        1302 TCCTCGCATAAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 1361
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Db          301 TCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 360

Qy         1362 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGG 1421
                |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db          361 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTNGCACCAAGCAGCCGTTTTGA 420

Qy         1422 AACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 1481
                ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 AACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 480

Qy         1482 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 1541
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 540

Qy         1542 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 1601
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 600

Qy         1602 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 1661
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 660

Qy         1662 GTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTA 1721
                |||||||||||||| ||||||||:||||||||||||||||||||||||||||||||||||
Db          661 GTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 720

Qy         1722 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 1781
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 780

Qy         1782 AACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTT 1841
                |||||||||:|||||||  |||||||||||||||| ||||||||||||||||||||||||
Db          781 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 840

Qy         1842 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGT 1901
                |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db          841 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGT 900

Qy         1902 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 1961
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 960

Qy         1962 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 2021
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1020

Qy         2022 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 2081
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1080

Qy         2082 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTT 2141
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         1081 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1140

Qy         2142 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2201
                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 GGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 1200

Qy         2202 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2261
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 1260

Qy         2262 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 2321
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Db         1261 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 1320

Qy         2322 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2381
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 1380

Qy         2382 TTTAAGATACCGT 2394
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Db         1381 TTTAAGATACCGT 1393
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RESULT 4
US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/09/658,499
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER: 09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   NAME/KEY: misc_feature
;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-658-499-3

  Query Match             43.5%;  Score 1372.2;  DB 4;  Length 1393;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1377;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         1002 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 1061
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

Qy         1062 CATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 1121
                 ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 120

Qy         1122 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 1181
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 180

Qy         1182 TGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 1241
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 240

Qy         1242 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 1301
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 300

Qy       1302 TCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 1361
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 360

Qy       1362 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGG 1421
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||| 
Db        361 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGA 420

Qy       1422 AACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 1481
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 480

Qy       1482 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 1541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 540

Qy       1542 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 1601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 600

Qy       1602 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 1661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGIATCTTCTCTCAAATGCGAGATG 660

Qy       1662 GTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTA 1721
              |||||||||||||| ||||||||:||||||||||||||||||||||||||||||||||||
Db        661 GTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 720

Qy       1722 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 1781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 780

Qy       1782 AACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTT 1841
              |||||||||:|||||||  |||||||||||||||| ||||||||||||||||||||||||
Db        781 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 840

Qy       1842 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGT 1901
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Db        841 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGT 900

Qy       1902 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 1961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 960

Qy       1962 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 2021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1020

Qy       2022 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 2081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1080

Qy       2082 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTT 2141
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1081 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1140

Qy       2142 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2201
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 1200

Qy       2202 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 1260

Qy       2262 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 2321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 1320

Qy       2322 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 1380

Qy       2382 TTTAAGATACCGT 2394
              |||||||||||||
Db       1381 TTTAAGATACCGT 1393


RESULT 5
US-09-257-894-1
; Sequence 1, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:     2665 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..2476
US-09-257-894-1

  Query Match             38.0%;  Score 1200.4;  DB 4;  Length 2665;
  Best Local Similarity   73.3%;  Pred. No. 0;
  Matches 1534;  Conservative    2;  Mismatches  558;  Indels    0;  Gaps    0;

Qy        663 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 722
              |||||     |    || |||||   | |   |||| |||||  |   ||| || || ||
Db        381 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 440

Qy        723 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 782
               |   | || |||||| | |||  |  ||||    | || ||||| ||  ||||    | 
Db        441 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 500

Qy        783 GTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCG 842
               || |  | |||  |    |  |||||  |  |||| || || |||||||| || || ||
Db        501 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 560
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Qy    843 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 902
Db    561 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 620

Qy    903 TCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 962
Db    621 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACTTCAACAACTGGGATCCAAATGCAGA 680

Qy    963 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 1022
Db    681 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 740

Qy   1023 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGT 1082
Db    741 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 800

Qy   1083 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 1142
Db    801 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 860

Qy   1143 TAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCC 1202
Db    861 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 920

Qy   1203 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
Db    921 TAAACGACCAAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 980

Qy   1263 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGG 1322
Db    981 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 1040

Qy   1323 GTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTA 1382
Db   1041 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1100

Qy   1383 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1442
Db   1101 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1160

Qy   1443 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1502
Db   1161 TTTGATTGATAGAGCACATGAGCTTGGTTTGCTAGTTCTCATGGATGTGGTTCATAGTCA 1220

Qy   1503 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTT 1562
Db   1221 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 1280

Qy   1563 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1622
Db   1281 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAA 1340

Qy   1623 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATT 1682
Db   1341 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 1400

Qy   1683 TGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGT 1742
Db   1401 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 1460

Qy   1743 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGT 1802
Db   1461 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 1520

Qy   1803 GTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1862
Db   1521 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 1580

Qy   1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTT 1922
Db   1581 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1640

Qy   1923 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1982
Db   1641 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1700

Qy   1983 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2042
Db   1701 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 1760

Qy   2043 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 2102
Db   1761 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 1820

Qy   2103 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATT 2162
Db   1821 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1880

Qy   2163 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2222
Db   1881 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1940

Qy   2223 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2282
Db   1941 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 2000

Qy   2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGA 2342
Db   2001 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 2060

Qy   2343 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2402
Db   2061 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2120

Qy   2403 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2462
Db   2121 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATTCATGACATCTGATCA 2180

Qy   2463 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2522
Db   2181 CCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTGTGTTCGAAAAGGGAGATTT 2240

Qy   2523 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCT 2582
Db   2241 GGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTTGACTACCGTATTGGTTGTCG 2300

Qy   2583 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2642
Db   2301 AAAGCCTGGGGTGTATAAGGTGGTCTTGGACTCCGACGCTGGACTATTTGGTGGATTTAG 2360

Qy   2643 GAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2702
Db   2361 CAGGATCCATCACGCAGCCGAGCACTTCACCGCCGACTGTTCGCATGATAATAGGCCATA 2420

Qy   2703 TTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGA 2756
Db   2421 TTCATCCTCGGTTTATACACCAAGCAGAACATGTGTCGTCTATGCTCCAGTGGA 2474
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RESULT 6
US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/941,445A
;      FILING DATE:  30-SEP-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,855
;      FILING DATE:  30-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winner, Ellen P
;      REGISTRATION NUMBER:  28,547
;      REFERENCE/DOCKET NUMBER:  89-97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2725 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  mRNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Zea mays
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  91..264
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  265..2487
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  91..2490
US-08-941-445A-14

  Query Match             38.0%;  Score 1200.4;  DB 3;  Length 2725;
  Best Local Similarity   73.3%;  Pred. No. 0;
  Matches 1534;  Conservative    2;  Mismatches  558;  Indels    0;  Gaps    0;

Qy        663 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 722
Db        393 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 452

Qy        723 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 782
Db        453 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 512

Qy        783 GTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCG 842
Db        513 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 572

Qy        843 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 902
Db        573 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 632

Qy        903 TCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 962
Db        633 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACGTCAACAACTGGGATCCAAATGCAGA 692

Qy        963 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 1022
Db        693 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 752

Qy       1023 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGT 1082
Db        753 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 812

Qy       1083 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 1142
Db        813 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 872

Qy       1143 TAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCC 1202
Db        873 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 932

Qy       1203 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
Db        933 TAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 992

Qy       1263 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGG 1322
Db        993 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 1052

Qy       1323 GTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTA 1382
Db       1053 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1112

Qy       1383 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1442
Db       1113 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTGGTACCCCAGAAGATTTGAAGTC 1172

Qy       1443 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1502
Db       1173 TTTGATTGATAGAGCACATGAGCTTGGTTTGCTAGTTCTCATGGATGTGGTTCATAGTCA 1232

Qy       1503 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTT 1562
Db       1233 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 1292

Qy       1563 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1622
Db       1293 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAA 1352

Qy       1623 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATT 1682
Db       1353 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 1412

Qy       1683 TGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGT 1742
Db       1413 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 1472

Qy       1743 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGT 1802
Db       1473 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 1532

Qy       1803 GTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1862
Db       1533 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 1592

Qy       1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTT 1922
Db       1593 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1652

Qy       1923 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1982
Db       1653 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1712

Qy       1983 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2042
Db       1713 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 1772

Qy       2043 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 2102
Db       1773 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 1832

Qy       2103 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATT 2162
Db       1833 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1892

Qy       2163 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2222
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Db      1893 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1952

Qy      2223 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2282
Db      1953 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 2012

Qy      2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGA 2342
Db      2013 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 2072

Qy      2343 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2402
Db      2073 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2132

Qy      2403 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2462
Db      2133 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATTCATGACATCTGATCA 2192

Qy      2463 CCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCT 2522
Db      2193 CCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTGTGTTCGAAAAGGGAGATTT 2252

Qy      2523 AGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCT 2582
Db      2253 GGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTTGACTACCGTATTGGTTGTCG 2312

Qy      2583 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2642
Db      2313 AAAGCCTGGGGTGTATAAGGTGGTCTTGGACTCCGACGCTGGACTATTTGGTGGATTTAG 2372

Qy      2643 GAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2702
Db      2373 CAGGATCCATCACGCAGCCGAGCACTTCACCGCCGACTGTTCGCATGATAATAGGCCATA 2432

Qy      2703 TTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGA 2756
Db      2433 TTCATTCTCGGTTTATACACCAAGCAGAACATGTGTCGTCTATGCTCCAGTGGA 2486
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RESULT 7
US-09-257-894-9
; Sequence 9, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-257-894-9

Query Match 33.3%; Score 1049.8; DB 4; Length 2087;
Best Local Similarity 74.2%; Pred. No. 4.3e-308;
Matches 1324; Conservative 2; Mismatches 459; Indels 0; Gaps 0;

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Qy       663 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 722
Db       303 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 362

Qy       723 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 782
Db       363 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 422

Qy       783 GTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCG 842
Db       423 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 482

Qy       843 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 902
Db       483 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 542

Qy       903 TCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 962
Db       543 TCCTGGAGCATTTTCTGCAGCATTGGTGGGTGACTTCAACAACTGGGATCCAAATGCAGA 602

Qy       963 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 1022
Db       603 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 662

Qy      1023 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGT 1082
Db       663 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 722

Qy      1083 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 1142
Db       723 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 782

Qy      1143 TAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCC 1202
Db       783 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 842

Qy      1203 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
Db       843 TAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 902

Qy      1263 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGG 1322
Db       903 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 962

Qy      1323 GTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTA 1382
Db       963 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1022

Qy      1383 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1442
Db      1023 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1082

Qy      1443 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1502
Db      1083 TTTGATTGATAGAGCACATGAGCTTGGTTTGCTAGTTCTCATGGATGTGGTTCATAGTCA 1142
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Qy   1503 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTT 1562
Db   1143 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 1202

Qy   1563 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1622
Db   1203 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAA 1262

Qy   1623 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATT 1682
Db   1263 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 1322

Qy   1683 TGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGT 1742
Db   1323 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 1382

Qy   1743 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGT 1802
Db   1383 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 1442

Qy   1803 GTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1862
Db   1443 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 1502

Qy   1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTT 1922
Db   1503 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1562

Qy   1923 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1982
Db   1563 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1622

Qy   1983 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2042
Db   1623 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 1682

Qy   2043 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 2102
Db   1683 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 1742

Qy   2103 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATT 2162
Db   1743 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1802

Qy   2163 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2222
Db   1803 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 1862

Qy   2223 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2282
Db   1863 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 1922

Qy   2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGA 2342
Db   1923 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 1982

Qy   2343 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2402
Db   1983 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 2042

Qy   2403 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTT 2447
Db   2043 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATT 2087
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RESULT 8
US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-257-894-8

Query Match 33.2%; Score 1048.2; DB 4; Length 2165;
Best Local Similarity 74.1%; Pred. No. 1.4e-307;
Matches 1323; Conservative 2; Mismatches 460; Indels 0; Gaps 0;

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Qy    663 TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGAT 722
Db   1785 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTCCCCCCACCAAGCGATGGACAAAAAAT 1726

Qy    723 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 782
Db   1725 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 1666

Qy    783 GTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCG 842
Db   1665 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 1606

Qy    843 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 902
Db   1605 TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGGAAGGTATCACATATCGAGAATGGGC 1546

Qy    903 TCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 962
Db   1545 TCCTGGAGCATTTTCTCGCAGCATTGGTGGGTGACGTCAACAACTGGGATCCAAATGCAGA 1486

Qy    963 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGG 1022
Db   1485 TCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAATGCAGATGG 1426

Qy   1023 TTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGT 1082
Db   1425 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 1366
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Qy       1083 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 1142
Db       1365 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 1306

Qy       1143 TAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCC 1202
Db       1305 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 1246

Qy       1203 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
Db       1245 TAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAATGAGTAGCCCGGAACC 1186

Qy       1263 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGG 1322
Db       1185 GAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAATAAAAAAACTTGG 1126

Qy       1323 GTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTA 1382
Db       1125 ATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGGAAGCTTTGGATA 1066

Qy       1383 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1442
Db       1065 CCATGTAACTAATTTTTTTGCGCCAAGTAGTCGTTTTGGTACCCCAGAAGATTTGAAGTC 1006

Qy       1443 TTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCA 1502
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Qy       1503 TGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTT 1562
Db        945 TGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTT 886

Qy       1563 TCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAA 1622
Db        885 TCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAA 826

Qy       1623 CTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATT 1682
Db        825 CTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCGAGGAATATAAGTT 766

Qy       1683 TGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGT 1742
Db        765 TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACCACGGATTACAAGT 706

Qy       1743 GGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGT 1802
Db        705 AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCAGTGGT 646

Qy       1803 GTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGG 1862
Db        645 TTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTAACCATTGG 586

Qy       1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTT 1922
Db        585 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 526

Qy       1923 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1982
Db        525 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 466

Qy       1983 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2042
Db        465 TGAAACTTGGAAGATGGGTGATATTGTGCACACACTGACAAATAGGAGGTGGTTAGAGAA 406

Qy       2043 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT 2102
Db        405 GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTT 346

Qy       2103 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATT 2162
Db        345 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 286

Qy       2163 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2222
Db        285 CATTGATCGTGGGATAGCATTACATAAGATGATTAGACTTATCACAATGGGTTTAGGAGG 226

Qy       2223 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2282
Db        225 AGAGGGCTATCTTAATTTCATGGGAAATGAGTTTGGACATCCTGAATGGATAGATTTTCC 166

Qy       2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGA 2342
Db        165 AAGAGGTCCGCAAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATAACAACAGTTATGA 106

Qy       2343 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2402
Db        105 CAAATGTCGTCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA 46

Qy       2403 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTT 2447
Db         45 AGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATATGAATT 1
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RESULT 9
~~US-08-716-449-1~~

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; Sequence 1, Application US/08716449
; Patent No. 6103893
;  GENERAL INFORMATION:
;    APPLICANT:  National Starch and Chemical Investment
;    APPLICANT:  Holding Corporation
;    TITLE OF INVENTION:  Method for Producing Altered Starch
;    TITLE OF INVENTION:  from Potato Plants
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scott & Aylen
;      STREET:  Box 194, 24th Floor, Toronto-Dominion Bank Tower
;      CITY:  Toronto
;      STATE:  Canada M5K 1H6
;      COUNTRY:  Canada
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  IMB 1.44 MB High Density Diskette
;      COMPUTER:  COMPAQ Deskpro 590 (IBM PC compatible)
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  Word 7.0 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/716,449
;      FILING DATE:  FILED CONCURRENTLY HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/00634
;      FILING DATE:  22.03.95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Anita E.Nador
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  1552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 368-2400
;      TELEFAX:  (416) 363-7246
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3128 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  cDNA encoding starch branching enzyme
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:  clone 1.2.1 and E2
;      ORGANISM:  Solanum tuberosum
;      STRAIN:  cv desiree
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:  mature tuber
;      HAPLOTYPE:
;      TISSUE TYPE:
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;       CELL TYPE:
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:  lambda Zap tuber cDNA
;       CLONE:  1.2.1 and E2
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:  open reading frame
;       NAME/KEY:  starch branching enzyme
;       LOCATION:  44-2788
;       IDENTIFICATION METHOD:  lone ORF with homology to other starch
;       IDENTIFICATION METHOD:  branching enzymes
;       OTHER INFORMATION:  complements KV832 E. coli glycogen
;       OTHER INFORMATION:  branching enzyme mutant
US-08-716-449-1

  Query Match             20.2%;  Score 637.4;  DB 3;  Length 3128;
  Best Local Similarity   60.3%;  Pred. No. 7.3e-183;
  Matches 1190;  Conservative    1;  Mismatches  727;  Indels   57;  Gaps    6;

Qy        731 TAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGA 790
Db        345 TGGATCCAACTTTGGAACCTTATCTAGATCACTTCAGACACAGAATGAAGAGATATGTGG 404

Qy        791 AAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATG 850
Db        405 ATCAGAAAATGCTCATTGAAAAATATGAGGGACCCCTTGAGGAATTTGCTCAAGGTTATT 464

Qy        851 AAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTG 910
Db        465 TAAAATTTGGATTCAACAGGGAAGATGGTTGCATAGTCTATCGTGAATGGGCTCCTGCTG 524

Qy        911 CCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGA 970
Db        525 CTCAGGAAGCAGAAGTTATTGGCGATTTCAATGGATGGAACGGTTCTAACCACATGATGG 584

Qy        971 CTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTG 1030
Db        585 AGAAGGACCAGTTTGGTGTTTGGAGTATTAGAATTCC---TGATGTTGACAGTAAGCCAG 641

Qy       1031 CAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAG---G 1087
Db        642 TCATTCCACACAACTCCAGAGTTAAGTTTCGTTTCAAACATGGTAATGGAGTGTGGGTAG 701

Qy       1088 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCC------TGATGAAATTCCAT 1141
Db        702 ATCGTATCCCTGCTTGGATAAAGTATGCCACTGCAGACGCCACAAAGTTTGCAGCACCAT 761

Qy       1142 ATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGC 1201
Db        762 ATGATGGTGTCTACTGGGACCCACCACCTTCAGAAAGGTACCACTTCAAATACCCTCGCC 821

Qy       1202 CAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGC 1261
Db        822 CTCCCAAACCCCGAGCCCCACGAATCTACGAAGCACATGTCGGCATGAGCAGCTCTGAGC 881

Qy       1262 CTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTG 1321
Db        882 CACGTGTAAATTCGTATCGTGAGTTTGCAGATGATGTTTTACCTCGGATTAAGGCAAATA 941

Qy       1322 GGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTT 1381
Db        942 ACTATAATACTGTCCAGTTGATGGCCATAATGGAACATTCTTACTATGGATCATTTGGAT 1001

Qy       1382 ATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGT 1441
Db       1002 ATCATGTTACAAACTTTTTTGCTGTGAGCAATAGATATGGAAACCCGGAGGACCTAAAGT 1061

Qy       1442 CTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCC 1501
Db       1062 ATCTGATAGATAAAGCACATAGCTTGGGTTTACAGGTTCTGGTGGATGTAGTTCACAGTC 1121

Qy       1502 ATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACGGCACAGATA 1552
Db       1122 ATGCAAGCAATAATGTCACTGATGGCCTCAATGGCTTTGATATTGGCCAAGGTTCTCAAG 1181

Qy       1553 GTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTA 1612
Db       1182 AATCCTACTTTCATGCTGGAGAGCGAGGGTACCATAAGTTGTGGGATAGCAGGCTGTTCA 1241

Qy       1613 ACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATG 1672
Db       1242 ACTATGCCAATTGGGAGGTTCTTCGTTTCCTTCTTTCCAACTTGAGGTGGTGGCTAGAAG 1301

Qy       1673 AGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACG 1732
Db       1302 AGTATAACTTTGACGGATTTCGATTTGATGGAATAACTTCTATGCTGTATGTTCATCATG 1361

Qy       1733 GATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRG 1792
Db       1362 GAATCAATATGGGATTTACAGGAAACTATAATGAGTATTTCAGCGAGGCTACAGATGTTG 1421

Qy       1793 ATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAA 1852
Db       1422 ATGCTGTGGTCTATTTAATGTTGGCCAATAATCTGATTCACAAGATTTTCCCAGACGCAA 1481

Qy       1853 TTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGG 1912
Db       1482 CTGTTATTGCCGAAGATGTTTCTGGTATGCCGGGCCTTAGCCGGCCTGTTTCTGAGGGAG 1541

Qy       1913 GTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCA 1972
Db       1542 GAATTGGTTTTGATTACCGCCTGGCAATGGCAATCCCAGATAAGTGGATAGATTATTTAA 1601

Qy       1973 AGAAACGG---GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAA 2029
Db       1602 AGAATAAGAATGATGAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGA 1661

Qy       2030 GATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATA 2089
Db       1662 GATATACAGAGAAGTGTATAGCATATGCGGAGAGCCATGATCAGTCTATTGTCGGTGACA 1721

Qy       2090 AAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGAC 2149
Db       1722 AGACCATTGCATTTCTCCTAATGGACAAAGAGATGTATTCTGGCATGTCTTGCTTGACAG 1781

Qy       2150 CGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTA 2209
Db       1782 ATGCTTCTCCTGTTGTTGATCGAGGAATTGCGCTTCACAAGATGATCCATTTTTTCACAA 1841

Qy       2210 TGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGT 2269
Db       1842 TGGCCTTGGGAGGAGAGGGGTACCTCAATTTCATGGGTAACGAGTTTGGCCATCCTGAGT 1901

Qy       2270 GGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACC 2329
Db       1902 GGATTGACTTCCCTAGAG-------------------------------AGGGCAATA 1928

Qy       2330 AATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGAT 2389
Db       1929 ATTGGAGTTATGACAAATGTAGACGCCAGTGGAACCTCGCAGATAGCGAACACTTGAGAT 1988

Qy       2390 ACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTA 2449
Db       1989 ACAAGTTTATGAATGCATTTGATAGAGCTATGAATTCGCTCGATGAAAAGTTCTCATTCC 2048

Qy       2450 TGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTG 2509
Db       2049 TCGCATCAGGAAAACAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTGTTTG 2108

Qy       2510 AAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATC 2569
Db       2109 AACGTGGTGACCTGGTATTTGTATTCAACTTCCACCCAAATAACACATACGAAGGGTATA 2168
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Qy       2570 GCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTT 2629
Db       2169 AAGTTGGATGTGACTTGCCAGGGAAGTACAGAGTTGCACTGGGCAGTGATGCTTGGGAAT 2228

Qy       2630 TTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATG 2684
Db       2229 TTGGTGGCCATGGAAGAGCTGGTCATGATGTTGACCATTTCACATCACCAGAAGG 2283
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RESULT 10
US-09-257-894-19/c
; Sequence 19, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
;   APPLICANT: Broglie, Karen E.
;   APPLICANT: Klein, Theodore M.
;   APPLICANT: Hubbard, Natalie L.
;   APPLICANT: Lightner, Jonathan E.
;   TITLE OF INVENTION: No. 6376749el Starches via Modification of
;   TITLE OF INVENTION: Expression of Starch Biosynthesis
;   TITLE OF INVENTION: Enzyme Genes
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: E. I. du Pont de Nemours and Company
;   STREET: 1007 Market Street
;   CITY: Wilmington
;   STATE: Delaware
;   COUNTRY: USA
;   ZIP: 19898
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: Microsoft Windows 95
;   SOFTWARE: Version 7.0A
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/257,894
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/091,052
;   FILING DATE: JUNE 10, 1998
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Majarian, William R.
;   REGISTRATION NUMBER: 41,173
;   REFERENCE/DOCKET NUMBER: BB-1066-A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 302-992-4926
;   TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 19:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2487 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-09-257-894-19

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  Query Match            20.0%;  Score 632.4;  DB 4;  Length 2487;
  Best Local Similarity   59.7%;  Pred. No. 2.1e-181;
  Matches 1178;  Conservative    2;  Mismatches  738;  Indels   54;  Gaps    5;

Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
Db       2124 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 2065

Qy        781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
Db       2064 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 2005

Qy        841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
Db       2004 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 1945

Qy        901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
Db       1944 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 1885

Qy        961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGGAT 1020
Db       1884 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 1828

Qy       1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
Db       1827 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 1768

Qy       1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 1136
Db       1767 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 1708

Qy       1137 --TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db       1707 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 1648

Qy       1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db       1647 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 1588

Qy       1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db       1587 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 1528

Qy       1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
Db       1527 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 1468

Qy       1375 TTTGGTTATCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1434
Db       1467 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 1408

Qy       1435 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1494
Db       1407 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1348

Qy       1495 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACG---------GC 1545
Db       1347 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1288

Qy       1546 ACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1605
Db       1287 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1228

Qy       1606 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1665
Db       1227 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1168

Qy       1666 TTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACT 1725
Db       1167 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1108

Qy       1726 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1785
Db       1107 CACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACA 1048

Qy       1786 GATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCA 1845
Db       1047 GCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCA 988

Qy       1846 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAA 1905
Db        987 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 928

Qy       1906 GATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAG 1965
Db        927 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 868
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Qy       1966 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 2022
Db        867 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 808

Qy       2023 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082
Db        807 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 748

Qy       2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142
Db        747 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 688

Qy       2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202
Db        687 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 628

Qy       2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262
Db        627 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 568

Qy       2263 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2322
Db        567 CCAGAATGGATTGACTTTCCAAGAGAA--------------------------------- 541

Qy       2323 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2382
Db        540 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 481

Qy       2383 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2442
Db        480 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 421

Qy       2443 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2502
Db        420 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 361

Qy       2503 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2562
Db        360 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 301

Qy       2563 GACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2622
Db        300 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 241

Qy       2623 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCT 2674
Db        240 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 189
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RESULT 11
US-09-257-894-24
; Sequence 24, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-257-894-24

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  Query Match             20.0%;  Score 632.4;  DB 4;  Length 2565;
  Best Local Similarity   59.7%;  Pred. No. 2.1e-181;
  Matches 1178;  Conservative    2;  Mismatches  738;  Indels   54;  Gaps    5;

Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
Db        253 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 312

Qy        781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
Db        313 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 372

Qy        841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
Db        373 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 432

Qy        901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
Db        433 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 492

Qy        961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
Db        493 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 549

Qy       1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
Db        550 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 609

Qy       1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 1136
Db        610 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 669

Qy       1137 --TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db        670 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 729

Qy       1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db        730 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 789

Qy       1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db        790 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 849

Qy       1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
Db        850 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 909

Qy       1375 TTTGGTTATCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1434
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Db        910 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 969

Qy       1435 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1494

Db        970 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1029

Qy       1495 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACG---------GC 1545

Db       1030 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1089

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Db       1150 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTCTTCTTTCTAACCTGAGATATTGG 1209

Qy       1666 TTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACT 1725

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Qy       1846 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAA 1905

Db       1390 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 1449

Qy       1906 GATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAG 1965

Db       1450 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 1509

Qy       1966 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 2022

Db       1510 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 1569

Qy       2023 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082

Db       1570 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1629

Qy       2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142

Db       1630 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1689

Qy       2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202

Db       1690 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 1749

Qy       2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262

Db       1750 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 1809

Qy       2263 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2322

Db       1810 CCAGAATGGATTGACTTTCCAAGAGAA--------------------------------- 1836

Qy       2323 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2382

Db       1837 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 1896

Qy       2383 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2442

Db       1897 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 1956

Qy       2443 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2502

Db       1957 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 2016

Qy       2503 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2562

Db       2017 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 2076

Qy       2563 GACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2622

Db       2077 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 2136

Qy       2623 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCT 2674

Db       2137 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 2188
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RESULT 12
US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
;   APPLICANT: Keeling, Peter
;   APPLICANT: Guan, Hanping
;   TITLE OF INVENTION: Starch Encapsulation
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
;   STREET: 5370 Manhattan Circle
;   CITY: Boulder
;   STATE: CO
;   COUNTRY: US
;   ZIP: 80303
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/941,445A
;   FILING DATE: 30-SEP-1997
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/026,855
;   FILING DATE: 30-SEP-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Winner, Ellen P
;   REGISTRATION NUMBER: 28,547
;   REFERENCE/DOCKET NUMBER: 89-97
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (303) 499-8080
;   TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2763 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: mRNA
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: transit_peptide
;   LOCATION: 2..190
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: 191..2467
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 2..2470
US-08-941-445A-16

Query Match 20.0%; Score 632.4; DB 3; Length 2763;
Best Local Similarity 59.7%; Pred. No. 2.2e-181;

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Matches 1178;  Conservative    2;  Mismatches  738;  Indels   54;  Gaps    5;

Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
Db        251 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 310

Qy        781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
Db        311 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 370

Qy        841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
Db        371 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 430

Qy        901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
Db        431 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 490

Qy        961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
Db        491 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 547

Qy       1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
Db        548 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 607

Qy       1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 1136
Db        608 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 667

Qy       1137 --TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db        668 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 727

Qy       1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db        728 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 787

Qy       1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db        788 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 847

Qy       1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
Db        848 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 907

Qy       1375 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGAC 1434
Db        908 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 967

Qy       1435 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1494
Db        968 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1027

Qy       1495 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACG---------GC 1545
Db       1028 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1087

Qy       1546 ACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1605
Db       1088 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1147

Qy       1606 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1665
Db       1148 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1207

Qy       1666 TTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACT 1725
Db       1208 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1267

Qy       1726 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1785
Db       1268 CACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACA 1327

Qy       1786 GATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCA 1845
Db       1328 GCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCA 1387

Qy       1846 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAA 1905
Db       1388 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 1447

Qy       1906 GATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAG 1965
Db       1448 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 1507

Qy       1966 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 2022
Db       1508 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 1567

Qy       2023 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082
Db       1568 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1627

Qy       2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142
Db       1628 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1687

Qy       2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202
Db       1688 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 1747

Qy       2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262
Db       1748 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 1807

Qy       2263 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2322
Db       1808 CCAGAATGGATTGACTTTCCAAGAGAA--------------------------------- 1834

Qy       2323 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2382
Db       1835 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 1894

Qy       2383 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2442
Db       1895 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 1954

Qy       2443 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2502
Db       1955 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 2014

Qy       2503 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2562
Db       2015 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 2074

Qy       2563 GACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2622
Db       2075 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 2134

Qy       2623 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCT 2674
Db       2135 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 2186
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RESULT 13
US-09-257-894-12
; Sequence 12, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis

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;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2772 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  49..2580
US-09-257-894-12

  Query Match              20.0%;  Score 632.4;  DB 4;  Length 2772;
  Best Local Similarity    59.7%;  Pred. No. 2.2e-181;
  Matches 1178;  Conservative    2;  Mismatches  738;  Indels   54;  Gaps    5;

Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
Db        364 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 423

Qy        781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
Db        424 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 483

Qy        841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
Db        484 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 543

Qy        901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
Db        544 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 603

Qy        961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
Db        604 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 660

Qy       1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
Db        661 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 720

Qy       1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 1136
Db        721 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 780

Qy       1137 --TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db        781 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 840

Qy       1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db        841 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 900

Qy       1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db        901 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 960

Qy       1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
Db        961 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 1020

Qy       1375 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1434
Db       1021 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 1080

Qy       1435 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1494
Db       1081 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1140

Qy       1495 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACG---------GC 1545
Db       1141 CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC 1200

Qy       1546 ACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGC 1605
Db       1201 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1260

Qy       1606 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1665
Db       1261 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1320

Qy       1666 TTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACT 1725
Db       1321 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1380

Qy       1726 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1785
Db       1381 CACCATGGTATCAATGTGGGGTTTACTGGAAACTACCAGGAATATTTCAGTTTGGACACA 1440

Qy       1786 GATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCA 1845
Db       1441 GCTGTGGATGCAGTTGTTTACATGATGCTTGCAAACCATTTAATGCACAAACTCTTGCCA 1500

Qy       1846 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAA 1905
Db       1501 GAAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTGCCGGCCAGTTGAT 1560

Qy       1906 GATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAG 1965
Db       1561 GAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC 1620

Qy       1966 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGACA 2022
Db       1621 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAAATAGCGCATACTTTGACT 1680

Qy       2023 AATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082
Db       1681 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1740

Qy       2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142
Db       1741 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1800

Qy       2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202
Db       1801 TTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTC 1860

Qy       2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262
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Db       1861 ATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 1920

Qy       2263 CCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCC 2322

Db       1921 CCAGAATGGATTGACTTTCCAAGAGAA--------------------------------- 1947

Qy       2323 GGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATAT 2382

Db       1948 GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 2007

Qy       2383 TTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATAT 2442

Db       2008 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 2067

Qy       2443 GAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATT 2502

Db       2068 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTATT 2127

Qy       2503 GTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCA 2562

Db       2128 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGAG 2187

Qy       2563 GACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGAT 2622

Db       2188 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCT 2247

Qy       2623 CCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCT 2674

Db       2248 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGT 2299
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RESULT 14
US-08-104-158-1
; Sequence 1, Application US/08104158
; Patent No. 6215042
; GENERAL INFORMATION:
;   APPLICANT: Willmitzer, Lothar
;   APPLICANT: Sonnewald, Uwe
;   APPLICANT: Kossmann, Jens
;   APPLICANT: Mueller-Roeber, Bernd
;   APPLICANT: Visser, Richard Gerardus Francisus
;   APPLICANT: Jacobsen, Evert
;   TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
;   TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
;   TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
;   TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
;   STREET: 1180 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10036-8403
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/104,158
;   FILING DATE: 13-AUG-1993
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP PCT/EP92/00302
;   FILING DATE: 11-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE P 41 04 782.6
;   FILING DATE: 13-FEB-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Meilman, Edward A.
;   REGISTRATION NUMBER: 24,735
;   REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-382-0700
;   TELEFAX: 212-382-0888
;   TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2909 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Solanum tuberosum cv. Desiree
;   STRAIN: Desiree
;   DEVELOPMENTAL STAGE: growing tuber
;   TISSUE TYPE: tuber
;   CELL TYPE: total tuber
;   IMMEDIATE SOURCE:
;   LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 2..1699
;   OTHER INFORMATION: /note= "for Branching enzyme I
;   OTHER INFORMATION: (partial) truncated protein; 97,11 % identity to
;   OTHER INFORMATION: active potato branching enzyme"
US-08-104-158-1

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  Query Match             19.7%;  Score 623.2;  DB 4;  Length 2909;
  Best Local Similarity   60.1%;  Pred. No. 1.4e-178;
  Matches 1188;  Conservative    1;  Mismatches  729;  Indels   58;  Gaps    7;

Qy        731 TAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGA 790

Db        165 TGGATCCAACTTTGGAACCTTATCTAGATCACTTCAGACACAGAATGAAGAGATATGTGG 224

Qy        791 AAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTITATG 850

Db        225 ATCAGAAAATGCTCATTGAAAAATATGAGGGACCCCTTGAGGAATTTGCTCAAGGTTATT 284

Qy        851 AAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTG 910

Db        285 TAAAATTTGGATTCAACAGGGAAGATGGTTGCATAGTCTATCGTGAATGGGCTCCTGCTG 344

Qy        911 CCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGA 970

Db        345 CTCAGGAAGCAGAAGTTATTGGCGATTTCAATGGTAGGAACGGTTCTAACCACATGATGG 404

Qy        971 CTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTG 1030

Db        405 AGAAGGACCAGTTTGGTGTTTGGAGTATTAGAATTCC---TGATGTTGACAGTAAGCCAG 461

Qy       1031 CAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAG---G 1087

Db        462 TCATTCCACACAACTCCAGAGTTAAGTTTCGTTTCAAACATGGTAATGGAGTGTGGGTAG 521

Qy       1088 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCC------TGATGAAATTCCAT 1141

Db        522 ATCGTATCCCTGCTTGGATAAAGTATGCCACTGCAGACGCCACAAAGTTTGCAGCACCAT 581

Qy       1142 ATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGC 1201

Db        582 ATGATGGTGTCTACTGGGACCCACCACCTTCAGAAAGGTACCACTTCAAATACCCTCGCC 641

Qy       1202 CAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGC 1261

Db        642 CTCCCAAACCCCGAGCCCCACGAATCTACGAAGCACATGTCGGCATGAGCAGCTCTGAGC 701

Qy       1262 CTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTG 1321

Db        702 CACGTGTAAATTCGTATCGTGAGTTTGCAGATGATGTTTACCTCGGATTAAGGCAAATA 761
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Qy       1322 GGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTT 1381
Db        762 ACTATAATACTGTCCAGTTGATGGCCATAATGGAACATTCTTACTATGGATCATTTGGAT 821

Qy       1382 ATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGT 1441
Db        822 ATCATGTTACAAACTTTTTTGCTGTGAGCAATAGATATGGAAACCCGGAGGACCTAAAGT 881

Qy       1442 CTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCC 1501
Db        882 ATCTGATAGATAAAGCACATAGCTTGGGTTTACAGGTTCTGGTGGATGTAGTTCACAGTC 941

Qy       1502 ATGCATCAAATAATACTTTAGATGGACTGAACATGTTTG---------ACGGCACAGATA 1552
Db        942 ATGCAAGCAATAATGTCACTGATGGCCTCAATGGCTTTGATATTGGCCAAGGTTCTCAAG 1001

Qy       1553 GTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTA 1612
Db       1002 AATCCTACTTTCATGCTGGAGAGCGAGGGTACCATAAGTTGTGGGATAGCAGGCTGTTCA 1061

Qy       1613 ACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATG 1672
Db       1062 ACTATGCCAATTGGGAGGTTCTTCGTTTCCTTCTTTCCAACTTGAGGTGGTGGCTAGAAG 1121

Qy       1673 AGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACG 1732
Db       1122 AGTATAACTTTGACGGATTTCGATTTGATGGAATAACTTCTATGCTGTATGTTCATCATG 1181

Qy       1733 GATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRG 1792
Db       1182 GAATCAATATGGGATTTACAGGAAACTATAATGAGTATTTCAGCGAGGCTACAGATGTTG 1241

Qy       1793 ATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAA 1852
Db       1242 ATGCTGTGGTCTATTTAATGTTGGCCAATAATCTGATTCACAAGATTTTCCCAGACGCAA 1301

Qy       1853 TTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGG 1912
Db       1302 CTGTTATTGCCGAAGATGTTTCTGGTATGCCGGGCCTTAGCCGGCCTGTTTCTGAGGGAG 1361

Qy       1913 GTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCA 1972
Db       1362 GAATTGGTTTTGATTACCGCCTGGCAATGGCAATCCCAGATAAGTGGATAGATTATTTAA 1421

Qy       1973 AGAAACGG---GATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAA 2029
Db       1422 AGAATAAGAATGATGAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGA 1481

Qy       2030 GATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATA 2089
Db       1482 GATATACAGAGAAGTGTATAGCATATGCGGAGAGCCATGATCAGTCTATTGTCGGTGACA 1541

Qy       2090 AAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGAC 2149
Db       1542 AGACCATTGCATTTCTCCTAATGAACAAAGAGATGTATTCTGGCATGTCTTGCTTGACAG 1601

Qy       2150 CGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGAT-TAGGCTTGTAACT 2208
Db       1602 ATGCTTCTCCTGTTGTTGATGCAGGAATTGCGCTTGACAAGATGATCCATTTTTTTCACA 1661

Qy       2209 ATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAG 2268
Db       1662 ATGGCCTTGGGAGGAGAGGGGTACCTCAATTTCATGGGTAACGAGTTTGGCCATCCTGAG 1721

Qy       2269 TGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAAC 2328
Db       1722 TGGATTGACTTCCCTAGTGAG--------------------------------GGCAAT 1748

Qy       2329 CAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGA 2388
Db       1749 AATTGGAGTTATGACAAATGTAGACGCCAGTGGAACCTCGCAGATAGCGAACACTTGAGA 1808

Qy       2389 TACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTT 2448
Db       1809 TACAAGTTTATGAATGCATTTGATAGAGCTATGAATTCGCTCGATGAAAAGTTCTCATTC 1868

Qy       2449 ATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTT 2508
Db       1869 CTCGCATCAGGAAAACAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTGTTT 1928

Qy       2509 GAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTAT 2568
Db       1929 GAACGTGGTGACCTGGTATTTGTATTCAACTTCCACCCAAATAACACATACGAAGGGTAT 1988

Qy       2569 CGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTT 2628
Db       1989 AAAGTTGGATGTGACTTGCCAGGGAAGTACAGAGTTGCACTGGACAGTGATGCTTGGGAA 2048

Qy       2629 TTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATG 2684
Db       2049 TTTGGTGGCCATGGAAGAGCTGGTCATGATGTTGACCATTTCACATCACCAGAAGG 2104

RESULT 15
US-09-257-894-25
; Sequence 25, Application US/09257894
; Patent No. 6376749
;  GENERAL INFORMATION:
;    APPLICANT:  Broglie, Karen E.
;    APPLICANT:  Klein, Theodore M.
;    APPLICANT:  Hubbard, Natalie L.
;    APPLICANT:  Lightner, Jonathan E.
;    TITLE OF INVENTION:  No. 6376749el Starches via Modification of
;    TITLE OF INVENTION:  Expression of Starch Biosynthesis
;    TITLE OF INVENTION:  Enzyme Genes
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Version 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/257,894
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/091,052
;      FILING DATE:  JUNE 10, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Majarian, William R.
;      REGISTRATION NUMBER:  41,173
;      REFERENCE/DOCKET NUMBER:  BB-1066-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4926
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-257-894-25

  Query Match             17.3%;  Score 546;  DB 4;  Length 1809;
  Best Local Similarity   61.2%;  Pred. No. 2.7e-155;
  Matches  955;  Conservative    2;  Mismatches  582;  Indels   21;  Gaps    4;

Qy        721 ATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCA 780
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Db     253 ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTCAGGTACCGGATGAAA 312

Qy     781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
Db     313 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 372

Qy     841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
Db     373 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 432

Qy     901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
Db     433 GCACCTGCTGCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAAC 492

Qy     961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
Db     493 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 549

Qy    1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
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Qy    1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 1136
Db     610 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 669

Qy    1137 --TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db     670 GCTCCCTATGATGGTGTTCATTGGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 729

Qy    1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db     730 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 789

Qy    1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
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Qy    1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
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Qy    1546 ACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGATTCCCGC 1605
Db    1090 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1149

Qy    1606 CTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGG 1665
Db    1150 CTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTTCTAACCTGAGATATTGG 1209

Qy    1666 TTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACT 1725
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Qy    1726 CACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACT 1785
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Qy    1846 GATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAA 1905
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Db    1570 AACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGTT 1629

Qy    2083 GGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTG 2142
Db    1630 GGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGAC 1689

Qy    2143 GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTT 2202
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Qy    2203 GTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCAC 2262
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Search completed: July 5, 2003, 20:15:12
Job time : 160.619 secs

14

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                 GenCore version 5.1.6
        Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          July  5, 2003, 13:51:57 ; Search time 486.292 Seconds
                                          (without alignments)
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Perfect score:   3156
Sequence:        1 AAAAACCTCCTCCACTCAGT..........TGCTGATCTAATGATGTTTT 3156

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters:      2171862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2955.2	93.6	3074	9	US-10-254-534-1	Sequence 1, Appli
	2	1372.2	43.5	1393	9	US-10-254-534-3	Sequence 3, Appli
	3	1323	41.9	2418	9	US-09-938-842A-872	Sequence 872, App
	4	1296	41.1	2577	9	US-09-938-842A-337	Sequence 337, App
	5	1185.6	37.6	3039	10	US-09-792-127-3	Sequence 3, Appli
	6	1185	37.5	2559	10	US-09-792-127-1	Sequence 1, Appli
	7	598.2	19.0	2994	9	US-10-084-817-92	Sequence 92, Appl
	8	596.6	18.9	2955	9	US-09-918-624B-30	Sequence 30, Appl
	9	596.6	18.9	2955	10	US-09-880-107-2148	Sequence 2148, Ap
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	11	139.6	4.4	604	10	US-09-925-300-453	Sequence 453, App
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c	15	108	3.4	601	10	US-09-833-263-304	Sequence 304, App
	16	88.2	2.8	1877	10	US-09-974-300-653	Sequence 653, App
	17	87.2	2.8	204	10	US-09-878-574-12567	Sequence 12567, A
	18	85.4	2.7	1830121	9	US-10-329-960-1	Sequence 1, Appli
	19	81.4	2.6	2193	9	US-09-738-626-1354	Sequence 1354, Ap
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	22	69.8	2.2	543	10	US-09-815-343-373	Sequence 373, App
	23	68.8	2.2	576	10	US-09-815-343-924	Sequence 924, App
	24	59	1.9	261	10	US-09-864-761-19524	Sequence 19524, A
c	25	59	1.9	261	10	US-09-864-761-25517	Sequence 25517, A
	26	59	1.9	448	10	US-09-864-761-557	Sequence 557, App
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	29	54.6	1.7	381	10	US-09-864-761-21610	Sequence 21610, A
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c	33	53.8	1.7	8895	9	US-10-091-438-256	Sequence 256, App
c	34	53.8	1.7	8895	10	US-09-764-853-887	Sequence 887, App
c	35	53.8	1.7	8895	10	US-09-764-853-937	Sequence 937, App
c	36	53.8	1.7	9656	9	US-10-091-438-246	Sequence 246, App
c	37	53.8	1.7	9656	9	US-10-091-438-255	Sequence 255, App
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	45	52.4	1.7	288	9	US-09-728-444-165	Sequence 165, App

ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/10/254,534
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: US/09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (189)..(2825)
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (189)..(332)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (333)..(2825)
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;    NAME/KEY: misc_feature
;    LOCATION: (92)..(2156)
;    OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
;    OTHER INFORMATION: n wherein n = A, C, G or T.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (285)..(287)
;    OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
;    OTHER INFORMATION: or Phe.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1404)..(1406)
;    OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1428)..(1430)
;    OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1896)..(1898)
;    OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
;    OTHER INFORMATION: or Phe.
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (2154)..(2156)
;    OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-10-254-534-1

  Query Match             93.6%;  Score 2955.2;  DB 9;  Length 3074;
  Best Local Similarity   98.1%;  Pred. No. 0;
  Matches 3019;  Conservative    2;  Mismatches   41;  Indels   14;  Gaps    3;

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Db        1739 ATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGA 1798

Qy        1794 TGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1853
               |||||  |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        1799 TGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAAT 1858

Qy        1854 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGG 1913
               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        1859 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGTTCAAGATGGGGG 1918

Qy        1914 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1973
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1919 TGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAA 1978

Qy        1974 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2033
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1979 GAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATG 2038

Qy        2034 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2093
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2039 GTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAAC 2098

Qy        2094 TATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTC 2153
               ||||||||||||||||||||| |||||||||||||||||||||||| |||||||||| ||
Db        2099 TATAGCATTCTGGCTGATGGAGAAGGATATGTATGATTTTATGGCTCTGGATAGACCNTC 2158

Qy        2154 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2159 AACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGG 2218

Qy        2214 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2219 ATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGAT 2278

Qy        2274 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2279 TGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATT 2338

Qy        2334 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2339 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2398

Qy        2394 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2399 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2458

Qy        2454 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2513
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2459 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2518

Qy        2514 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2573
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2519 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2578

Qy        2574 AGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2633
               |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2579 AGGCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2638

Qy        2634 TGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGA 2693
               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        2639 TGGCTTCGGGAGAATTGATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGA 2698

Qy        2694 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2699 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2758

Qy        2754 AGACA---AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2810
               |||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2759 AGACAAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGA 2818

Qy        2811 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        2819 AGAATGAACGAACTTGTGATCGCGTTGAAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878

Qy        2871 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2930
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2879 TATCTGGCAATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCT 2938

Qy        2931 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAA 2990
               ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        2939 TTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGCACAAACATATGTAA 2998

Qy        2991 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3050
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2999 AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3058

Qy        3051 TGTAAATTGTCATCTC 3066
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Db        3059 TGTAAATTGTCATCTC 3074
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RESULT 2
US-10-254-534-3
; Sequence 3, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
;  APPLICANT: EK, Bo
;  APPLICANT:  KHOSNOODI, Jamshid
;  APPLICANT:  LARSSON, Clas-Tomas
;  APPLICANT:  LARSSON, Hakan
;  APPLICANT:  RASK, Lars
;  TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
;  FILE REFERENCE: 003300-486
;  CURRENT APPLICATION NUMBER: US/10/254,534
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: US/09/087,277
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: PCT/SE96/01558
;  PRIOR FILING DATE: 1996-11-28
;  PRIOR APPLICATION NUMBER: SE 9504272-7
;  PRIOR FILING DATE: 1995-11-29
;  PRIOR APPLICATION NUMBER: SE 9601506-0
;  PRIOR FILING DATE: 1996-04-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1393
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
;   OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
;   OTHER INFORMATION: (potato)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1393)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(1150)
;   OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
;   OTHER INFORMATION: C, G or T.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (422)..(424)
;   OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(892)
;   OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
;   OTHER INFORMATION: or Phe.
;   FEATURE:
;   NAME/KEY: misc_feature
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;   LOCATION: (1148)..(1150)
;   OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-10-254-534-3

  Query Match             43.5%;  Score 1372.2;  DB 9;  Length 1393;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1377;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       1002 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 1061
Db          1 TCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

Qy       1062 CATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 1121
Db         61 TATGGACACTCCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACA 120

Qy       1122 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 1181
Db        121 GCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTA 180

Qy       1182 TGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 1241
Db        181 TATCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATAT 240

Qy       1242 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 1301
Db        241 TGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCT 300

Qy       1302 TCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 1361
Db        301 TCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTC 360

Qy       1362 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGG 1421
Db        361 TTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTNGCACCAAGCAGCCGTTTTGA 420

Qy       1422 AACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 1481
Db        421 AACNCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCT 480

Qy       1482 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 1541
Db        481 CATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGA 540

Qy       1542 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 1601
Db        541 CGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTC 600

Qy       1602 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 1661
Db        601 CCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATG 660

Qy       1662 GTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTA 1721
Db        661 GTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTA 720

Qy       1722 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 1781
Db        721 TACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGC 780

Qy       1782 AACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTT 1841
Db        781 AACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTT 840

Qy       1842 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGT 1901
Db        841 CCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTNTATTCCCGT 900

Qy       1902 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 1961
Db        901 TCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGAT 960

Qy       1962 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 2021
Db        961 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 1020

Qy       2022 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 2081
Db       1021 AAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT 1080

Qy       2082 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTT 2141
Db       1081 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTCT 1140

Qy       2142 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2201
Db       1141 GGATAGACCNTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 1200

Qy       2202 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2261
Db       1201 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 1260

Qy       2262 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 2321
Db       1261 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 1320

Qy       2322 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2381
Db       1321 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 1380

Qy       2382 TTTAAGATACCGT 2394
Db       1381 TTTAAGATACCGT 1393


RESULT 3
US-09-938-842A-872
; Sequence 872, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 872
;   LENGTH: 2418
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

  Query Match             41.9%;  Score 1323;  DB 9;  Length 2418;
  Best Local Similarity   76.9%;  Pred. No. 0;
  Matches 1604;  Conservative    2;  Mismatches  480;  Indels    0;  Gaps    0;

Qy        677 GGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACC 736
Db        329 GGGTGAAACCAAGAATAGTTCCCCCACCGGGTGATGGCAAGAAAATTTATGAGATAGACC 388

Qy        737 CCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGA 796
Db        389 CCATGTTACGAACTTACAACAATCATCTTGATTACCGTTATGGACAGTATAAAAGATTGC 448

Qy        797 GGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAA 856
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Db    449 GTGAGGAAATAGACAAGTATGAGGGTGGTCTTGAGGCATTCTCTCGTGGCTATGAAAAGT 508

Qy    857 TGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGT 916
Db    509 TAGGATTTTCGCGCAGTGATGCCGGTATAACTTATAGAGAGTGGGCGCCTGGAGCTAAGG 568

Qy    917 CAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGA 976
Db    569 CTGCATCACTTATCGGAGATTTCAACAACTGGAATTCTAATGCAGATATCATGACTCGGA 628

Qy    977 ATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTC 1036
Db    629 ATGAATTTGGTGTTTGGGAGATCTTTTTGCCCAACAACACTGATGGTTCGCCTGCAATTC 688

Qy   1037 CTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTC 1096
Db    689 CTCATGGCTCACGTGTAAAGATTCGTATGGATACTCCATCTGGCATTAAAGACTCAATTC 748

Qy   1097 CTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATT 1156
Db    749 CTGCTTGGATCAAGTTCTCGGTGCAAGCTCCAGGTGAAATCCCATTCAATGGCATATACT 808

Qy   1157 ATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGT 1216
Db    809 ATGATCCTCCAGAAGAGGAGAAGTATGTATTCAAACATCCTCAACCAAAGAGACCTAAGT 868

Qy   1217 CGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCAT 1276
Db    869 CGCTAAGGATTTATGAAGCACATGTTGGCATGAGTAGCACGGAACCAATGGTCAATACGT 928

Qy   1277 ACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGC 1336
Db    929 ATGCTAACTTTAGAGATGATGTTCTTCCCCGCATCAAAAAGCTTGGATATAATGCTGTTC 988

Qy   1337 AAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATT 1396
Db    989 AAATTATGGCCATACAAGAACATTCATATTATGCCAGCTTTGGGTACCATGTCACAAACT 1048

Qy   1397 TTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAG 1456
Db   1049 TTTTTGCCCCAAGCAGTCGCTGTGGGACCCCAGAGGAACTAAAATCACTGATAGATAGAG 1108

Qy   1457 CTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATA 1516
Db   1109 CTCACGAGTTAGGCCTGGTAGTTCTGATGGATATCGTTCATAGCCATGCTTCAAAAAACA 1168

Qy   1517 CTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTC 1576
Db   1169 CATTGGATGGACTGAACATGTTTGATGGAACTGATGCTCACTATTTTCACTCTGGACCTC 1228

Qy   1577 GTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTA 1636
Db   1229 GGGGATACCATTGGATGTGGGATTCACGACTTTTCAATTATGGGAGCTGGGAAGTATTAC 1288

Qy   1637 GGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGAT 1696
Db   1289 GATATCTCCTTTCAAATGCACGGTGGTGGCTAGAAGAATACAAGTTTGATGGATTTAGAT 1348

Qy   1697 TTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGA 1756
Db   1349 TTGATGGTGTAACCTCAATGATGTATACTCATCATGGACTCTCGGTTGGATTTACTGGGA 1408

Qy   1757 ACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGG 1816
Db   1409 ACTACACCGAATACTTTGGATTGGAAACTGATGTGGATGCTGTGAATTATCTCATGCTGG 1468

Qy   1817 CCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCG 1876
Db   1469 TTAATGATATGATTCATGGGCTCTACCCTGAAGCGATTACCGTTGGTGAAGATGTTAGTG 1528

Qy   1877 GAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGC 1936
Db   1529 GTATGCCAACATTCTGTATTCCTGTCCAAGATGGTGGCGTTGGATTTGACTACCGTTTAC 1588

Qy   1937 ATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAG 1996
Db   1589 ACATGGCCATAGCTGATAAGTGGATAGAAATGCTCAAGAAGAGAGATGAAGACTGGCAAA 1648

Qy   1997 TGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACG 2056
Db   1649 TGGGCGACATCATTTACACACTTACCAACAGAAGGTGGTCAGAGAAGTGTATCTCTTATG 1708

Qy   2057 CTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACA 2116
Db   1709 CTGAAAGTCACGATCAAGCTCTTGTTGGTGATAAAACAATTGCCTTCTGGTTAATGGACA 1768

Qy   2117 AGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGA 2176
Db   1769 AGGATATGTATGATTTCATGGCAGTAGACAGACCATCAACTCCTCTTATCGATAGAGGAA 1828

Qy   2177 TAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAA 2236
Db   1829 TAGCTTTGCACAAAATGATTAGGCTTATAACTATGGGATTAGGCGGTGAAGGTTACTTAA 1888

Qy   2237 ATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAAC 2296
Db   1889 ATTTTATGGGAAACGAATTCGGACATCCAGAATGGATTGATTTTCCCAGAGGCGAGCAGC 1948

Qy   2297 ACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGA 2356
Db   1949 GTCTTTCTGATGGTAGCGTGATTCCTGGCAACAATTTCAGTTATGACAAATGCCGCCGCA 2008

Qy   2357 GATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGG 2416
Db   2009 GATTTGATCTTGGGGATGCAGATTATCTCAGATACCGCGGACTACAAGAATTTGATCAGG 2068

Qy   2417 CTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCAC 2476
Db   2069 CAATGCAACATCTTGAAGAGAATTACGGTTTTATGACTTCGGAGCACCAATTCATATCAC 2128

Qy   2477 GAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTA 2536
Db   2129 GAAAAGACGAAGCAGATAGAGTAATCGTATTCGAAAGAGGTGATCTCGTCTTTGTCTTTA 2188

Qy   2537 ATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAAT 2596
Db   2189 ACTTTCACTGGACCAGCAGCTACTTTGATTACCGCATTGGTTGCTCCAAGCCTGGAAAAT 2248

Qy   2597 ACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATA 2656
Db   2249 ATAAGATCGTATTGGACTCGGACGATCCTCTCTTTGGTGGATTCAATAGGCTCGATCGCA 2308

Qy   2657 ATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGT 2716
Db   2309 AGGCAGAGTACTTCACTTATGATGGCTTATACGACGAACGACCCTGCTCCTTCATGGTCT 2368

Qy   2717 ATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGA 2762
Db   2369 ATGCACCGTGTAGAACCGCCGTGGTTTATGCTTTAGCAAACCACGA 2414
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RESULT 4
US-09-938-842A-337
; Sequence 337, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866

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;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
;   LENGTH: 2577
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

  Query Match            41.1%;  Score 1296;  DB 9;  Length 2577;
  Best Local Similarity  76.2%;  Pred. No. 0;
  Matches 1593;  Conservative    1;  Mismatches  496;  Indels    0;  Gaps    0;

Qy     686 AGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGA 745
Db     443 AGAGGAAGATTCCACCTCCTGGAGATGGGAAGAGAATATATGACATTGATCCTATGTTGA 502

Qy     746 CAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAA 805
Db     503 ACAGTCATCGTAATCATCTTGATTACCGATATGGGCAGTACAGAAAACTGCGTGAAGAAA 562

Qy     806 TTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCA 865
Db     563 TTGACAAGAATGAAGGTGGTTTGGAGGCATTTTCTCGTGGTTATGAAATATTTGGCTTCA 622

Qy     866 CTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTC 925
Db     623 CTCGAAGCGCCACTGGTATCACTTACCGGGAATGGGCACCGGGAGCTAAGGCAGCATCAC 682

Qy     926 TCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTG 985
Db     683 TGATCGGAGATTTTAATAACTGGAATGCGAAATCTGATGTTATGGCTCGGAACGACTTTG 742

Qy     986 GTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGT 1045
Db     743 GTGTGTGGGAAATATTTCTGCCAAATAATGCTGATGGCTCACCAGCAATTCCCCATGGCT 802

Qy    1046 CCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGA 1105
Db     803 CCCGTGTGAAGATCCGCATGGATACCCCATCTGGTATTAAAGACTCCATTCCAGCTTGGA 862

Qy    1106 TCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCAC 1165
Db     863 TCAAGTATTCTGTCCAGCCACCTGGCGAGATCCCATATAATGGAGTATATTATGACCCTC 922

Qy    1166 CCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAA 1225
Db     923 CTGAGGAGGATAAATATGCGTTCAAACATCCTCGTCCAAAGAAACCCACATCGCTGCGTA 982

Qy    1226 TATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATT 1285
Db     983 TATATGAATCACATGTTGGAATGAGTAGTACGGAACCAAAGATAAATACATATGCCAACT 1042

Qy    1286 TTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGG 1345
Db    1043 TTAGAGATGATGTACTTCCCCGTATAAAAAAGCTAGGCTATAATGCTGTGCAGATAATGG 1102

Qy    1346 CTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCAC 1405
Db    1103 CCATTCAAGAGCATGCCTACTATGCCAGCTTTGGGTATCATGTGACAAATTTTTTCGCAC 1162

Qy    1406 CAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGC 1465
Db    1163 CTAGCAGCCGCTTTGGAACACCTGATGACCTTAAATCTTTGATAGACAAAGCTCATGAGC 1222

Qy    1466 TAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATG 1525
Db    1223 TAGGTCTGGTTGTTCTGATGGATATTGTGCACAGCCATGCATCAAAAAACACACTGGATG 1282

Qy    1526 GACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATC 1585
Db    1283 GCCTGGACATGTTTGATGGTACTGATGGTCAATATTTCCACTCTGGATCGCGTGGTTATC 1342

Qy    1586 ATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTC 1645
Db    1343 ATTGGATGTGGGATTCTCGTCTTTTCAATTACGGAAGCTGGGAAGTGCTTAGGTATCTTC 1402

Qy    1646 TCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTG 1705
Db    1403 TTTCCAACGCGAGATGGTGGCTGGAAGAATACAAGTTTGATGGGTTCAGATTTGATGGTG 1462

Qy    1706 TGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGG 1765
Db    1463 TGACTTCCATGATGTACACTCATCATGGACTGCAGGTCGAATTTACTGGGAATTACAATG 1522

Qy    1766 AATACTTTGGACTCGCAACTGATGTGRTGATGCTGCCGTGTATCTGATGCTGGCCAACGATC 1825
Db    1523 AGTACTTTGGATATTCTACTGATGTTGACGCTGTGGTCTATCTAATGCTGGTGAACGATT 1582

Qy    1826 TTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGA 1885
Db    1583 TGATTCATGGGCTATACCCTGAGGCTATTGTTGTCGGCGAAGATGTTAGCGGGATGCCAG 1642

Qy    1886 CATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAA 1945
Db    1643 CTTTTTGCGTTCCTGTCGAAGACGGTGGTGTGGGTTTTGACTACCGTCTACACATGGCAG 1702

Qy    1946 TTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATA 2005
Db    1703 TGGCAGATAAATGGATTGAGCTTCTTAAGAAGAGAGACGAGGACTGGCAGGTTGGTGATA 1762

Qy    2006 TTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTC 2065
Db    1763 TAACTTTCACGCTTACCAACAGGAGGTGGGGAGAAAAATGTGTCGTCTATGCAGAGAGTC 1822

Qy    2066 ATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGT 2125
Db    1823 ATGATCAAGCCCTTGTTGGAGACAAAACGATAGCTTTCTGGCTAATGGATAAGGACATGT 1882

Qy    2126 ATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGC 2185
Db    1883 ATGATTTCATGGCCGTTGATAGACAGGCCACTCCGCGTGTAGACCGTGGGATTGCTTTAC 1942

Qy    2186 ACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGG 2245
Db    1943 ACAAAATGATCCGTCTCATTACGATGGGATTGGGTGGAGAAGGATACCTCAATTTCATGG 2002

Qy    2246 GAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTG 2305
Db    2003 GAAACGAATTTGGACACCCAGAATGGATCGACTTCCCAAGGACCGACCAGCACCTTCCTG 2062

Qy    2306 ATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACC 2365
Db    2063 ATGGCAGAGTCATCGCTGGGAATAATGGTAGTTATGATAAATGCCGACGTAGGTTTGATC 2122

Qy    2366 TGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGT 2425
Db    2123 TGGGAGATGCAGAATATCTTAGATACCATGGACTACAAGAGTTTGATCGAGCAATGCAAA 2182

Qy    2426 ATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATG 2485
Db    2183 ATCTAGAGGAGACGTATGGTTTCATGACTTCAGAGCACCAGTACATATCCCGCAAGGATG 2242

Qy    2486 AAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACT 2545
Db    2243 AAGGAGACAGAGTCATTGTATTCGAGAGAGGTAACTTGCTCTTCGTCTTCAACTTCCACT 2302

Qy    2546 GGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTG 2605
Db    2303 GGACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAAGTACAAAATCG 2362

Qy    2606 CCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAAT 2665
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Db       2363 TTTTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGACTCCGCGGAGT 2422

Qy       2666 GTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTA 2725
Db       2423 TTTTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGTGTATGCACCGT 2482

Qy       2726 GTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAA 2775
Db       2483 GCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGAA 2532

RESULT 5
US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
;  APPLICANT:  Allen, Steve
;  APPLICANT:  Beckles, Diane M.
;  APPLICANT:  Butler, Karla
;  APPLICANT:  Pearlstein, Rich
;  TITLE OF INVENTION:  Starch Branching Enzyme IIb
;  FILE REFERENCE:  BB1439 US NA
;  CURRENT APPLICATION NUMBER: US/09/792,127
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER:  60/186098
;  PRIOR FILING DATE:  2000-03-01
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  Microsoft Office 97
; SEQ ID NO 3
;   LENGTH: 3039
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-792-127-3

  Query Match             37.6%;  Score 1185.6;  DB 10;  Length 3039;
  Best Local Similarity   71.9%;  Pred. No. 0;
  Matches 1545;  Conservative    2;  Mismatches  601;  Indels    0;  Gaps    0;

Qy        664 GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT 723
Db        474 GAATCATCTACGAGGGAGAAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATA 533

Qy        724 TATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG 783
Db        534 TACGAGATTGACCCAACGCTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA 593

Qy        784 TACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGT 843
Db        594 TACAGGAGAATACGTTCAGACATTGATGAACACGAAGGAGGCATGGATGTATTTTCCCGC 653

Qy        844 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 903
Db        654 GGTTACGAGAAGTTTGGATTTATGCGCAGCGCTGAAGGTATCACTTACCGAGAATGGGCT 713

Qy        904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db        714 CCTGGAGCAGATTCTGCAGCATTAGTTGGCGACTTCAACAATTGGGATCCAAATGCAGAC 773

Qy        964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
Db        774 CATATGAGCAAAAATGACCTTGGTGTTTGGGAGATTTTTCTGCCAAACAATGCAGATGGT 833

Qy       1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTT 1083
Db        834 TCGCCACCAATTCCTCACGGCTCACGGGTGAAGGTGAGAATGGATACTCCATCTGGGATA 893

Qy       1084 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1143
Db        894 AAGGATTCAATTCCTGCTTGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATAC 953

Qy       1144 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCA 1203
Db        954 AATGGAATATATTATGATCCTCCCGAAGAGGAGAAGTATGTATTCAAGCATCCTCAACCT 1013

Qy       1204 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1263
Db       1014 AAACGACCAAAATCATTGCGGATATATGAAACACATGTTGGCATGAGTAGCCCGGAACCA 1073

Qy       1264 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGG 1323
Db       1074 AAGATCAACACATATGCAAACTTCAGGGATGAGGTGCTTCCAAGAATTAAAAGACTTGGA 1133

Qy       1324 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1383
Db       1134 TACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATACTATGGAAGCTTTGGGTAC 1193

Qy       1384 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1443
Db       1194 CATGTTACCAATTTCTTTGCACCAAGTAGCCGTTTTGGGTCCCCAGAAGATTTAAAATCT 1253

Qy       1444 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1503
Db       1254 TTGATTGATAGAGCTCACGAGCTTGGCTTGGTTGTCCTCATGGATGTTGTTCACAGTCAC 1313

Qy       1504 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1563
Db       1314 GCGTCAAATAATACCTTGGACGGGTTGAATGGTTTTGATGGCACGGATACACATTACTTC 1373

Qy       1564 CACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAAC 1623
Db       1374 CATGGCGGTTCACGGGGCCATCACTGGATGTGGGATTCCCGTGTGTTTAACTATGGGAAT 1433

Qy       1624 TGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAATTT 1683
Db       1434 AAGGAAGTTATAAGGTTTCTACTTTCCAATGCAAGATGGTGGCTAGAGGAGTATAAGTTT 1493

Qy       1684 GRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCGGTG 1743
Db       1494 GATGGTTTCCGATTCGATGGCGCGACCTCCATGATGTATACCCATCATGGATTACAAGTA 1553

Qy       1744 GGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCCGTG 1803
Db       1554 ACCTTTACAGGAAGCTACCATGAATATTTTGGCTTTGCCACTGATGTAGATGCGGTCGTT 1613

Qy       1804 TATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGT 1863
Db       1614 TACTTGATGCTGATGAATGATCTAATTCATGGGTTTTATCCTGAAGCCGTAACTATCGGT 1673

Qy       1864 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTT 1923
Db       1674 GAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGGTTGGTTTT 1733

Qy       1924 GACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGAT 1983
Db       1734 GACTATCGCTTACATATGGCTGTTGCCGACAAATGGATTGAACTTCTCAAAGGAAACGAT 1793

Qy       1984 GAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAG 2043
Db       1794 GAAGCTTGGGAGATGGGTAATATTGTGCACACACTAACAAACAGAAGGTGGCTGGAAAAG 1853

Qy       2044 TGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTC 2103
Db       1854 TGTGTTACTTATGCTGAAAGTCACGATCAAGCACTTGTTGGAGACAAGACTATTGCATTC 1913

Qy       2104 TGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTA 2163
Db       1914 TGGTTGATGGACAAGGATATGTATGATTTCATGGCGCTGAACGGACCTTCGACGCCTAAT 1973

Qy       2164 ATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGA 2223
Db       1974 ATTGATCGTGGAATAGCACTGCATAAAATGATTAGACTTATCACAATGGGTCTAGGAGGA 2033

Qy       2224 GAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCT 2283
Db       2034 GAGGGTTATCTTAACTTTATGGGAAATGAGTTCGGGCATCCTGAATGGATAGACTTTCCA 2093
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Qy       2284 AGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGAT 2343
Db       2094 AGAGGCCCACAAGTACTTCCAAGTGGTAAGTTCATCCCAGGAAACAACAACAGTTACGAC 2153

Qy       2344 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAA 2403
Db       2154 AAATGCCGTCGAAGATTTGACCTGGGTGATGCAGAATTTCTTAGGTATCATGGTATGCAG 2213

Qy       2404 GAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACAC 2463
Db       2214 CAGTTTGATCAGGCAATGCAGCATCTTGAGGAAAAATATGGTTTTATGACATCAGACCAC 2273

Qy       2464 CAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTA 2523
Db       2274 CAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTGTTTGAAAAAGGGGACTTG 2333

Qy       2524 GTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTG 2583
Db       2334 GTATTTGTGTTCAACTTCCACTGGAGTAGTAGCTATTTCGACTACCGGGTCGGCTGTTTA 2393

Qy       2584 AAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGG 2643
Db       2394 AAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGACTCTTTGGTGGATTTGGT 2453

Qy       2644 AGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGT 2703
Db       2454 AGGATCCATCACACTGCAGAGCACGTCACTTCTGACTGCCAACATGACAACAGGCCCCAT 2513

Qy       2704 TCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAA 2763
Db       2514 TCATTCTCAGTGTACACTCCTAGCAGAACCTGTGTTGTCTATGCTCCAATGAACTAACAG 2573

Qy       2764 GAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAA 2811
Db       2574 CAAAGTGCAGCATACGCGTCGCGCTGTTGTTGCTAGTAGCAAGAAAA 2621
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RESULT 6
US-09-792-127-1
; Sequence 1, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIb
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
;   LENGTH: 2559
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-792-127-1

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  Query Match             37.5%;  Score 1185;  DB 10;  Length 2559;
  Best Local Similarity   72.4%;  Pred. No. 0;
  Matches 1533;  Conservative    2;  Mismatches  582;  Indels    0;  Gaps    0;

Qy        695 TCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATC 754
Db         25 TGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACGCTCCGAGACTTTA 84

Qy        755 GTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGT 814
Db         85 AGTACCATCTTGAGTATCGATATAGCCTATACAGGAGAATACGTTCAGACATTGATGAAC 144

Qy        815 ATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTG 874
Db        145 ACGAAGGAGGCATGGATGTATTTTCCCGCGGTTACGAGAAGTTTGGATTTATGCGCAGCG 204

Qy        875 CTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAG 934
Db        205 CTGAAGGTATCACTTACCGAGAATGGGCTCCTGGAGCAGATTCTGCAGCATTAGTTGGCG 264

Qy        935 ATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGG 994
Db        265 ACTTCAACAATTGGGATCCAAATGCAGACCATATGAGCAAAAATGACCTTGGTGTTTGGG 324

Qy        995 AGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGA 1054
Db        325 AGATTTTTCTGCCAAACAATGCAGATGGTTCGCCACCAATTCCTCACGGCTCACGGGTGA 384

Qy       1055 AGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACT 1114
Db        385 AGGTGAGAATGGATACTCCATCTGGGATAAAGGATTCAATTCCTGCTTGGATCAAGTACT 444

Qy       1115 CTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGG 1174
Db        445 CCGTGCAGACTCCAGGAGATATACCATACAATGGAATATATTATGATCCTCCCGAAGAGG 504

Qy       1175 AGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAAT 1234
Db        505 AGAAGTATGTATTCAAGCATCCTCAACCTAAACGACCAAAATCATTGCGGATATATGAAA 564

Qy       1235 CTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATG 1294
Db        565 CACATGTTGGCATGAGTAGCCCGGAACCAAAGATCAACACATATGCAAACTTCAGGGATG 624

Qy       1295 AAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAG 1354
Db        625 AGGTGCTTCCAAGAATTAAAAGACTTGGATACAATGCAGTGCAAATAATGGCAATCCAAG 684

Qy       1355 AGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCC 1414
Db        685 AGCACTCATACTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTTGCACCAAGTAGCC 744

Qy       1415 GTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTG 1474
Db        745 GTTTTGGGTCCCCAGAAGATTTAAAATCTTTGATTGATAGAGCTCACGAGCTTGGCTTGG 804

Qy       1475 TTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACA 1534
Db        805 TTGTCCTCATGGATGTTGTTCACAGTCACGCGTCAAATAATACCTTGGACGGGTTGAATG 864

Qy       1535 TGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGT 1594
Db        865 GTTTTGATGGCACGGATACACATTACTTCCATGGCGGTTCACGGGGCCATCACTGGATGT 924

Qy       1595 GGGATTCCCGCCTCTTTAACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATG 1654
Db        925 GGGATTCCCGTGTGTTTAACTATGGGAATAAGGAAGTTATAAGGTTTCTACTTTCCAATG 984

Qy       1655 CGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAA 1714
Db        985 CAAGATGGTGGCTAGAGGAGTATAAGTTTGATGGTTTCCGATTCGATGGCGCGACCTCCA 1044

Qy       1715 TGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTG 1774
Db       1045 TGATGTATACCCATCATGGATTACAAGTAACCTTTACAGGAAGCTACCATGAATATTTTG 1104

Qy       1775 GACTCGCAACTGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATG 1834
Db       1105 GCTTTGCCACTGATGTAGATGCGGTCGTTTACTTGATGCTGATGAATGATCTAATTCATG 1164

Qy       1835 GGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTA 1894
Db       1165 GGTTTTATCCTGAAGCCGTAACTATCGGTGAAGATGTTAGTGGAATGCCTACATTTGCCC 1224

Qy       1895 TTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATA 1954
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Db   1225 TTCCTGTTCAAGTTGGTGGGGTTGGTTTTGACTATCGCTTACATATGGCTGTTGCCGACA 1284

Qy   1955 AATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATA 2014
Db   1285 AATGGATTGAACTTCTCAAAGGAAACGATGAAGCTTGGGAGATGGGTAATATTGTGCACA 1344

Qy   2015 CACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAG 2074
Db   1345 CACTAACAAACAGAAGGTGGCTGGAAAAGTGTGTTACTTATGCTGAAAGTCACGATCAAG 1404

Qy   2075 CTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTA 2134
Db   1405 CACTTGTTGGAGACAAGACTATTGCATTCTGGTTGATGGACAAGGATATGTATGATTTCA 1464

Qy   2135 TGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGA 2194
Db   1465 TGGCGCTGAACGGACCTTCGACGCCTAATATTGATCGTGGAATAGCACTGCATAAAATGA 1524

Qy   2195 TTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAAT 2254
Db   1525 TTAGACTTATCACAATGGGTCTAGGAGGAGAGGGTTATCTTAACTTTATGGGAAATGAGT 1584

Qy   2255 TCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAG 2314
Db   1585 TCGGGCATCCTGAATGGATAGACTTTCCAAGAGGCCCACAAGTACTTCCAAGTGGTAAGT 1644

Qy   2315 TAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATG 2374
Db   1645 TCATCCCAGGAAACAACAACAGTTACGACAAATGCCGTCGAAGATTTGACCTGGGTGATG 1704

Qy   2375 CAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAG 2434
Db   1705 CAGAATTTCTTAGGTATCATGGTATGCAGCAGTTTGATCAGGCAATGCAGCATCTTGAGG 1764

Qy   2435 ATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATA 2494
Db   1765 AAAAATATGGTTTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATA 1824

Qy   2495 GGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAA 2554
Db   1825 AGGTGATCGTGTTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAGTA 1884

Qy   2555 GCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACT 2614
Db   1885 GCTATTTCGACTACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACT 1944

Qy   2615 CAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCT 2674
Db   1945 CGGACGCTGGACTCTTTGGTGGATTTGGTAGGATCCATCACACTGCAGAGCACGTCACTT 2004

Qy   2675 TTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAG 2734
Db   2005 CTGACTGCCAACATGACAACAGGCCCCATTCATTCTCAGTGTACACTCCTAGCAGAACCT 2064

Qy   2735 CAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAG 2794
Db   2065 GTGTTGTCTATGCTCCAATGAACTAACAGCAAAGTGCAGCATACGCGTGCGCGCTGTTGT 2124

Qy   2795 AAGTAGTAGTAGAAGAA 2811
Db   2125 TGCTAGTAGCAAGAAAA 2141
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RESULT 7
US-10-084-817-92
; Sequence 92, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 92
; LENGTH: 2994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CB1
US-10-084-817-92

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Query Match              19.0%;  Score 598.2;  DB 9;  Length 2994;
Best Local Similarity    58.0%;  Pred. No. 2.5e-158;
Matches 1175;  Conservative    2;  Mismatches  800;  Indels   48;  Gaps    5;

Qy    727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db    215 GAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 274

Qy    787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846
Db    275 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 334

Qy    847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 903
Db    335 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAATGGGCC 394

Qy    904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db    395 CCGGGAGCAGAAGGAGTTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 454

Qy    964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
Db    455 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 514

Qy   1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTG-- 1081
Db    515 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 574

Qy   1082 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
Db    575 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 634

Qy   1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
Db    635 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGA 688

Qy   1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
Db    689 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 748

Qy   1261 CCTAAAATTAACTCATACGTGAATTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1320
Db    749 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTT 808

Qy   1321 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1380
Db    809 GGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGT 868

Qy   1381 TATCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAG 1440
Db    869 TACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAA 928

Qy   1441 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1500
Db    929 GAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGC 988

Qy   1501 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1560
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Db        989 CATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTAT 1048

Qy       1561 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1620
Db       1049 TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC 1108

Qy       1621 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1680
Db       1109 AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC 1168

Qy       1681 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1740
Db       1169 TTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGT 1228

Qy       1741 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1800
Db       1229 CAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTG 1288

Qy       1801 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1860
Db       1289 ACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATA 1348

Qy       1861 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGC 1920
Db       1349 GCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGT 1408

Qy       1921 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCA---AGAAA 1977
Db       1409 TTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1468

Qy       1978 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 2037
Db       1469 AAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTT 1528

Qy       2038 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 2097
Db       1529 GAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTG 1588

Qy       2098 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACA 2157
Db       1589 GCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACT 1648

Qy       2158 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2217
Db       1649 CCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTT 1708

Qy       2218 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2277
Db       1709 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGGCATCCTGAATGGTTAGAC 1768

Qy       2278 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGT 2337
Db       1769 TTCCCAAGAAAA--------------------------------GGAAATAATGAGAGT 1795

Qy       2338 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2397
Db       1796 TACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1855

Qy       2398 TTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2457
Db       1856 CTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCT 1915

Qy       2458 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2517
Db       1916 CCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCA 1975

Qy       2518 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGC 2577
Db       1976 GGTCTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGA 2035

Qy       2578 TGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2637

Db       2036 ACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGG 2095

Qy       2638 TTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGT 2697
Db       2096 CATCAGAGACTGGACCACAGCACTGACTTTTTTTCTGAGGCTTTTGAACATAATGGGCGT 2155

Qy       2698 CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2742
Db       2156 CCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATC 2200
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RESULT 8
US-09-918-624B-30
; Sequence 30, Application US/09918624B
; Publication No. US20030113720A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
; FILE REFERENCE: PA-0033 US
; CURRENT APPLICATION NUMBER: US/09/918,624B
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/222,470
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PERL Program
; SEQ ID NO 30
;   LENGTH: 2955
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
US-09-918-624B-30

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  Query Match             18.9%;  Score 596.6;  DB 9;  Length 2955;
  Best Local Similarity   58.0%;  Pred. No. 7e-158;
  Matches 1174;  Conservative    2;  Mismatches  801;  Indels   48;  Gaps    5;

Qy        727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db        187 GAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 246

Qy        787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846
Db        247 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 306

Qy        847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGCCT 903
Db        307 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTCCAAAGAATGGGCC 366

Qy        904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db        367 CCGGGAGCAGAAGGAGTTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 426

Qy        964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
Db        427 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 486

Qy       1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTG-- 1081
Db        487 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 546

Qy       1082 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
Db        547 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 606

Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
Db        607 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGA 660

Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
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Db     661 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720

Qy    1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1320
Db     721 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTT 780

Qy    1321 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1380
Db     781 GGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGT 840

Qy    1381 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTGGAACGCCCGACGACCTTAAG 1440
Db     841 TACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAA 900

Qy    1441 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1500
Db     901 GAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGC 960

Qy    1501 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1560
Db     961 CATGCTTCAAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTAT 1020

Qy    1561 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1620
Db    1021 TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC 1080

Qy    1621 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1680
Db    1081 AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC 1140

Qy    1681 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1740
Db    1141 TTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGT 1200

Qy    1741 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1800
Db    1201 CAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTG 1260

Qy    1801 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1860
Db    1261 ACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATA 1320

Qy    1861 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGC 1920
Db    1321 GCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGT 1380

Qy    1921 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCA---AGAAA 1977
Db    1381 TTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1440

Qy    1978 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 2037
Db    1441 AAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTT 1500

Qy    2038 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 2097
Db    1501 GAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTG 1560

Qy    2098 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACA 2157
Db    1561 GCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACT 1620

Qy    2158 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2217
Db    1621 CCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGGCTT 1680

Qy    2218 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2277
Db    1681 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGCATCCTGAATGGTTAGAC 1740

Qy    2278 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGT 2337
Db    1741 TTCCCAAGAAAA--------------------------------GGAAATAATGAGAGT 1767

Qy    2338 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2397
Db    1768 TACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1827

Qy    2398 TTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2457
Db    1828 CTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCT 1887

Qy    2458 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2517
Db    1888 CCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCA 1947

Qy    2518 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGC 2577
Db    1948 GGTCTTCTTTTCATTTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGA 2007

Qy    2578 TGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2637
Db    2008 ACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGG 2067

Qy    2638 TTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGT 2697
Db    2068 CATCAGAGACTGGACCACAGCACTGACTTTTTTTCTGAGGCTTTTGAACATAATGGGCGT 2127

Qy    2698 CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2742
Db    2128 CCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATC 2172
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RESULT 9
US-09-880-107-2148
; Sequence 2148, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2148
;   LENGTH: 2955
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

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  Query Match             18.9%;  Score 596.6;  DB 10;  Length 2955;
  Best Local Similarity   58.0%;  Pred. No. 7e-158;
  Matches 1174;  Conservative    2;  Mismatches  801;  Indels   48;  Gaps    5;

Qy     727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db     187 GAGATCGACCCGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 246

Qy     787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846
Db     247 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 306

Qy     847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 903
Db     307 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTCCAAAGAATGGGCC 366
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Qy    904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db    367 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 426
Qy    964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGGATGGT 1023
Db    427 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 486
Qy   1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTG-- 1081
Db    487 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 546
Qy   1082 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
Db    547 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 606
Qy   1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
Db    607 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCAGA 660
Qy   1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
Db    661 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720
Qy   1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1320
Db    721 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAAGGCCTT 780
Qy   1321 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1380
Db    781 GGATACAACTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGT 840
Qy   1381 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1440
Db    841 TACCAAATCACAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAA 900
Qy   1441 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1500
Db    901 GAACTGGTAGACACAGCTCATTCCATGGGTATCATAGTCCTCTTAGATGTGGTACACAGC 960
Qy   1501 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1560
Db    961 CATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATGGGACAGATTCCTGTTAT 1020
Qy   1561 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1620
Db   1021 TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC 1080
Qy   1621 AACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAAA 1680
Db   1081 AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC 1140
Qy   1681 TTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATCG 1740
Db   1141 TTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATGGAGTGGGT 1200
Qy   1741 GTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGCC 1800
Db   1201 CAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAGATGCCTTG 1260
Qy   1801 GTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATT 1860
Db   1261 ACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTATAACAATA 1320
Qy   1861 GGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGC 1920
Db   1321 GCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAGGGGGTGGT 1380
Qy   1921 TTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCA---AGAAA 1977
Db   1381 TTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1440
Qy   1978 CGGGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCG 2037
Db   1441 AAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGCGCTACCTT 1500
Qy   2038 GAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 2097
Db   1501 GAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCATTGGTTGGGGATAAGTCGCTG 1560
Qy   2098 GCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACA 2157
Db   1561 GCATTTTGGTTGATGGATGCCGAAATGTATACAAACATGAGTGTCCTGACTCCTTTTACT 1620
Qy   2158 TCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTA 2217
Db   1621 CCAGTTATTGATCGTGGAATACAGCTTCATAAAATGATTCGACTCATTACGCATGGCTT 1680
Qy   2218 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2277
Db   1681 GGTGGAGAAGGCTATCTCAATTTCATGGGTAATGAATTTGGCATCCTGAATGGTTAGAC 1740
Qy   2278 TTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGT 2337
Db   1741 TTCCCAAGAAAA----------------------------------GGAAATAATGAGAGT 1767
Qy   2338 TATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGG 2397
Db   1768 TACCATTATGCCAGGCGGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1827
Qy   2398 TTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCA 2457
Db   1828 CTAAATAATTTTGACAGGGATATGAATAGATTGGAAGAAAGATATGGTTGGCTTGCAGCT 1887
Qy   2458 GAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAGGA 2517
Db   1888 CCACAGGCCTACGTGAGTGAAAAACATGAAGGCAATAAGATCATTGCTTTTGAAAGAGCA 1947
Qy   2518 AACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGC 2577
Db   1948 GGTCTTCTTTTCATTTCAACTTCCATCCAAGCAAGAGCTACACTGACTACCGAGTTGGA 2007
Qy   2578 TGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGC 2637
Db   2008 ACAGCATTGCCAGGGAAATTCAAAATTGTGCTAGATTCAGATGCAGCGGAATATGGAGGG 2067
Qy   2638 TTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGT 2697
Db   2068 CATCAGAGACTGGACCACAGCACTGACTTTTTTTCTGAGGCTTTGAACATAATGGGCGT 2127
Qy   2698 CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTC 2742
Db   2128 CCCTATTCTCTTTTGGTGTACATTCCAAGCAGAGTGGCCCTCATC 2172
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RESULT 10
US-09-770-149-955/c
; Sequence 955, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.

```
; APPLICANT:  Allen, Keith
; APPLICANT:  Hoffman, Neil
; APPLICANT:  Hurban, Patrick
; TITLE OF INVENTION:  Expressed Sequences of Arabidopsis
; TITLE OF INVENTION:  thaliana
; FILE REFERENCE:  2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE:  2001-01-26
; PRIOR APPLICATION NUMBER:  60/178,506
; PRIOR FILING DATE:  2000-01-27
; NUMBER OF SEQ ID NOS:  999
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 602
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-770-149-955

  Query Match             8.2%;  Score 257.8;  DB 10;  Length 602;
  Best Local Similarity  75.1%;  Pred. No. 2.5e-62;
  Matches  322;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy       2334 CAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCG 2393
Db        602 CAGTTATGACAAATGCCGCCGCAGATTTGATCTTGGGGATGCAGATTATCTCAGATACCG 543

Qy       2394 TGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGAC 2453
Db        542 CGGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGAC 483

Qy       2454 TTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAA 2513
Db        482 TTCGGAGCACCAATTCATATCACGAAAAGACGAAGCAGATAGAGTAATCGTATTCGAAAG 423

Qy       2514 AGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCAT 2573
Db        422 AGGTGATCTCGTCTTTGTCTTTAACTTTCACTGGACCAGCAGCTACTTTGATTACCGCAT 363

Qy       2574 AGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGG 2633
Db        362 TGGTTGCTCCAAGCCTGGAAAATATAAGATCGTATTGGACTCGGACGATCCTCTCTTTGG 303

Qy       2634 TGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGA 2693
Db        302 TGGATTCAATAGGCTCGATCGCAAGGCAGAGTACTTCACTTATGATGGCTTATACGACGA 243

Qy       2694 TCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
Db        242 ACGACCCTGCTCCTTCATGGTCTATGCACCGTGTAGAACCGCCGTGGTTTATGCTTTAGC 183

Qy       2754 AGACAAAGA 2762
Db        182 AAACCACGA 174

RESULT 11
US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
;   LENGTH: 604
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (12)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (517)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (540)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (567)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (593)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-453

  Query Match             4.4%;  Score 139.6;  DB 10;  Length 604;
  Best Local Similarity  62.4%;  Pred. No. 8e-29;
  Matches  217;  Conservative    1;  Mismatches  130;  Indels    0;  Gaps    0;

Qy       1170 AGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATA 1229
Db        125 AGAACACTCATATGAGTTTAAGCATTCCAGACCAAAGAAGCCACGGAGTCTAAGAATTTA 184

Qy       1230 TGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAG 1289
Db        185 TGAATCTCATGTGGGAATTTCTTCCCATGAAGGAAAAGTAGCTTCTTATAAACATTTTAC 244

Qy       1290 AGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1349
Db        245 ATGCAATGTACTACCAAGAATCAAAGGCCTTGGATACAACTGCATTCAGTTGATGGCAAT 304

Qy       1350 TCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAG 1409
Db        305 CATGGAGCATGCTTACTATGCCAGCTTTGGTTACCAAATCACAAGCTTCTTTGCAGCTTC 364

Qy       1410 CAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGG 1469
Db        365 CAGCCGTTATGGAACACCTGAAGAGCTACAAGAACTGGTAGACACAGCTCATTYCATGGG 424

Qy       1470 AATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATAC 1517
Db        425 TATCATAGTCCTCTTAGATGTGGTACAAGCSCATGCTTCAAAAAATTC 472

RESULT 12
US-09-770-444-893
; Sequence 893, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
;  APPLICANT: Gorlach, Jorn
;  .APPLICANT:  An, Yong-Qiang
;  APPLICANT:  Hamilton, Carol M.
;  APPLICANT:  Price, Jennifer L.
;  APPLICANT:  Raines, Tracy M.
;  APPLICANT:  Yu, Yang
;  APPLICANT:  Rameaka, Joshua G.
;  APPLICANT:  Page, Amy
;  APPLICANT:  Matthew, Abraham V.
;  APPLICANT:  Ledford, Brooke L.
;  APPLICANT:  Woessner, Jeffrey P.
;  APPLICANT:  Haas, William David
;  APPLICANT:  Garcia, Carlos A.
;  APPLICANT:  Kricker, Maja
;  APPLICANT:  Slader, Ted
;  APPLICANT:  Davis, Keith R.
;  APPLICANT:  Allen, Keith
;  APPLICANT:  Hoffman, Neil
```

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;  APPLICANT:  Hurban, Patrick
;  TITLE OF INVENTION: Expressed Sequences of Arabidopsis
;  TITLE OF INVENTION:  thaliana
;  FILE REFERENCE: 2027 (PARA-016PRV)
;  CURRENT APPLICATION NUMBER: US/09/770,444
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 60/178,502
;  PRIOR FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 999
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 893
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-770-444-893

  Query Match              3.6%;  Score 114.6;  DB 10;  Length 441;
  Best Local Similarity   67.2%;  Pred. No. 7.8e-22;
  Matches  162;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;

Qy       2535 TAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAA 2594
Db          1 TAACTTCCACTGGACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCCCGGAAA 60

Qy       2595 ATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCA 2654
Db         61 GTACAAAATCGTTTTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGA 120

Qy       2655 TAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGT 2714
Db        121 CTCCGCGGAGTTTTTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGT 180

Qy       2715 GTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGA 2774
Db        181 GTATGCACCGTGCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGATGA 240

Qy       2775 A 2775
Db        241 A 241

RESULT 13
US-10-025-380-304/c
; Sequence 304, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Smith, Carole L.
;  APPLICANT:  King, Gordon E.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Clapper, Jonathan D.
;  APPLICANT:  Skeiky, Yasir A. W.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick Thomas S.
;  APPLICANT:  Carter, Darrick
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF COLON CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.471C14
;  CURRENT APPLICATION NUMBER: US/10/025,380
;  CURRENT FILING DATE:  2001-12-19
;  NUMBER OF SEQ ID NOS: 1129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-025-380-304

  Query Match              3.4%;  Score 108;  DB 9;  Length 601;
  Best Local Similarity   52.5%;  Pred. No. 7.2e-20;
  Matches  312;  Conservative    0;  Mismatches  270;  Indels   12;  Gaps    3;

Qy        727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db        590 GAGATCGACCGGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 531

Qy        787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846
Db        530 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 471

Qy        847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 903
Db        470 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAATGGGCC 411

Qy        904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db        410 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 351

Qy        964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
Db        350 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 291

Qy       1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTG-- 1081
Db        290 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 231

Qy       1082 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
Db        230 ATCTTGTATCGTATTTCACCGTGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 171

Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
Db        170 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCGGA 117

Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
Db        116 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 57

Qy       1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db         56 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAA 3

RESULT 14
US-09-922-217-304/c
; Sequence 304, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Smith, Carole Lynn
;  APPLICANT:  King, Gordon E.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Clapper, Jonathan D.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF COLON CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.471C13
;  CURRENT APPLICATION NUMBER: US/09/922,217
;  CURRENT FILING DATE:  2001-08-03
;  NUMBER OF SEQ ID NOS: 1124
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304
;   LENGTH: 601
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-922-217-304

  Query Match              3.4%;  Score 108;  DB 10;  Length 601;
  Best Local Similarity   52.5%;  Pred. No. 7.2e-20;
  Matches  312;  Conservative    0;  Mismatches  270;  Indels   12;  Gaps    3;

Qy        727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db        590 GAGATCGACCGGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 531

Qy        787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846
Db        530 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 471

Qy        847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 903
Db        470 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAATGGGCC 411

Qy        904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db        410 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 351

Qy        964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
Db        350 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 291

Qy       1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTG-- 1081
Db        290 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 231

Qy       1082 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
Db        230 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 171

Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
Db        170 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCGGA 117

Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
Db        116 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 57

Qy       1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db         56 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAA 3

RESULT 15
US-09-833-263-304/c
; Sequence 304, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Aijun
;  APPLICANT:  Clapper, Jonathan D.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Meagher, Madeleine J.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.471C12
;  CURRENT APPLICATION NUMBER: US/09/833,263
;  CURRENT FILING DATE:  2001-04-10
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 304
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-833-263-304

  Query Match              3.4%;  Score 108;  DB 10;  Length 601;
  Best Local Similarity   52.5%;  Pred. No. 7.2e-20;
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  Matches  312;  Conservative    0;  Mismatches  270;  Indels   12;  Gaps    3;

Qy        727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db        590 GAGATCGACCGGTACTTGAAGCCCTACGCCGTGGACTTCCAGCGCAGGTATAAGCAGTTT 531

Qy        787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846
Db        530 AGCCAAATTTTGAAGAACATTGGAGAAAATGAAGGTGGTATTGATAAGTTTTCCAGAGGC 471

Qy        847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 903
Db        470 TATGAATCATTTGGCGTCCACAGATGTGCTGATGGTGGTTTATACTGCAAAGAATGGGCC 411

Qy        904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
Db        410 CCGGGAGCAGAAGGAGTTTTCTTACTGGAGATTTTAATGGTTGGAATCCATTTTCGTAC 351

Qy        964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
Db        350 CCATACAAAAAACTGGATTATGGAAAATGGGAGCTGTATATCCCACCAAAGCAGAATAAA 291

Qy       1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTG-- 1081
Db        290 TCTGTACTCGTGCCTCATGGATCCAAATTAAAGGTAGTTATTACTAGTAAAAGCGGAGAG 231

Qy       1082 -TTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCA 1140
Db        230 ATCTTGTATCGTATTTCACCGTGGGCAAAGTATGTGGTTCGTGAAGGTGATAATGTGAAT 171

Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200
Db        170 TATGATTGGATACACTGGGATCC------AGAACACTCATATGAGTTTAAGCATTCCGGA 117

Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260
Db        116 CCAAAGAAGCCACGGAGTCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 57

Qy       1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db         56 GGAAAAGTAGCTTCTTATAAACATTTTACATGCAATGTACTACCAAGAATCAAA 3

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          Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         July  5, 2003, 13:27:32 ; Search time 4280.35 Seconds
                                          (without alignments)
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Scoring table:  IDENTITY_NUC
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Searched:       16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 4:  em_estmu:*
                 5:  em_estov:*
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                 7:  em_estro:*
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                 10:  gb_est2:*
                 11:  gb_htc:*
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                 17:  gb_gss:*
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                 20:  em_gss_pln:*
                 21:  em_gss_vrt:*
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                 23:  em_gss_mam:*
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                 26:  em_gss_pro:*
                 27:  em_gss_rod:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result              Query
  No.     Score     Match  Length DB  ID                   Description
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    6     488.6      15.5     728 14  BU008463             BU008463 QGH7K17.y
    7     479.4      15.2     713 14  BQ986883             BQ986883 QGF10L08.
    8       441      14.0     689 13  BI308555             BI308555 EST529965
    9       436      13.8     801 10  BE195628             BE195628 HVSMEh008
   10     430.6      13.6     678 10  AV939010             AV939010 AV939010
   11       417      13.2     731 10  BE602527             BE602527 HVSMEh009
   12     413.8      13.1     573 13  BM526229             BM526229 sal38f02.
   13     411.8      13.0     717 14  BU005876             BU005876 QGG9F08.y
   14     402.4      12.8     603 10  AW930851             AW930851 EST356694
   15       398      12.6     825 12  BF065047             BF065047 HV_CEb002
   16     391.6      12.4     695 14  BQ240494             BQ240494 TaE05016F
   17       387      12.3     621 12  BG521671             BG521671 13-3 Stev
   18       384      12.2     650 10  BE427534             BE427534 PSR7153 I
   19       383      12.1     646  9  AU238577             AU238577 AU238577
   20     381.4      12.1     639 10  AW065909             AW065909 687002G09
   21       381      12.1     651 12  BG526727             BG526727 63-11 Ste
   22     378.6      12.0     571 13  BI699680             BI699680 sai25g09.
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   24     373.6      11.8     576 10  AW244197             AW244197 687050F06
   25     372.6      11.8     571 13  BI469105             BI469105 sai07e09.
   26     372.6      11.8     575 13  BI425610             BI425610 sah69a11.
   27     371.4      11.8     560 14  BM885252             BM885252 sal97a08.
   28     366.8      11.6     589 10  AW596011             AW596011 si96g03.y
   29     363.4      11.5     582 13  BM309136             BM309136 sak55b02.
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   34     345.6      11.0     704 14  BU008407             BU008407 QGH7I04.y
   35     344.8      10.9     516 14  BQ253050             BQ253050 sao05e05.
   36     341.2      10.8     761 13  BM411030             BM411030 EST585357
   37     340.4      10.8     592 10  BE402623             BE402623 CSB009H05
   38     340.4      10.8     592 14  BQ608128             BQ608128 BRY_4030
   39     337.6      10.7     568 14  BQ240653             BQ240653 TaE05014F
   40     337.2      10.7     569 13  BJ233506             BJ233506 BJ233506
   41     334.2      10.6     509 12  BG651974             BG651974 sad72d10.
   42     327.8      10.4     573  9  AJ432886             AJ432886 AJ432886
   43     313.6       9.9     898 14  BQ716536             BQ716536 AGENCOURT
   44     312.4       9.9     615 14  BQ606935             BQ606935 BRY_2812
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                              ALIGNMENTS

RESULT 1
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LOCUS       AY109521                2766 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays CL1245_1 mRNA sequence.
ACCESSION   AY109521
VERSION     AY109521.1  GI:21213273
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 2766)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 2766)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
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                  Library"
                  /note="this sequence is part of a project of EST
                  assemblies resulting from the application of public
                  contigs to seed DuPont contigs; this resource was
                  assembled by DuPont as part of a collaboration for the
                  overgo addressing of BACs in conjunction with the Maize
                  Mapping Project"
BASE COUNT     715 a    546 c    689 g    718 t     98 others
ORIGIN

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  Best Local Similarity  71.1%;  Pred. No. 3.2e-294;
  Matches 1488;  Conservative    1;  Mismatches  604;  Indels    0;  Gaps    0;

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Db        363 GAGTTATCCCACCACCAGGAGATGGCCAACGAATATATGAGATTGACCCAATGTTGGAAG 422

Qy        749 ACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTG 808
Db        423 GGTTTCGGGGTCACCTTGACTACCGATACAGTGAATATAAGAGATTACGTGCGGCTATTG 482

Qy        809 ACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTC 868
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Qy        869 GTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCA 928
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Qy        929 TTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTG 988
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Qy       1169 AAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATAT 1228
Db        843 AAGAGGAGAAATATGTATTCAAACACCCTCAACCTAAGCGGCCCAAGTCACTGCGGATAT 902

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Db        903 ATGAATCACATGTTGGAATGAGTAGCCCGGAACCAAAGATAAATACATATGCTAACTTCA 962

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Qy       1469 GAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGAC 1528
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Qy       1649 CAAATGCGAGATGGTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGA 1708
Db       1323 CAAATGCGAGATGGTGGCTTGAAGAATATAAATTTGATGGGTTTCGATTTGATGGGGTGA 1382

Qy       1709 CATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAAT 1768
Db       1383 CCTCCATGATGTATACTCACCATGGATTACAAGTGACATTCACTGGGAACTATGGCGAGT 1442

Qy       1769 ACTTTGGACTCGCAACTGATGTGRATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTA 1828
Db       1443 ATTTGGATTTGCCACTGATGTTGATGCAGTAGTTTACCTAATGCTGGTAAACGATCTTA 1502

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Db       1503 TTCGTGGGCTTTATCCAGAAGCTGTATCCATTGGCGAAGATGTCAGCGGAATGCCNNNNN 1562

Qy       1889 TTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTG 1948
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Qy       2009 TTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATG 2068
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Qy       2069 ATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATG 2128
Db       1743 ATCAAGCTCTTGTTGGTGACAAGACAATTGCATTCTGGTTGATGGATAAGGATATGTATG 1802

Qy       2129 ATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACA 2188
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Qy       2189 AGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAA 2248
Db       1863 AAATGATTAGGCTTGTCACAATGGGTTTAGGAGGTGAAGGCTATCTAAATTTCATGGGAA 1922

Qy       2249 ATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATG 2308
Db       1923 ATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGAGGTCCTCAAAGTCTTCCAAATG 1982

Qy       2309 GCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGG 2368
Db       1983 GCTCCGTCATTCCTGGGAATAACAATAGCTTTGATAAATGCCGCCGTAGATTTGACCTTG 2042

Qy       2369 GAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATC 2428
Db       2043 GAGATGCAGATTATCTTAGATATCGTGGTATGCAAGAGTTTGACCAGGCAATGCAGCACC 2102

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Qy       2549 CAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCT 2608
Db       2223 GCAATAGCTATTTTGACTATCGCGTTGGTTGTTTCAAGCCTGGGAAGTACAAGATCGTTT 2282

Qy       2609 TGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTT 2668
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Qy       2729 GAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGAAGTA 2781
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LOCUS       AY109532                2732 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays CL1742_1 mRNA sequence.
ACCESSION   AY109532
VERSION     AY109532.1  GI:21213287
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 2732)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 2732)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
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                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      659 a    506 c    679 g    710 t    178 others
ORIGIN

  Query Match             36.2%;  Score 1142.6;  DB 11;  Length 2732;
  Best Local Similarity   69.9%;  Pred. No. 2.8e-283;
  Matches 1463;  Conservative    2;  Mismatches  629;  Indels    0;  Gaps    0;

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Db        403 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTNNNNNNACCAAGCGATGGACNNNNNNT 462

Qy        723 TTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACA 782
Db        463 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCCT 522

Qy        783 GTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCG 842
Db        523 CTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAGCCTTCTCCCG 582

Qy        843 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGC 902
Db        583 TAGTTATGAGAAGTTTGGATTTAATCGCAGCGCGGAAGGTATCACATATCGAGAATGGGC 642

Qy        903 TCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGA 962
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Db        763 TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCATCAGGGAT 822

Qy       1083 TAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATA 1142
Db        823 AAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATA 882

Qy       1143 TAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCC 1202
Db        883 TGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATGCGCAACC 942

Qy       1203 AAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
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Qy       1263 TAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGG 1322
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Qy       1383 TCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTC 1442
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Qy       1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTT 1922
Db       1603 TGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCACGATGGTGGGGTAGGTTT 1662

Qy       1923 TGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGA 1982
Db       1663 TGACTATCGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAAGTGA 1722

Qy       1983 TGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAA 2042
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Qy   2103 CTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATT 2162
Db   1843 TTGGTTGATGGACAAGGATATGTATGATTTCATGGCCCTCGATAGACCTTCAACTCCTAC 1902

Qy   2163 AATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG 2222
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Qy   2223 AGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCC 2282
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Qy   2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGA 2342
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Qy   2343 TAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCA 2402
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Qy   2403 AGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACA 2462
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Qy   2583 GAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGG 2642
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Qy   2643 GAGAATTGATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCG 2702
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Qy   2703 TTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGA 2756
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RESULT 3
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LOCUS       AY105679             3012 bp    mRNA    linear   HTC 25-MAY-2002
DEFINITION  Zea mays PCO072723 mRNA sequence.
ACCESSION   AY105679
VERSION     AY105679.1  GI:21208757
KEYWORDS    HTC.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 3012)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 3012)
  AUTHORS   Coe,E.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
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                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      837 a    628 c    790 g    756 t      1 others
ORIGIN

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Qy    781 CAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCT 840
Db    467 AGATTCCTAGAGCAGAAAGGATCAATTGAAGAAAATGAGGGAAGTCTTGAATCTTTTTCT 526

Qy    841 CGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGG 900
Db    527 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 586

Qy    901 GCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCT 960
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Qy    961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGAT 1020
Db    647 CATAAGATGGAGAAGGATAAATTTGGTGTTTGGTCGATCAAAAT---TGACCATGTCAAA 703

Qy   1021 GGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGT 1080
Db    704 GGGAAACCTGCCATCCCTCACAATTCCAAGGTTAAATTTCGCTTTCTACATGGTGGAGTA 763

Qy   1081 GTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAAT---- 1136
Db    764 TGGGTTGATCGTATTCCAGCATTGATTCGTTATGCGACTGTTGATGCCTCTAAATTTGGA 823

Qy   1137 --TCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db    824 GCTCCCTATGATGGTGTTCATTGGATCCTCCTGCTTCTGAAAGGTACACATTTAAGCAT 883

Qy   1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db    884 CCTCGGCCTTCAAAGCCTGCTGCTCCACGTATCTATGAAGCCCATGTAGGTATGAGTGGT 943

Qy   1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db    944 GAAAAGCCAGCAGTAAGCACATATAGGGAATTTGCAGACAATGTGTTGCCACGCATACGA 1003

Qy   1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
Db   1004 GCAAATAACTACAACACAGTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 1063

Qy   1375 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1434
Db   1064 TTCGGGTACCATGTGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACACCAGAGGAC 1123

Qy   1435 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1494
Db   1124 CTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTGCGAGTTCTGATGGATGTTGTC 1183

Qy   1495 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACG---------GC 1545
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Db   1244 ACCCAAGAGTCCTATTTTCATGCGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1303

Qy   1606 CTCTTT-AACTATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTG 1664

Db   1304 CTGTTTCAACTATGCTAACTGGGAGGTATTAACGTTTCTTCTTTCTAACCTGAGATATTG 1363

Qy   1665 GTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATAC 1724

Db   1364 GTTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCA 1423

Qy   1725 TCACCACGGATTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAAC 1784

Db   1424 TCACCATGGTATCAATGTGGGGCTTACTGGAAACTACCAGGAATATTTCAGTTTGGACAC 1483

Qy   1785 TGATGTRGATGCTGCCGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCC 1844

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Db   1604 TGAAGGTGGGGTTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGA 1663

Qy   1965 GTTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTGTTCATACACTGAC 2021

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Db   1724 TAACAGGAGATATACTGAAAAATGCATCGCATATGCTGAGAGCCATGATCAGTCTATTGT 1783

Qy   2082 CGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTT 2141

Db   1784 TGGCGACAAAACTATTGCATTTCTCCTGATGGACAAGGAAATGTACACTGGCATGTCAGA 1843

Qy   2142 GGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCT 2201

Db   1844 CTTGCAGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTT 1903

Qy   2202 TGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCA 2261

Db   1904 CATCACAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCA 1963

Qy   2262 CCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCC 2321

Db   1964 CCCAGAATGGATTGACTTTCCAAGAGAA-------------------------------- 1991

Qy   2322 CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATA 2381

Db   1992 -GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCA 2050

Qy   2382 TTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATA 2441

Db   2051 CTTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATT 2110

Qy   2442 TGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGAT 2501

Db   2111 TTCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAAGGTTAT 2170

Qy   2502 TGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTC 2561

Db   2171 TGTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACTTACGA 2230

Qy   2562 AGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGA 2621

Db   2231 GGGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGC 2290

Qy   2622 TCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCT 2674

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RESULT 4
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LOCUS       AK009815                2738 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
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            ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME) (BRANCHER ENZYME),
            full insert sequence.
ACCESSION   AK009815
VERSION     AK009815.1  GI:12844841
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2310045H19.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
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            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
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PUBMED      11217851
REFERENCE   5  (bases 1 to 2738)
AUTHORS     Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0 and subtraction to
            Rot = 25.0. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
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                     FNLTDDDLLRYKFLNNFDRDMNRLEERCGWLSAPQAYVSEKHEANKTITFERAGLLFI
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     polyA_signal    2714..2719
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BASE COUNT      780 a    562 c    624 g    772 t
ORIGIN

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  Best Local Similarity   57.0%;  Pred. No. 1.1e-136;
  Matches 1172;  Conservative    2;  Mismatches  835;  Indels   48;  Gaps    5;

Qy        727 GAAATAGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786

Db        117 GAGATTGACCCGTACCTGAAGCCCTTCGCCGCGGACTTCCAGCGCAGGTATAAGAAGTTT 176

Qy        787 AAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGT 846

Db        177 AGCCAGGTTTTGCATGACATTGGAGAGAATGAAGGTGGGATCGATAAGTTCTCCAGAGGC 236

Qy        847 TATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGT---GAGTGGGCT 903

Db        237 TATGAGTCATTTGGCATCCACAGATGTTCTGATGGTGGCATCTACTGCAAAGAATGGGCC 296

Qy        904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963

Db        297 CCAGGAGCAGAAGGAGTTTTTCTTACTGGAGAATTCAGTGGTTGGAATCCATTTTCTCAC 356

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Qy       1141 TATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGG 1200

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Qy       1201 CCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAG 1260

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Qy       1261 CCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTT 1320

Db        651 GGAAAAATAGCTTCTTACAAACATTTTACCAGCAATGTACTACCAAGAATCAAAGACCTT 710

Qy       1321 GGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGT 1380

Db        711 GGGTATAACTGCATTCAGTTGATGGCGATCATGGAACATGCTTACTATGCCAGTTTTGGG 770

Qy       1381 TATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAG 1440

Db        771 TACCAAATCACGAGCTTTTTTGCAGCTTCAAGTCGTTATGGAACTCCTGAAGAGCTGAAA 830

Qy       1441 TCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGC 1500

Db        831 GAACTTGTTGACACAGCACATTCGATGGGCATTGTAGTCCTCCTAGATGTGGTTCATAGC 890

Qy       1501 CATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTAC 1560

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Qy       1561 TTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGA 1620

Db        951 TTTCACTCTGGACCCCGAGGGACCCATGATCTTTGGGACAGTAGATTATTTATCTATTCC 1010

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Qy       2218 GGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGAT 2277
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RESULT 5
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ACCESSION   AI487345
VERSION     AI487345.1  GI:4382716
KEYWORDS    EST.
SOURCE      tomato.
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE   1  (bases 1 to 656)
  AUTHORS   Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
            , Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
            ,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
            ,S.D. and Giovannoni,J.
  TITLE     Generation of ESTs from tomato carpel tissue
  JOURNAL   Unpublished (1999)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES             Location/Qualifiers
     source          1..656
                     /organism="Lycopersicon esculentum"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="cLED13M4"
                     /clone_lib="tomato ovary, TAMU"
                     /tissue_type="carpel"
                     /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
                     /lab_host="XL1-Blue MRF'"
                     /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
                     XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
                     directionally cloned cDNA in vector Lamda ZAP II with 5'
                     and 3' ends located at the EcoRI and XhoI sites,
                     respectively."
BASE COUNT      207 a    106 c    149 g    194 t
ORIGIN

  Query Match             15.8%;  Score 499.6;  DB 9;  Length 656;
  Best Local Similarity   90.7%;  Pred. No. 1.2e-117;
  Matches  584;  Conservative    0;  Mismatches   39;  Indels   21;  Gaps    4;

Qy       2428 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2487
Db          1 CTTGAAGATAAATATGAGTTTATGACTTCAGAACATCAGTTCATATCACGAAAGGATGAA 60

Qy       2488 GGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 2547
Db         61 GGAGATAGGATGATTGTATTTGAAAGAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGG 120

Qy       2548 ACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCC 2607
Db        121 ACAAATAGCTATTCAGACTATCGCATAGGCTGCCTAAAACCTGGAAAATACAAGGTTGTC 180

Qy       2608 TTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGT 2667
Db        181 TTGGACTCAGATGATCCACCTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATAT 240

Qy       2668 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 2727
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Db          241 TTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGT 300

Qy         2728 AGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGAAGTAGCAGTA 2787
                |||||||||| ||||||||||||||||||||||||||||||||||| || ||  |||| || |
Db          301 AGAACAGCAGTTGTCTATGCACTAGTAGACAAAGAAGAAGAAGTAGTAGTCGTAGAAGAA 360

Qy         2788 GTAGAAGAAGTAGTAGTAGAA------GAAGAATGAACGAACTTGTGATCGCGTTGAAAG 2841
                |||| || || || || ||||      ||||||||||||||||||||| ||||| |||
Db          361 GTAGTAGTAGAAGAAGAAGAACACGTTGAAGAATGAACGAACTTGTGATCTCGTTGGAAG 420

Qy         2842 ATTTGAACGCT-----------ACATAGAGCTTCTTGACGT--ATCTGGCAATATTGCA 2887
                ||||||||||            |||||||||||||||||       |  |||||||||
Db          421 ATTTGAACGCTACTTGGTCATCGACATAGAGCTTCTTGACGTTATCTGGCAAATATTGCA 480

Qy         2888 TCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTCTTTCCACTATTAGTAGTG 2947
                 |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Db          481 CCAGTCTTGGCGGAATTTCACGTGACAAAAGGTTTGCAGTTCTTTCCACTATTAGTAGTC 540

Qy         2948 CAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTAA-AATCGATGAATTTATG 3006
                |||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db          541 CAACGACATACGCAGAGATGAAGTGCTGAACAAACATATGTAACAATCGATGAATTTATG 600

Qy         3007 TCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGTTC 3050
                ||||||  | ||||| |||||||||||||||||||| |||||||
Db          601 TCGAATCATAGGACGTGCTTCAGCAGGTTTTGCTTAATGAGTTC 644


RESULT 6
BU008463
LOCUS       BU008463                 728 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGH7K17.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGH7K17, mRNA sequence.
ACCESSION   BU008463
VERSION     BU008463.1  GI:22442858
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGH7  row: K  column: 17.
FEATURES             Location/Qualifiers
     source          1..728
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGH7K17"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=leaves dark grow
                     TAG_SEQ=GCTAGTCGGG"
BASE COUNT      227 a    133 c    149 g    218 t      1 others
ORIGIN

  Query Match             15.5%;  Score 488.6;  DB 14;  Length 728;
  Best Local Similarity   79.4%;  Pred. No. 8.5e-115;
  Matches  578;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy          844 GGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCT 903
                ||||||||||||| | |||||||||| ||      |||||||||||||  | || |||||
Db            1 GGTTATGAAAAATTAGGTTTCACTCGAAGCAAAACAGGTATCACTTATAGAGAATGGGCA 60

Qy          904 CCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGAC 963
                ||||| ||  |||| ||| | || | ||||||||||||||| ||| |  ||||||||||
Db           61 CCTGGGGCAAAGTCTGCTTCACTTACTGGAGATTTCAACAACTGGAATCCAAATGCTGAT 120

Qy          964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT 1023
                 ||||||| |||||||||||||||| |||||||| ||| ||||||| ||||| |||| |
Db          121 GTTATGACCCGGAATGAATTTGGTGTGTGGGAGATCTTTTTGCCAAACAATGTTGATGAT 180

Qy         1024 TCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTT 1083
                ||| |   | ||||||||||| ||   ||||  ||||| ||  |||||  ||||| ||  ||
Db          181 TCTTCACCTATTCCTCATGGTTCTCGAGTAAAGATTCGTATGGATACGCCATCTGGCATT 240

Qy         1084 AAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATAT 1143
                || || || ||  |||||||||||||||||  |   ||  ||||     |||| ||| ||||| |||
Db          241 AAAGACTCGATTCCTGCTTGGATCAAGTTTCAGTACAAGCACCTGGTGAGATTCCTTAT 300

Qy         1144 AATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCA 1203
                |||||||||| ||||||||| ||  ||||||| |  || || || |||||  ||| | |||
Db          301 AATGGAATATACTATGATCCCCCACAAGAGGAAAAATACGTGTTTCAACATCCAAGACCA 360

Qy         1204 AAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCT 1263
                ||||| || || || || || || || |||||  | ||| | |||||||||||| |||| ||
Db          361 AAGAAGCCGAAATCTCTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCA 420

Qy         1264 AAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGG 1323
                |  || ||| | || |  || |||||||| || ||||| ||||||||||||||||||| ||
Db          421 ATGATCAACACGTATGCTAACTTTAGAGACGATGTTCTCCCTCGCATAAAAAAACTCGGT 480

Qy         1324 TACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTAT 1383
                ||||||| || ||||| |||||||||||||||||||| |||||||||| ||||| ||
Db          481 TACAATGCAGTTCAAATCATGGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTAC 540

Qy         1384 CATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCT 1443
                ||||| |||||||||||||||||| || ||  | |||||| || || || ||||| ||
Db          541 CATGTGACAAATTTTTTTGCACCAAGTAGTCGATGTGGAACTCCAGATGATCTTAAATCA 600

Qy         1444 TTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCAT 1503
                |||||||||||| |||||  ||||  |||||||||||||||| ||||| || || |||
Db          601 ATGATTGATAAAGCACATGAATTAGGTCTTGTTGTTCTCATGGATATTGTGCATAGTCAT 660

Qy         1504 GCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTT 1563
                ||||||| || || |||||||||| |  | |||||||| || || ||||||     |||||
Db          661 TCATCAAACAACACATTAGATGGATTANATATGTTTGATGGAACTGATAGTCAATACTTT 720

Qy         1564 CACTCTGG 1571
                || |||||
Db          721 CATTCTGG 728


RESULT 7
BQ986883
LOCUS       BQ986883                 713 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  QGF10L08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGF10L08, mRNA sequence.
ACCESSION   BQ986883
VERSION     BQ986883.1  GI:22404408
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KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGF10  row: L  column: 08.
FEATURES             Location/Qualifiers
     source          1..713
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGF10L08"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=flowers post-fertilized
                     TAG_SEQ=TGCCATCGGG"
BASE COUNT      221 a    132 c    146 g    214 t
ORIGIN

  Query Match             15.2%;  Score 479.4;  DB 14;  Length 713;
  Best Local Similarity   79.5%;  Pred. No. 2e-112;
  Matches  567;  Conservative    0;  Mismatches  146;  Indels    0;  Gaps    0;

Qy        859 GGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCA 918
              |||||||||| ||    |||||||||||||   | || ||||| ||||| ||    ||||
Db          1 GGTTTCACTCGAAGCAAAACAGGTATCACTTATAGAGAATGGGCACCTGGGGCAAAGTCT 60

Qy        919 GCTGCTCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAAT 978
              |||  | || ||||||||||||||||| |||  |   |||||||||  ||||||| ||||||
Db         61 GCTTCACTTATTGGAGATTTCAACAACTGGAATCCAAATGCTGATGTTATGACCCGGAAT 120

Qy        979 GAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCT 1038
              |||||||||| |||||||| ||| ||||||| ||||| |||| ||||  |   ||||||
Db        121 GAATTTGGTGTGTGGGAGATCTTTTTGCCAAACAATGTTGATGATTCTTCACCTATTCCT 180

Qy       1039 CATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCT 1098
              ||||| ||   ||||  |||||  || ||||| ||   ||||  ||    |||| || || ||||||
Db        181 CATGGTTCTCGAGTAAAGATTCGTATGGATACGCCATCTGGCATTAAAGACTCGATTCCT 240

Qy       1099 GCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAATATATTAT 1158
              |||||||||| |  ||  ||||       |||| ||| ||||| |||||||||||||| |||
Db        241 GCTTGGATCAAGTTTTCAGTACAAGCACCTGGTGAGATTCCTTATAATGGAATATACTAT 300

Qy       1159 GATCCACCCGAAGAGGAGAGGTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCG 1218
              ||||| ||  ||||||| |  || || ||||| ||| | |||||||| || || ||
Db        301 GATCCCCCACAAGAGGAAAAATACGTGTTTCAACATCCAAGACCAAAGAAGCCGAAATCT 360

Qy       1219 CTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATAC 1278
              || || || |||||   | |||  | ||||||||||| |||| ||  |  ||| |  ||
Db        361 CTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCAATGATCAACACGTAT 420

Qy       1279 GTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAA 1338
              |  ||  |||||||| || ||||| |||||||||||||| || || ||||||| || |||
Db        421 GCTAACTTTAGAGACGATGTTCTCCCTCGCATAAAAAAACTCGGTTACAATGCAGTTCAA 480

Qy       1339 ATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTT 1398
              || ||||||||||||||||||| |||||||||||| ||||| || ||||| ||||||||
Db        481 ATCATGGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTACCATGTGACAAATTTT 540

Qy       1399 TTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCT 1458
              ||||||||||  || ||  |  ||||||  || || || ||||| ||    ||||||||||||
Db        541 TTTGCACCAAGTAGTCGATGTGGAACTCCAGATGATCTTAAATCAATGATTGATAAAGCA 600

Qy       1459 CATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAATAATACT 1518
              |||||  ||||  |||||||||||||||| ||||| || ||  ||| |||||||  || ||
Db        601 CATGAATTAGGTCTTGTTGTTCTCATGGATATTGTGCATAGTCATTCATCAAACAACACA 660

Qy       1519 TTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGG 1571
              |||||||| |  || |||||||| || || ||||||     ||||||| |||||
Db        661 TTAGATGGATTAAATATGTTTGATGGAACTGATAGTCAATACTTTCATTCTGG 713


RESULT 8
BI308555
LOCUS       BI308555              689 bp    mRNA    linear   EST 20-JUL-2001
DEFINITION  EST529965 GPOD Medicago truncatula cDNA clone pGPOD-7017 5' end,
            mRNA sequence.
ACCESSION   BI308555
VERSION     BI308555.1  GI:14982882
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
            ,J. and Fraser,C.M.
  TITLE     ESTs from developing reproductive tissues of Medicago truncatula
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Michael A. Grusak
            USDA/ARS Children's Nutrition Research Center
            Baylor College of Medicine
            1100 Bates Street, Houston, TX 77030-2600, USA
            Tel: 713-798-7044
            Fax: 713-798-7078
            Email: mgrusak@bcm.tmc.edu
            B395410e
             TIGR sequence name: MTOAQ93TK
             More information is available at: www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES             Location/Qualifiers
     source          1..689
                     /organism="Medicago truncatula"
                     /cultivar="A17"
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                     /clone="pGPOD-7017"
                     /clone_lib="GPOD"
                     /tissue_type="immature pod walls"
                     /dev_stage="Immature pods, ranging in age from 15 to 30
                     days after pollination"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Immature pods, ranging in age from 15 to 30 days
                     after pollination,  were collected from greenhouse-grown
                     plants.  At harvest, seeds were removed from pods and
                     isolated pod walls were collected and  immediately frozen
```

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               in liquid nitrogen.  Pod walls were pooled for  mRNA
               extraction. cDNA was prepared from polyA+ enriched RNA.
               The cDNA was directionally  ligated into the Unizap XR
               vector from Stratagene and packaged using  Gigapack III
               Gold packaging extracts.  Plasmids containing cDNA inserts
               were excised from the recombinant lambda-Zap phage using
               Ex-assist helper phage and propogated in XLOLR cells."
BASE COUNT      198 a    112 c    165 g    214 t
ORIGIN

  Query Match             14.0%;  Score 441;  DB 13;  Length 689;
  Best Local Similarity   77.5%;  Pred. No. 1.6e-102;
  Matches  534;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy       2078 TAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATGATTTTATGG 2137
Db          1 TGGTTGGTGACAAGACACTAGCATTTTGGTTGATGGACAAGGATATGTATGACTTCATGG 60

Qy       2138 CTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACAAGATGATTA 2197
Db         61 CTTTAGACAGACCATCTACTCCTCTAATCGATCGTGGTATTGCATTACACAAAATGATTA 120

Qy       2198 GGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAAATGAATTCG 2257
Db        121 GGCTTATTACTATGGGCCTTGGTGGTGAAGGGTATTTAAATTTTATGGGGAATGAATTCG 180

Qy       2258 GCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATGGCTCAGTAA 2317
Db        181 GCCATCCTGAGTGGATCGATTTTCCAAGGGGTGATCAACATCTTCCTAATGGCACAGTAG 240

Qy       2318 TTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAG 2377
Db        241 TTCCTGGGAATAACAACAGTTATGATAAATGCAGGCGTAGATTTGACTTGGGTGATGCAG 300

Qy       2378 AATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCTTGAAGATA 2437
Db        301 AATATCTAAGATATCATGGAATGCAAGAATTTGATCGAGCTATGCAGCACCTAGAAGAAA 360

Qy       2438 AATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGA 2497
Db        361 GATATGGTTTCATGATTTCTGAGCACCAATATATTTCAAGGAAAAATGAAGGTGACAGAG 420

Qy       2498 TGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCT 2557
Db        421 TTATAATCTTTGAAAGGGACAACCTGGTCTTTGTATTCAATTTTCACTGGACCAACAGTT 480

Qy       2558 ATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAG 2617
Db        481 ATTCAGATTACAAAGTTGGCTGTTTAAAGCCAGGGAAATATAAGATTGTCTTGGATTCAG 540

Qy       2618 ATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTTTCACCTTTG 2677
Db        541 ATGAGTCCTTGTTTGGTGGCTTCAATAGGCTCAATCATACTGCTGAGTACTTCACTTCGG 600

Qy       2678 AAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAG 2737
Db        601 AAGGATGGTATGATGACCGGCCTCGTTCCTTCCTCGTTTATGCACCTTGTAGAACAGCAG 660

Qy       2738 TGGTCTATGCACTAGTAGACAAAGAAGAA 2766
Db        661 TGGTATATGCTCTTGTAGATGGAGTTGAA 689

RESULT 9
BE195628
LOCUS       BE195628                 801 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0089P20f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0089P20f,
            mRNA sequence.
ACCESSION   BE195628
VERSION     BE195628.2  GI:13188305
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 26, 2000 this sequence version replaced gi:8707823.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 408
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 611.
FEATURES             Location/Qualifiers
     source          1..801
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEh0089P20f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      220 a    146 c    198 g    236 t      1 others
ORIGIN

  Query Match             13.8%;  Score 436;  DB 10;  Length 801;
  Best Local Similarity   76.1%;  Pred. No. 3.2e-101;
  Matches  549;  Conservative    0;  Mismatches  171;  Indels    1;  Gaps    1;

Qy       1828 ATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA 1887
Db          2 ATTCATGGACTTTATCCGGATGCTGTATCCATTGGTGAAGATGTCAGCGGAATGCCTACA 61

Qy       1888 TTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATT 1947
Db         62 TTTTGCATCCCTGTCCCAGATGGTGGTGTTGGTTTTGACTATCGCCTGCATATGGCTGTA 121

Qy       1948 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTGATATT 2007
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Db      122 GCAGATAAATGGATTGAACTCCTCAAGCAAAGTGACGAATCTTGGAAAATGGGCGATATT 181

Qy     2008 GTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 2067

Db      182 GTGCACACCCTAACAAATAGAAGGTGGCTTGAGAAGTGTGTCACTTATGCAGAAAGTCAT 241

Qy     2068 GATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTAT 2127

Db      242 GATCAAGCACTAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTAT 301

Qy     2128 GATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCAC 2187

Db      302 GATTTCATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACAT 361

Qy     2188 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGA 2247

Db      362 AAAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTAATTTCATGGGA 421

Qy     2248 AATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2307

Db      422 AATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGGGGTCCGCANACTCTTCCAACC 481

Qy     2308 GGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2367

Db      482 GGCAAAGTTCTCCCTGGCAATAACAATAGTTATGATAAATGCCGCCGTAAATTTGATCTT 541

Qy     2368 GGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTAT 2427

Db      542 GGAGATGCAGATTTTCTTAGATATCGTGGAATGCAAGAGTTCGATCAGGCAATGCCCCAT 601

Qy     2428 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAA 2487

Db      602 CTTGAGGGAAAAATAGGGTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACTTGAG 661

Qy     2488 GGAGATAGGATGATTGT-ATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTG 2546

Db      662 GAAGATAAGGTGAACATCTTTTGAAAGAGGAAATTTGGTATTTGTTTTCAACTTTCCCTG 721

Qy     2547 G 2547

Db      722 G 722
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RESULT 10
AV939010
LOCUS AV939010 678 bp mRNA linear EST 18-JAN-2002
DEFINITION AV939010 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah20e24 5', mRNA sequence.
ACCESSION AV939010
VERSION AV939010.1 GI:18234807
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 678)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .678
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah20e24"
/clone_lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 193 a 135 c 154 g 194 t 2 others
ORIGIN

Query Match 13.6%; Score 430.6; DB 10; Length 678;
Best Local Similarity 78.3%; Pred. No. 7.6e-100;
Matches 528; Conservative 0; Mismatches 145; Indels 1; Gaps 1;

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Qy      880 GGTATCACTTACCGTG-AGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTT 938

Db        5 GGTATCACTTACCGAGNAATGGGCTCCTGGNGCGCATTCTGCAGCATTAGTAGGTGACTT 64

Qy      939 CAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGAT 998

Db       65 CAACAATTGGAACCCAAATGCAGATACTATGACCAGAGATGATTATGGTGTTTGGGAGAT 124

Qy      999 TTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGAT 1058

Db      125 TTTCCTCCCTAACAATGCTGATGGATCCCCTGCTATTCCTCATGGCTCACGTGTAAAGAT 184

Qy     1059 ACGCATGGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTT 1118

Db      185 ACGGATGGATACTCCATCTGGTGTGAAGGATTCAATTTCTGCTTGGATCAAGTTCTCTGT 244

Qy     1119 ACAGCTTCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAG 1178

Db      245 GCAGGCTCCAGGTGAAATACCATTCAATGGCATATATTATGATCCACCTGAAGAGGAGAA 304

Qy     1179 GTATGTCTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCA 1238

Db      305 GTATGTCTTCCAACATCCTCAACCTAAACGACCAGAGTCACTAAGGATATATGAATCACA 364

Qy     1239 TATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGT 1298

Db      365 CATTGGAATGAGCAGCCCGGAACCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGT 424

Qy     1299 TCTTCCTCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCA 1358

Db      425 GCTGCCAAGAATTAAAAGGCTTGGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCA 484

Qy     1359 TTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTT 1418

Db      485 TTCATACTATGCGAGCTTTGGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTT 544

Qy     1419 TGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGT 1478

Db      545 TGGAACTCCAGAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGT 604

Qy     1479 TCTCATGGACATTGTTCACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTT 1538

Db      605 TCTTATGGATATTGTTCATAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTT 664

Qy     1539 TGACGGCACAGATA 1552

Db      665 CGATGGCACTGATA 678
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RESULT 11
BE602527
LOCUS BE602527 731 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f, mRNA sequence.
ACCESSION BE602527
VERSION BE602527.2 GI:13190371
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare

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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
          ; Triticeae; Hordeum.
REFERENCE 1  (bases 1 to 731)
  AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
          ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
          ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE   Development of a genetically and physically anchored EST resource
          for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL Unpublished (2001)
COMMENT   On Aug 21, 2000 this sequence version replaced gi:9860088.
          Contact: Wing RA
          Clemson University Genomics Institute
          Clemson University
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Total hq bases = 322
          Seq primer: AATTAACCCTCACTAAAGGG
          High quality sequence stop: 680.
FEATURES             Location/Qualifiers
     source          1..731
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEh0099J22f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      194 a    132 c    186 g    216 t      3 others
ORIGIN

  Query Match            13.2%;  Score 417;  DB 10;  Length 731;
  Best Local Similarity  74.0%;  Pred. No. 2.5e-96;
  Matches  537;  Conservative    2;  Mismatches  185;  Indels    2;  Gaps    1;

Qy       1560 CTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGG 1619
              ||||||    ||  |  || ||  ||||  |||||||||||||| ||   | || ||||| ||
Db          7 CTTTCATGGCGGCTCACGGGGCCATCACTGGATGTGGGATTCTCGTGTGTTCAACTACGG 66

Qy       1620 AAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTGCAA 1679
                ||    ||| ||    | |||   ||| || || ||||| |||||| || | || || |  ||
Db         67 GAATAAGGAAGTTATAAGGGTTCTACTTTCCAATGCCAGATGGGGCTTGAGGAATATAA 126

Qy       1680 ATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATACTCACCACGGATTATC 1739
                ||   :||| ||     ||| || ||        || |   ||||||||||| | ||| ||||||
Db        127 GTTCCATGGGTTCCCATTCGACGGGCCCACCTTCATGATGTATACCCCCCATGGATTACA 186

Qy       1740 GGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTRGATGCTGC 1799
                ||      ||        ||| |||| | ||||| |||||    | ||  || ||||:||||| |
Db        187 AGTACCTTT--ACAGGAGCTACCATGAATATTTTGGCTTTGCCACGGATGTAGATGCAGT 244

Qy       1800 CGTGTATCTGATGCTGGCCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATTACCAT 1859
                || ||   |||||||||   || |||||  |||||  | |||  |     || ||  ||    |||| ||
Db        245 TGTTTACTTGATGCTGGTGAATGATCTAATTCACGCGCTNATCCTGAAGCCGTTACTAT 304

Qy       1860 TGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGG 1919
              |||||||||||||| |||||||| ||||||       |||| ||||||| ||| || |||||
Db        305 TGGTGAAGATGTTAGTGGAATGCCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGGTTGG 364

Qy       1920 CTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACG 1979
               ||||||||||    |  ||||||||    ||||  |||||||||||||||   |  |||||     | |
Db        365 TTTTGACTATCGCTTACATATGGCCGTTGCCGATAAATGGATTGAACTTCTCAAAGGAAG 424

Qy       1980 GGATGAGGATTGGAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGA 2039
               ||||| | ||||       ||||| ||||||| || ||||| |||||||||||| |||| |||
Db        425 CGATGAAGGTTGGGAGATGGGTAATATTGTGCACACACTAACAAATAGAAGGTGGTTGGA 484

Qy       2040 AAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGC 2099
              ||||||||||  |  ||  |||||||||||||||||||| || || || || || |||||  ||
Db        485 AAAGTGTGTTACTTATGCTGAAAGTCATGATCAAGCACTTGTTGGAGACAAGACTATTGC 544

Qy       2100 ATTCTGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATC 2159
              |||||| ||||||||||||||||||||||||| |||||| || |    |||| || ||| |
Db        545 ATTCTGGTTGATGGACAAGGATATGTATGATTTCATGGCTCTGAACGGACCTTCGACACC 604

Qy       2160 ATTAATAGATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGG 2219
                     || ||||| || |||||| |||| || |||||||| ||| | || ||||     ||||
Db        605 TAATATTGATCGCGGAATAGCACTGCATAAAATGATTAGACTTATCACAATGGCTNTAGG 664

Qy       2220 AGGAGAAGGGTACCTAAATTTCATGGAAATGAATTCGGCCACCCTGAGTGGATTGATTT 2279
              |||||| || || || || || |||||||||| ||| | || ||||| ||||| ||| |
Db        665 AGGAGAGGGTTATCTTAACTTTATGGGAAATGAGTTCCGGCATCCTGAATGGATAGACTN 724

Qy       2280 CCCTAG 2285
                || ||
Db        725 TCCAAG 730


RESULT 12
BM526229
LOCUS       BM526229               573 bp    mRNA    linear   EST 19-FEB-2002
DEFINITION  sal38f02.y1 Gm-c1059 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1059-4491 5' similar to TR:Q9XIS5 Q9XIS5 BRANCHING ENZYME 1
            PRECURSOR ;, mRNA sequence.
ACCESSION   BM526229
VERSION     BM526229.1  GI:18731047
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
```

```
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact: ccu@resgen.com web site:
            www.resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1059-4491"
                     /clone_lib="Gm-c1059"
                     /tissue_type="Whole seedling, 2 week old, etiolated"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from 2 week old etiolated whole seedlings of PI468916.
                     Complementary DNA was synthesized from mRNA using a primer
                     consisting of a poly(dT) sequence with a XhoI restriction
                     site. EcoRI adapters were ligated to the blunt-ended cDNA
                     fragments followed by XhoI digestion. The cDNA fragments
                     were directionally cloned into the EcoRI- XhoI restriction
                     site of the pBluescript vector. The ligated cDNA fragments
                     were transformed into DH10B host cells (Gibco BRL). This
                     library was  constructed in the laboratory of Dr. Randy
                     Shoemaker at Iowa state university."
BASE COUNT       169 a     110 c     126 g     167 t       1 others
ORIGIN

  Query Match             13.1%;  Score 413.8;  DB 13;  Length 573;
  Best Local Similarity   82.5%;  Pred. No. 1.5e-95;
  Matches  472;  Conservative    1;  Mismatches   99;  Indels    0;  Gaps    0;

Qy       1135 ATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGTCTTCCAACAC 1194
Db          1 ATTCCATACAGCGGAATATACTATGATCCCCCAGAAGAGGAAAAATATGTCTTCAAACAT 60

Qy       1195 CCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGT 1254
Db         61 CCACAGCCAAAGAGACCAAAATCACTTAGAATATATGAGTCACACATCGGAATGAGCAGT 120

Qy       1255 CCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAA 1314
Db        121 CCGGAGCCAAAAATCAATACATATGTCAATTTTAGAGATGATGTACTGCCTCGCATTAAA 180

Qy       1315 AACCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGT 1374
Db        181 AGGCTTGGCTATAATGCTGTCCAGATTATGGCTATCCAAGAACATTCTTATTATGCCAGC 240

Qy       1375 TTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCCGACGAC 1434
Db        241 TTTGGGTACCATGTTACAAATTTCTTTGCACCTAGCAGCCGATTTGGAACTCCAGAGGAA 300

Qy       1435 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTT 1494
Db        301 CTTAAGTCTCTGATAGACAGAGCCCATGAACTGGGTCTGCTTGTTCTGATGGATATTGTA 360

Qy       1495 CACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGT 1554
Db        361 CACAGCCATGCATCAAATAATACATTGGATGGGCTGAACATGTTTGATGGAACTGATGGT 420

Qy       1555 TGTTACTTTCACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAAC 1614
Db        421 CATTACTTCCATCCTGGGTCACGAGGTTATCATTGGATGTGGGATTCTCGCCTTTTTAAC 480

Qy       1615 TATGGAAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAG 1674
Db        481 TATGGAAGCTGGGAAGTTCTAAGGTATCTACTTTCGAATGCACGATGGTGGCTGGATGAA 540

Qy       1675 TGCAAATTTGRTGGATTTAGATTTGATGGTGT 1706
Db        541 TACNAGTTTGATGGATTTCGATTTGATGGTGT 572
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RESULT 13
BU005876
LOCUS       BU005876                 717 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGG9F08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGG9F08, mRNA sequence.
ACCESSION   BU005876
VERSION     BU005876.1  GI:22440271
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGG9  row: F  column: 08.
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
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                     /clone="QGG9F08"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=germinating seeds
                     TAG_SEQ=TCTGTGCGGG"
BASE COUNT       233 a     122 c     155 g     206 t       1 others
ORIGIN

  Query Match             13.0%;  Score 411.8;  DB 14;  Length 717;
  Best Local Similarity   75.1%;  Pred. No. 5.4e-95;
  Matches  526;  Conservative    0;  Mismatches  173;  Indels    1;  Gaps    1;

Qy        645 TTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACC 704
Db         19 TTCTTTATTTGATATTGATAAAGAAAGTGAAGAAATTAGAAAATTATCGATTCCTCCTCC 78

Qy        705 TGGACTTGGTCAGAAGATTTATGAAATAGACCCCCTTTTGACAAACTATCGTCAACACCT 764
Db         79 TGGAAAAGGGGAGAGAATATATGAAATTGATCCACTTTTAAGCAATCATCGTGAACATCT 138

Qy        765 TGATTACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGG 824
Db        139 TGAGTATAGATATTCACATTACAAGAAGATACGTGAAGCAATTGACAAATATGAAGGTGG 198
```

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Qy         825 TTTGGAAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTAT 884
               |||||| || ||||| ||||||||||||||| | ||||||||||| ||      ||||||||
Db         199 TTTGGAGGCGTTTTCACGTGGTTATGAAAAATTAGGTTTCACTCGAAGCAAAACAGGTAT 258

Qy         885 CACTTACCGTGAGTGGGCTCCTGGTGCCCAGTCAGCTGCTCTCATTGGAGATTTCAACAA 944
               ||||||   | || ||||| ||||| ||    |||| |||  | || |||||||||||||||||
Db         259 CACTTATAGAGAATGGGCACCTGGGGCAAAGTCTGCTTCACTTATTGGAGATTTCAACAA 318

Qy         945 TTGGGACGCAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCT 1004
                ||| |  ||||||||||   |||||| ||||||||||||||||||||| |||||||| ||| |
Db         319 CTGGAATCCAAATGCTGATGTTATGACCCGGAATGAATTTGGTGTGTGGGAGATCTTTTT 378

Qy        1005 GCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGCAT 1064
               |||||| ||||| |||| ||||  |   | ||||||||||| ||  |||| |||||| || ||
Db         379 GCCAAACAATGTTGATGATTCTTCACCTATTCCTCATGGTTCTCGAGTAAAGATTCGTAT 438

Qy        1065 GGACACTTCATCAGGTGTTAAGGATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCT 1124
               ||| ||  |||| ||  |||| || || |||||||||||||||| |   ||   ||||
Db         439 GGATACGCCATCTGGCATTAAAGACTCGATTCCTGCTTGGATCAAGTTTTCAGTACAAGC 498

Qy        1125 TCCTGATGAAATTCCATATAATGGAATATATTATGATCCACCCGAAGAGGAGAGGTATGT 1184
                |||| ||| ||||| ||||||||||||||| |||||||| ||   ||||||| |     || ||
Db         499 ACCTGGTGAGATTCCTTATAATGGAATATACTATGATCCCCCACAAGAGGAAAAATACGT 558

Qy        1185 CTTCCAACACCCACGGCCAAAGAAACCAAAGTCGCTGAGAATATATGAATCTCATATTGG 1244
                || ||||| |||  |  |||||||| || |||| || ||   || |||||   | ||| | ||
Db         559 GTTTCAACATCCAAGACCAAAGAAGCCGAAATCTCTTANGATTTATGAGGCACATGTGGG 618

Qy        1245 AATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGAATTTTAGAGATGAAGTTCTTCC 1304
               ||||||||| |||| || |      | || | || |  || |||||||| || ||||| ||
Db         619 AATGAGTAGTACGGAACCAATGGATCACACGTATGCTAACTTTAGAGACGATGTTCTCCC 678

Qy        1305 TCGCATAAAAAACCTTGGGTACAATGCGGTGCAAATTATG 1344
               |||||||| || || || |||||||| || ||||| |||
Db         679 TCGCATAAAGAA-CTCGGTTACAATGCAGTTCAAATCATG 717
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RESULT 14
AW930851
LOCUS   AW930851   603 bp   mRNA   linear   EST 18-MAY-2001
DEFINITION EST356694 tomato fruit mature green, TAMU Lycopersicon esculentum
            cDNA clone cLEF41O9 5', mRNA sequence.
ACCESSION   AW930851
VERSION   AW930851.1 GI:8106252
KEYWORDS   EST.
SOURCE   tomato.
  ORGANISM Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE   1 (bases 1 to 603)
  AUTHORS   Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
            Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.
            , Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
  TITLE   Generation of ESTs from tomato fruit tissue
  JOURNAL   Unpublished (1999)
COMMENT   Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES   Location/Qualifiers
     source   1. .603
                     /organism="Lycopersicon esculentum"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="cLEF41O9"
                     /clone_lib="tomato fruit mature green, TAMU"
                     /tissue_type="fruit pericarp"
                     /dev_stage="mature green (3-5 days pre-ripening)"
                     /lab_host="SOLR"
                     /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
                     XhoI; cLEF - Fruit were tagged at the 1cm stage and
                     harvested 3-5 days prior to ripening. Fruit were cut in
                     half to verify the seeds were indeed 'immature' and the
                     seeds and locules were discarded prior to freezing the
                     pericarp"
BASE COUNT   186 a   105 c   132 g   180 t
ORIGIN

  Query Match   12.8%; Score 402.4; DB 10; Length 603;
  Best Local Similarity   89.5%; Pred. No. 1.4e-92;
  Matches 485; Conservative   0; Mismatches   36; Indels   21; Gaps   4;

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Qy        2530 GTCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCT 2589
               |||||||||||||||||||||||| |||||||||||||||||||||||||| || || |||
Db           1 GTCTTTAATTTTCACTGGACAAATAGCTATTCAGACTATCGCATAGGCTGCCTAAAACCT 60

Qy        2590 GGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAATT 2649
               |||||||||||||| |||||||||||||||||||| |||||||||||||||||||||
Db          61 GGAAAATACAAGGTTGTCTTGGACTCAGATGATCCACCTTTGGTGGCTTCGGGAGAATT 120

Qy        2650 GATCATAATGCCGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATT 2709
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         121 GATCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATT 180

Qy        2710 ATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAA 2769
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         181 ATGGTGTATGCACCTAGTAGAACAGCAGTTGTCTATGCACTAGTAGACAAAGAAGAAGAA 240

Qy        2770 GAA------GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAAC 2823
               | |      | ||||| || |||||||||||||| || |     |  ||||||||||||||
Db         241 GTAGTAGTCGTAGAAGAAGTAGTAGTAGAAGAAGAAGAACACGTTGAAGAATGAACGAAC 300

Qy        2824 TTGTGATCGCGTTGAAAGATTTGAACGCT-----------ACATAGAGCTTCTTGACGT 2871
               ||||||| ||||| |||||||||||||           |||||||||||||||||
Db         301 TTGTGATCTCGTTGGAAGATTTGAACGCTACTTGGTCATCGACATAGAGCTTCTTGACGT 360

Qy        2872 ATCTGGC--AATATTGCATCAGTCTTGGCGGAATTTCATGTGACAAAAGGTTTGCAATTC 2929
                      |  ||||||||| |||||||||||||||||| |||||||||||||||| |||
Db         361 TATCTGGCAAATATTGCACCAGTCTTGGCGGAATTTCACGTGACAAAAGGTTTGCAGTTC 420

Qy        2930 TTTCCACTATTAGTAGTGCAACGATATACGCAGAGATGAAGTGCTGAACAAACATATGTA 2989
               |||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db         421 TTTCCACTATTAGTAGTCCAACGACATACGCAGAGATGAAGTGCTGAACAAACATATGTA 480

Qy        2990 A-AATCGATGAATTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTTGCTTAGTGAGT 3048
               |  ||||||||||||||||||||||   | |||||  ||||||||||||||||||||||||
Db         481 ACAATCGATGAATTTATGTCGAATCATAGGACGTGCTTCAGCAGGTTTTGCTTAGTGAGT 540

Qy        3049 TC 3050
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Db         541 TC 542
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RESULT 15
BF065047
LOCUS   BF065047   825 bp   mRNA   linear   EST 23-OCT-2001
DEFINITION HV_CEb0022L05f Hordeum vulgare seedling green leaf EST library
            HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
            HV_CEb0022L05f, mRNA sequence.
ACCESSION   BF065047
VERSION   BF065047.1 GI:10841686
KEYWORDS   EST.
SOURCE   Hordeum vulgare.
  ORGANISM Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 825)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
            Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
            ,D.W., Fenton,R.D., Oates,R. and Main,D.
  TITLE   Development of a genetically and physically anchored EST resource

```
            for barley genomics: Blumeria infected incompatible (Mla6) seedling
            leaf cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 594
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1..825
                     /organism="Hordeum vulgare"
                     /cultivar="CI16151 (Mla6)"
                     /db_xref="taxon:4513"
                     /clone="HV_CEb0022L05f"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0005 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16151 (Mla6) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate 5874 (AvrMla6
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids (Choi, Close). Phagemids were plated and picked
                     at the Clemson University Genomics Institute (CUGI) (Begum
                     , Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT     220 a    167 c    212 g    226 t
ORIGIN

  Query Match             12.6%;  Score 398;  DB 12;  Length 825;
  Best Local Similarity   72.9%;  Pred. No. 2.1e-91;
  Matches  512;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy       2069 ATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATATGTATG 2128
Db         11 ATTCGGCACGAGTTGGTGACAAGACTATTGCATTCTGGTTGATGGATAAGGATATGTATG 70

Qy       2129 ATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTGCACA 2188
Db         71 ATTTCATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACATA 130

Qy       2189 AGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCATGGGAA 2248
Db        131 AAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTAATTTCATGGGAA 190

Qy       2249 ATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCTCTGATG 2308
Db        191 ATGAGTTTGGGCATCCTGAATGGATAGATTTTCCAAGGGGTCCGCAAACTCTTCCAACCG 250

Qy       2309 GCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGG 2368
Db        251 GCAAAGTTCTCCCTGGCAATAACAATAGTTATGATAAATGCCGCCGTAGATTTGATCTTG 310

Qy       2369 GAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTATC 2428
Db        311 GAGATGCAGATTTTCTTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATC 370

Qy       2429 TTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAG 2488
Db        371 TTGAGGAAAAATATGGGTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACATGAGG 430

Qy       2489 GAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGA 2548
Db        431 AAGATAAGGTGATCATCTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGA 490

Qy       2549 CAAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAAATACAAGGTTGCCT 2608
Db        491 GCAATAGCTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTGGCCT 550

Qy       2609 TGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCGAATGTT 2668
Db        551 TAGACTCTGATGATGCACTCTTTGGTGGATTCAGCAGGCTTGATCATGATGTCGACTACT 610

Qy.      2669 TCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTATGGTGTATGCACCTAGTA 2728
Db        611 TCACAACCGAACATCCGCATGACAACAGGCCACGCTCTTTCTCGGTGTACACTCCGAGCA 670

Qy       2729 GAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAG 2770
Db        671 GAACTGCGGTCGTGTATGCCCTTACAGAGTAAGAACCAGCAG 712

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Job time : 4287.35 secs
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